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(54) Title: BIALLELIC MARKERS (57) Abstract The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.		

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BIALLELIC MARKERS

RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996, the entire teachings of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution, generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; W090/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., W0 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include β -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater

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frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a

5 polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays

10 employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for

15 their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to

20 both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

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SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

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DETAILED DESCRIPTION OF THE INVENTION

DEFINITIONS

- An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.
- Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.
- Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).
- As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,

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and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

II. Analysis of Polymorphisms

A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); *PCR* (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988), transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,

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sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

3. Allele-Specific Primers

5 An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in
10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows
15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of
20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of
25 the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,
30 1988)).

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5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

10 6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

25 III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

:

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A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

$p(\text{ID})$ is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y , the probability of each genotype in a diploid organism is (see WO 95/12607):

- 10 Homozygote: $p(\text{AA}) = x^2$
 Homozygote: $p(\text{BB}) = y^2 = (1-x)^2$
 Single Heterozygote: $p(\text{AB}) = p(\text{BA}) = xy = x(1-x)$
 Both Heterozygotes: $p(\text{AB}+\text{BA}) = 2xy = 2x(1-x)$

The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(\text{ID}) = (x^2)^2 + (2xy)^2 + (y^2)^2.$$

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity $p(\text{ID})$ for a 3-allele system where the alleles have the frequencies in the population of x , y and z , respectively, is equal to the sum of the squares of the genotype frequencies:

25
$$p(\text{ID}) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$$

In a locus of n alleles, the appropriate binomial expansion is used to calculate $p(\text{ID})$ and $p(\text{exc})$.

The cumulative probability of identity ($\text{cum } p(\text{ID})$) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

30
$$\text{cum } p(\text{ID}) = p(\text{ID}_1)p(\text{ID}_2)p(\text{ID}_3) \dots p(\text{ID}_n)$$

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The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5 If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10 B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

- 15 Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20 If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child
- 25 attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- 30 The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3})\dots$$

$$p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

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circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert

5 phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an

10 individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan

15 syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos

20 syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous

25 system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers

30 of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of
5 individuals who have been tested for the presence or
absence of a phenotypic trait of interest and for
polymorphic markers sets. To perform such analysis, the
presence or absence of a set of polymorphisms (i.e. a
polymorphic set) is determined for a set of the
10 individuals, some of whom exhibit a particular trait, and
some of which exhibit lack of the trait. The alleles of
each polymorphism of the set are then reviewed to determine
whether the presence or absence of a particular allele is
associated with the trait of interest. Correlation can be
15 performed by standard statistical methods such as a κ -
squared test and statistically significant correlations
between polymorphic form(s) and phenotypic characteristics
are noted. For example, it might be found that the
presence of allele A1 at polymorphism A correlates with
20 heart disease. As a further example, it might be found
that the combined presence of allele A1 at polymorphism A
and allele B1 at polymorphism B correlates with increased
milk production of a farm animal.

Such correlations can be exploited in several ways. In
25 the case of a strong correlation between a set of one or
more polymorphic forms and a disease for which treatment is
available, detection of the polymorphic form set in a human
or animal patient may justify immediate administration of
treatment, or at least the institution of regular
30 monitoring of the patient. Detection of a polymorphic form
correlated with serious disease in a couple contemplating a
family may also be valuable to the couple in their
reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where Y_{ijkpn} is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record; μ is an overall mean; YS_i is the effect common to all cows calving in year $_i$ season; X_k is the effect common to cows in either the high or average selection line; β_1 to β_{17} are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms; PE_n is permanent environmental effect common to all records of cow n ; a_n is effect of animal n and is composed of the additive genetic contribution of sire and dam breeding values and a
5 Mendelian sampling effect; and e_p is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next
10 generation of the herd.

D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present
15 section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such
20 analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84,
25 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6
30 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

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for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-

5 segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the

10 odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction θ , versus the situation in which the two are not linked, and thus segregating independently (Thompson &

15 Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (θ),

20 ranging from $\theta = 0.0$ (coincident loci) to $\theta = 0.50$ (unlinked). Thus, the likelihood at a given value of θ is: probability of data if loci linked at θ to probability of data if loci unlinked. The computed likelihoods are usually expressed as the \log_{10} of this ratio (i.e., a lod

25 score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod

30 scores for differing values of θ (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

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Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of θ at which the lod score is the highest is considered to be the best estimate
5 of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of θ) than the possibility that the two loci are unlinked. By convention, a combined lod
10 score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared.
15 Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

IV. Modified Polypeptides and Gene Sequences

20 The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some
25 nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component)
30 except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

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corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby,
5 *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is
10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene
15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating
20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292
25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate

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the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and
5 antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to
10 corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A*
15 *Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of
20 immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

V. Kits

25 The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific
30 oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means
5 used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

15 EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to
20 microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference
25 sequences of the fragments shown in the Table, column 1.

The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154 (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.

5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three

10 additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in

15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included

20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or

25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For

30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by

5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined *a priori*, such

15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

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All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and
5 individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
WI-7070	226	C	T	---	---	TGTGAACCTCCACTTGAAGCCAAAGAAAGAACTCACACTTAAACACATGCCAGTTGGGAAGGCTCT GAAACTCAGTGCATAATAGGAACACTTGAGACTAATGAAAGAGAGAGTTGAGACCAATCTTTATTT GTACTGGCCAAATACTGAAATAACAGTTGAAGGAAGACATTTGGAAAAAGCTTTTGAGGATAATGT TACTAGACTTTATGCCATGGTGCTTTTC/TJAGTTTAAIGCTGCTCTGTCAAG
WI-10744	61	G	C	---	---	AAGCCATTGACGTAACATCTCAGAGGTTATTTGTCATGGATTGACTCTCTGGGACAAAGGAC[G/C]AA AAACACTCTTCTGTGGATATCTGTGCAGATAGATGACCCAAAGATCAGATGCTACCCAGATGTGTTT GATAATACATAAGCCCTAGGATTAGATACAATCTTGAAGAACTGAGACAGATAATCTGAAATT AAATGAGGTAAAGTTTCAGGCACTCA
WI-9975	126	C	T	---	---	GGGCAAAATTACCAGCAAAAGTCAAAATACCAGCATCAAAGTCAGGTGCAAGGAGGTAGAACA TTACAGTAACATATGTCAATCTTTTGTATATTAGTATTATCTGCCCAATGCCCTAGAATA[C/T]AGTG GGTCCCTAATAGTTATTAGTTCCTTTTCTCCTCTTCTCACTCTGAAATTTTATACTTAA GGGATTAGTTACCACCAAAATGTGTATGATCAATTTGATCTTACTGAA
WI-8010	247	G	T	---	---	GCTAGGTTTGTCTTCTGTTGGCTGCTTCACCTAGACTTGAGATGACTTGATTTACAGTAATCCCTATGT GATGTAACCTAGCTAGACCTTCCCCTCCTCCGAATCCAGCTCCAGTTCAGAAAGTATGCCACAC TCAACCCCTCTCTCCAGTTCATCCTGTATTAAATTTCTTCCCATAATTAATCAAGGGAGTGGACAGGT CCCTGGCTGAAAGAAATAAAGAGATCCCAAGTGGTGGG[G/T]CTT
WI-5:22b	85	G	C	---	---	GCCGGCCTATCTTTTAACTTTAAGTTGATCTTTGGTGTTCTCCATCCTAGGATTCGCCCTTATAAT CTTTGCTCTGTCTGTA[G/C]ATTACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGTGCCAAATCTTCAGGTCTCTTTGAAATTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA TCTCGACTCTATAACAACCTCCACAGAA
WI-5222	52	G	C	---	---	GCCCGGCTATCTTTTAACTTTAAGTTGATCTTTGGTGTTCTCCATCCTAG[G/C]GATTCGCCCTAT AATCTTTGCTGCTGTAGATTACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGTGCCAAATCTTCAGGTCTCTTTGAAATTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA TCTCGACTCTATAACAACCTCCACAGAA
WI-8007	242	C	A	---	---	TATGCACTTCCACAAAAGCGATATAATTTAAAGTTTTTTCATTAGAAATAAATGTATAAAAAATAA ATATGTTATTATAGGCATTATTACTAACTATATGCTCTCTTGGGAAGGAACACCCAAACCAATACTT ATAAAGTACATGTAAATTTATAGTAACATAATTTACTATATACATATGGAATAATCATATTTCTACA GAAGAGCTGAACAGACATTCACCAGGATACGACTGTTGGAC[C/A]AGCTGCTG
WI-9823	97	C	T	---	---	TCAGTTGCAAAAAATTGCTGCCATAAACATGCTTTGCTTATCTCTGTGCATATGATGTGTTTTGTTAG TCTATATTCACACATATGAGTGAATTT[C/T]GGGGCATGGGAAATACATCTTTATGAGACATTTGA ACTGCTCACCACATCATAGTATCCATTTAAACAGACCAACAATGTATAAGAAATTCCTTTGTTTTTAC ATGCTTTCCAACTGATTTGTATGACTATTGTATGACAGTTGGATCACC

WI-9651b	105	A T ---	---	TCTACATCTATGGACAACCTCCATGCCCTTTGCACATGCTGATCCCCTCCTCGGAATTCCTTTCCCT ACCTTGCTCCATGTACAAATTTCTGCTGCTCCTTCAATGGGGCAGCTTGAAGCCCTCCCTTTAGAC ACCTTACAGGTACAGCCGACCATGCCCTACCTCCATGCCACTGCCAGGGACCCCTTAGGCCCTCTG TCTTAAACCTGTAAATGGTATATTAAATCCTTGGTGTTTGAATGCTCTC
WI-9651	139	T C ---	---	TCTACATCTATGGACAACCTCCATGCCCTTTGCACATGCTGATCCCCTCCTCGGAATTCCTTTCCCT ACCTTGCTCCATGTACAAATTTCTGCTGCTCCTTCAAGGGCAGCTTGAAGCCCTCCCTTTAGACACCT CTTACAGGTACAGCCGACCATGCCCTACCTCCATGCCACTGCCAGGGACCCCTTAGGCCCTCTGT CTTAAACCTGTAAATGGTATATTAAATCCTTGGTGTTTGAATGCTCTC
WI-7676b	309	A C ---	---	GTGACCTTCTCGCAGCGTGAGATGGACATCCTTGTCTGGGACTTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCCAGGGTAGATGGGAGGGTCTGTGTGAAGGG GCCGGCTCTCTTGGTGGCTGCTGGGTTGCAGGGGCAGGAAGCGTGTGACTGCAGCTTCTGCTGGTGC TCCCCCGTCTCCTCGGAGGCAGTATAGGAGAGAGAGCAAGGATTGAGT
WI-7676	139	C T ---	---	GTGACCTTCTCGCAGCGTGAGATGGACATCCTTGTCTGGGACTTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCCAGGGTAGATGGGAGGGTCTGTGTGAAGGG GCCTGGCTCTCTTGGTGGCTGCTGGGTTGCAGGGGCAGGAAGCGTGTGACTGCAGCTTCTGCTG GTGCTCCCCCGTCTCCTCGGAGGCAGTATAGGAGAGAGAGCAAGGATT
WI-10072	105	G A ---	---	CATTATCTTGTCTGGGCTGTTCATTACCTTCTCTCTCCCAATGAAGAGGATATTTAAGCATCAT CATCTGGCCCTTTTGTAGTTTGAATATTTTGTGTGATGACTCCTATGCACATGATAAATTTGTTA TGCTTGCTCTTATCTTATCTTTTGTATAGGAGTTTGGCCATGACCCCTTATGAGGAGAAAGGGA TCACCCCTTTTGGCCTCTACAACCTTATAGATATTTAAATATCTTTT
WI-9986	42	T C ---	---	TTGGTGTGAACCTCAGAAATATAGGGAAATTAAGACAAATTTGAATTA/CJGTACCCCGAGGAACAAGAG CCCTGCACCTGACTCCAAAGGAGTTCTATTTCTGGCTGTTCCAGACTTTTATGTATCTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCATCATCTGATCCAGGGTAGTACTACAAGAACATGTCA ATATCAATAGCATGCATATGGGTTGTGGATTCTTAGAACTTATGCAATT
WI-7041	174	C A ---	---	GTCTATTGCAGGAGAAACGTCCCTTGCCACTCCCACTCTCATCAGGCCAAGTGGAGACTGGCCAGA GGCCCTGCACATGCAAACTCCAGTCCCTGCCTTCAGAGAGCTGAAAGGGTCCCTCGGCTCTTTATTT CAGGGCTTTGCATGCGCTCTATTCCTCTGCTGCTCTC/CJGCCACTTCTTTGGAGCAAGGAGATGC AGCTGTATTGTGTAACAAGCTCATTTGTACAGTGTCTGTTCATGTAATAA
WI-7224	134	T C ---	---	ATAAACCTTGTGTATGTATCACCCCACTCACTAATTAATCACTTAATGCTATCAGATATCCTCTCT ACCTTCACGTTATTTGAAGAAATCCTTAACATCAATATCTTTCATCCATAAAATGTCAGCATTT /CJATTAAGGATGGCCTGTGATTATCTTGGGAAGCAGAGTGATTCATGCTAG

WI-10826	132 A C ---	---	TCTATTGGCATTTCACAGTAGCCCCCATGAAGTAGGATGAACAGCCCTCTATTTTAAACATGAGAAGAT GGAGGCCCTTTCCAAATGGACTAAGTAATGTGTCTCAGGTTTTCTTAATAAGCAAAAGACCTGCA/WC JCCCTGGCTTCTGACTCCAAAGCTTATCCCTTCTCATGCTGTTGCTGTGAGCCAGGACCCCATGCGCA GAAAGCCAGCCTCTCCATCCCCAC
TIGR- A004S25	145 G A ---	---	AGATCTGCCATTAGTATTTATTCCTTTGAAGATACTTTGGAGATTCAATTTCTTGAGTGGCACTGCAT GCTCATTCAGTGAAAACCTTGTGGGGTATAGAAATGGAATGGAGAGTTTCAAACAGCTTTGCTGAAAC TGACTTTGG[G/A]CTCCAGACTTCACCTGCTCTAGGCATTGAAACCATCACCTGGTTTGCACTTCTC ATGACTGAGGTTAACTTAAATGACTGAGGTTAACTTAAAC
WI-1021	24 A T ---	---	AAACACACAGAATCATCAAMGCACI/AJATCTGTGTTTGAGATAAATGATAGTCTGAGTCACCTATG TAAGAAAGTAACCTCTGAAATAGTAGGATAGTATTAATTCCTGTAATAGATTACCTCTCAGCAAT TGGTCTGTTTTCATTCTATGGAACCTCTCCGTACTGTAATTTTCAATCTATGGAACCTCCCCATACTGT AATTGGACAGTTTGTGTTCCAC
WI-4687	121 G T ---	---	TAGTATGTCACCTGCCATGGTAAGGACTTTGATCACTAGGAAATAAGAACACATTTGAATGGTCTTGTCO TTTCAATAAAAAAGAGTGACATGATTGAACATGTGTTTAGATAAAGGGCACCTT[G/T]GCAGGAGTGT TTAGGATGAAGAGAGAGAGATTAAAGGAAGATCAGGAAGAAAAGTAGCAATGGGAATGAAAAATAG GAGGCCCTGAGATCCACTGGATAATCTAAAAAACCAAGAGAAAAGAACTTGAT
WI-4719b	107 T G ---	---	TTCATTCCCTTCCAAAATCCTTAGGAAATTTACATTATGGGCTAGTGTCTTTGGGTGTGAGCGGATT ATGCTGACGCCATGGGTGTTTCATAAGTGACTTGAGAGTTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGATTCATTCAACAAATTCCTGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCGCCACTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-4719	70 G A ---	---	TTCATTCCCTTCCAAAATCCTTAGGAAATTTACATTATGGGCTAGTGTCTTTGGGTGTGAGCGGATT AT[G/A]TCTGACGCCATGGGTGTTTCATAAGTGACTTGAGAGTTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGATTCATTCAACAAATTCCTGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCGCCACTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-9484b	216 G C ---	---	TCAACACGCTTTTATGCCACTTCTGGCTCCCTCGTCCCAGCAAGATTCTACCTCTTACCCCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTTCTCCTCTGCACACTGCCAAGT TAAAGAAACCCCTGCTTGTGAGAGGGAGGGCCAGACAGGAGGAATCAAGGGCATGTATGGCTC AGTCCCACTTCT[G/C]ACTGCAGAGTATAGGGACCCAGGGTTCCAAACTTT
WI-9484	178 G A ---	---	TCAACACGCTTTTATGCCACTTCTGGCTCCCTCGTCCCAGCAAGATTCTACCTCTTACCCCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTTCTCCTCTGCACACTGCCAAGT TAAAGAAACCCCTGCTTGTGAGAGGGAGGGCCAGACAGG[G/A]AGGAATTCAGGGCATGTATG GCTCAGTCCCACCTCTGACTGTCAGAGTATAGGGACCCAGGGTTCCAAACTTT

WI-7330	207	C T	---	---	AGGATGGAAGGAGACACGGGCGAGGAGAACTCTCTTCTGCTAAATCGATAGGAGTCAGTTTTGCTTAAATGCTGACTACAGCCACTGACATGGTGGCTGGAAATTTCTCTTTAAATGGCATATAGGTTGTGACACAAGAAAGTCATCTTTGGTGGCTAAGTTTACTAAGGAAAAATACTGAAAGATTAAAGTGAGAG[C/T]TGAAGAAGAGAAATGATAATGCTTCCAAACTGTAGCTGCACAGTTAAACACAGTTCAGGTTGGTGAAGCAGAAAAAGGGATGTGATTACAAATTTAAATGAATCAGTCACATTGCACAATTAATCCTTTGGCATCATACAACTGGGTTTTAATGGCAAAATGATGACATCATAGCATGACCAACTCATGGAAGGCAGTCTAGAGTCCATCACGCTCACACCTGAGGGGAAGGCACTGCACCCA CTGACGAGAC[G/A]CAGAGACCTTGGACTACAGATGACACCCACATGCCCACTTCTCTCAAAAGAGAAAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA[C/T]GGGATCATCAACAAGATTTCTTTGTGCAAAATATTTGACTATCTGTATCTTTTCATCCTTGACTAAATTCGTGATTTCAAGCAGCATCTTCTGGTTTAACTTTGCTGTGAACAATTTGCGAAAAAGAGTCTTCCAATTAATGCTTTTTATATCTAGGCTACCTGTGGTTAGATTCAAGGCCCGAGGCTTCTCCCGAAGCGGGGCTTGGCCTGGAACTTCCAGAGAGGAGCGGGAGCAATTTAGGCCCAACCTTGCTCCCATCTGCCCCCTGC AACAGCTGCAGGCTGCTTCTCTCTCTGAGTTCCCTCTGGGCTGCGCAGGCTCCCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAG[T/C]TGGGGGAGCAGAGCCAGGTTGGACAGGTGTTTGAGGGGCCCAACTTCCCTTGGAGCTCGCTTCTCCCGAAGCGGGGCTTGGCCTGGAACCTTCCAGAGAGGAGCGGGAGCAATTTAGGCCCAACCTTGCTCCCATCTGCCCCCTGC AACAGCTGCAGGCTGCTTCTCTCTCTGAGTTCCCTCTGGGCTGCGCAGGCTCCCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAG[T/C]TGGGGGAGCAGAGCCAGGTTGGACAGGTGTTTGAGGGGCCCAACTTCCCTTGGAGCTGTACTTTAGGCTGTGAGGTTGGGCAATTTAGTGTGACCTTGACACAGGGTTTTCTAACAGATGACCTGTGAATCATAAATTTAAACCTGCATATATTTATAGCCAGTCATCTTGGCCTCACCCCTATATG GCAATAAACTGCCTAAGCACTCAGGCTCCCACTCATCAACCCCTTTGACCAGAGAAAGCACTCTGGTTCTCTATCCCTTGTACATAGAGAGTTTGTGATGGGGCTCTGGCTGTCAGTTCTAGTCTCTGCGGGCCACACAGAAACTCTTTTTGGGCTCT[C/T]TTTTCTCCCTCTGGATCA AAGTAGGCAGGACCATGGGACCAGGCTTGGAGCTGAGCCTCTCACCTGTACTCTTCGGAATAATCCTCTTCTGAGGCTGGATCCTAGCCTTATCCTCTGATCTCCATGGCTTCCTCTCCCTCTGCGGACTCCTGGTTGAGCTGTGCTCAGTCCCAACAGATGCTTTCTGTCTCTGTGACCAATTTATTTAGAGGTTTAACAATGGCCTGACTATCACCTGATGGTGGCCAGAATTTCTGTGACCAATGCTACCTGACTCTAACCAATGCTGCTGAGGGAGGCTCCCCCT[G/A]CCCTGATCATGCTACCTAAGCTGCTGACTGCTGAGGCTGCTGAGTGTATGGGATCCTAAGCCAAAAAGCTGAAATGAACATGTTCTAGCACTACAGAAATCCCATACTGCCCTCAGTAAAGGCAATTTTAAATCTCTTTGGATAACCCAGGGCACAT
WI-9443	211	G A	---	---	TCCTCAAAAGAGAAAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA[C/T]GGGATCATCAACAAGATTTCTTTGTGCAAAATATTTGACTATCTGTATCTTTTCATCCTTGACTAAATTCGTGATTTCAAGCAGCATCTTCTGGTTTAACTTTGCTGTGAACAATTTGCGAAAAAGAGTCTTCCAATTAATGCTTTTTATATCTAGGCTACCTGTGGTTAGATTCAAGGCCCGAGGCTTCTCCCGAAGCGGGGCTTGGCCTGGAACTTCCAGAGAGGAGCGGGAGCAATTTAGGCCCAACCTTGCTCCCATCTGCCCCCTGC AACAGCTGCAGGCTGCTTCTCTCTCTGAGTTCCCTCTGGGCTGCGCAGGCTCCCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAG[T/C]TGGGGGAGCAGAGCCAGGTTGGACAGGTGTTTGAGGGGCCCAACTTCCCTTGGAGCTGTACTTTAGGCTGTGAGGTTGGGCAATTTAGTGTGACCTTGACACAGGGTTTTCTAACAGATGACCTGTGAATCATAAATTTAAACCTGCATATATTTATAGCCAGTCATCTTGGCCTCACCCCTATATG GCAATAAACTGCCTAAGCACTCAGGCTCCCACTCATCAACCCCTTTGACCAGAGAAAGCACTCTGGTTCTCTATCCCTTGTACATAGAGAGTTTGTGATGGGGCTCTGGCTGTCAGTTCTAGTCTCTGCGGGCCACACAGAAACTCTTTTTGGGCTCT[C/T]TTTTCTCCCTCTGGATCA AAGTAGGCAGGACCATGGGACCAGGCTTGGAGCTGAGCCTCTCACCTGTACTCTTCGGAATAATCCTCTTCTGAGGCTGGATCCTAGCCTTATCCTCTGATCTCCATGGCTTCCTCTCCCTCTGCGGACTCCTGGTTGAGCTGTGCTCAGTCCCAACAGATGCTTTCTGTCTCTGTGACCAATTTATTTAGAGGTTTAACAATGGCCTGACTATCACCTGATGGTGGCCAGAATTTCTGTGACCAATGCTACCTGACTCTAACCAATGCTGCTGAGGGAGGCTCCCCCT[G/A]CCCTGATCATGCTACCTAAGCTGCTGACTGCTGAGGCTGCTGAGTGTATGGGATCCTAAGCCAAAAAGCTGAAATGAACATGTTCTAGCACTACAGAAATCCCATACTGCCCTCAGTAAAGGCAATTTTAAATCTCTTTGGATAACCCAGGGCACAT
WI-7166	59	C T	---	---	TCCTCAAAAGAGAAAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA[C/T]GGGATCATCAACAAGATTTCTTTGTGCAAAATATTTGACTATCTGTATCTTTTCATCCTTGACTAAATTCGTGATTTCAAGCAGCATCTTCTGGTTTAACTTTGCTGTGAACAATTTGCGAAAAAGAGTCTTCCAATTAATGCTTTTTATATCTAGGCTACCTGTGGTTAGATTCAAGGCCCGAGGCTTCTCCCGAAGCGGGGCTTGGCCTGGAACTTCCAGAGAGGAGCGGGAGCAATTTAGGCCCAACCTTGCTCCCATCTGCCCCCTGC AACAGCTGCAGGCTGCTTCTCTCTCTGAGTTCCCTCTGGGCTGCGCAGGCTCCCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAG[T/C]TGGGGGAGCAGAGCCAGGTTGGACAGGTGTTTGAGGGGCCCAACTTCCCTTGGAGCTGTACTTTAGGCTGTGAGGTTGGGCAATTTAGTGTGACCTTGACACAGGGTTTTCTAACAGATGACCTGTGAATCATAAATTTAAACCTGCATATATTTATAGCCAGTCATCTTGGCCTCACCCCTATATG GCAATAAACTGCCTAAGCACTCAGGCTCCCACTCATCAACCCCTTTGACCAGAGAAAGCACTCTGGTTCTCTATCCCTTGTACATAGAGAGTTTGTGATGGGGCTCTGGCTGTCAGTTCTAGTCTCTGCGGGCCACACAGAAACTCTTTTTGGGCTCT[C/T]TTTTCTCCCTCTGGATCA AAGTAGGCAGGACCATGGGACCAGGCTTGGAGCTGAGCCTCTCACCTGTACTCTTCGGAATAATCCTCTTCTGAGGCTGGATCCTAGCCTTATCCTCTGATCTCCATGGCTTCCTCTCCCTCTGCGGACTCCTGGTTGAGCTGTGCTCAGTCCCAACAGATGCTTTCTGTCTCTGTGACCAATTTATTTAGAGGTTTAACAATGGCCTGACTATCACCTGATGGTGGCCAGAATTTCTGTGACCAATGCTACCTGACTCTAACCAATGCTGCTGAGGGAGGCTCCCCCT[G/A]CCCTGATCATGCTACCTAAGCTGCTGACTGCTGAGGCTGCTGAGTGTATGGGATCCTAAGCCAAAAAGCTGAAATGAACATGTTCTAGCACTACAGAAATCCCATACTGCCCTCAGTAAAGGCAATTTTAAATCTCTTTGGATAACCCAGGGCACAT
WI-7259b	189	T C	---	---	TCCTCAAAAGAGAAAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA[C/T]GGGATCATCAACAAGATTTCTTTGTGCAAAATATTTGACTATCTGTATCTTTTCATCCTTGACTAAATTCGTGATTTCAAGCAGCATCTTCTGGTTTAACTTTGCTGTGAACAATTTGCGAAAAAGAGTCTTCCAATTAATGCTTTTTATATCTAGGCTACCTGTGGTTAGATTCAAGGCCCGAGGCTTCTCCCGAAGCGGGGCTTGGCCTGGAACTTCCAGAGAGGAGCGGGAGCAATTTAGGCCCAACCTTGCTCCCATCTGCCCCCTGC AACAGCTGCAGGCTGCTTCTCTCTCTGAGTTCCCTCTGGGCTGCGCAGGCTCCCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAG[T/C]TGGGGGAGCAGAGCCAGGTTGGACAGGTGTTTGAGGGGCCCAACTTCCCTTGGAGCTGTACTTTAGGCTGTGAGGTTGGGCAATTTAGTGTGACCTTGACACAGGGTTTTCTAACAGATGACCTGTGAATCATAAATTTAAACCTGCATATATTTATAGCCAGTCATCTTGGCCTCACCCCTATATG GCAATAAACTGCCTAAGCACTCAGGCTCCCACTCATCAACCCCTTTGACCAGAGAAAGCACTCTGGTTCTCTATCCCTTGTACATAGAGAGTTTGTGATGGGGCTCTGGCTGTCAGTTCTAGTCTCTGCGGGCCACACAGAAACTCTTTTTGGGCTCT[C/T]TTTTCTCCCTCTGGATCA AAGTAGGCAGGACCATGGGACCAGGCTTGGAGCTGAGCCTCTCACCTGTACTCTTCGGAATAATCCTCTTCTGAGGCTGGATCCTAGCCTTATCCTCTGATCTCCATGGCTTCCTCTCCCTCTGCGGACTCCTGGTTGAGCTGTGCTCAGTCCCAACAGATGCTTTCTGTCTCTGTGACCAATTTATTTAGAGGTTTAACAATGGCCTGACTATCACCTGATGGTGGCCAGAATTTCTGTGACCAATGCTACCTGACTCTAACCAATGCTGCTGAGGGAGGCTCCCCCT[G/A]CCCTGATCATGCTACCTAAGCTGCTGACTGCTGAGGCTGCTGAGTGTATGGGATCCTAAGCCAAAAAGCTGAAATGAACATGTTCTAGCACTACAGAAATCCCATACTGCCCTCAGTAAAGGCAATTTTAAATCTCTTTGGATAACCCAGGGCACAT
WI-7259	188	G T	---	---	TCCTCAAAAGAGAAAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA[C/T]GGGATCATCAACAAGATTTCTTTGTGCAAAATATTTGACTATCTGTATCTTTTCATCCTTGACTAAATTCGTGATTTCAAGCAGCATCTTCTGGTTTAACTTTGCTGTGAACAATTTGCGAAAAAGAGTCTTCCAATTAATGCTTTTTATATCTAGGCTACCTGTGGTTAGATTCAAGGCCCGAGGCTTCTCCCGAAGCGGGGCTTGGCCTGGAACTTCCAGAGAGGAGCGGGAGCAATTTAGGCCCAACCTTGCTCCCATCTGCCCCCTGC AACAGCTGCAGGCTGCTTCTCTCTCTGAGTTCCCTCTGGGCTGCGCAGGCTCCCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAG[T/C]TGGGGGAGCAGAGCCAGGTTGGACAGGTGTTTGAGGGGCCCAACTTCCCTTGGAGCTGTACTTTAGGCTGTGAGGTTGGGCAATTTAGTGTGACCTTGACACAGGGTTTTCTAACAGATGACCTGTGAATCATAAATTTAAACCTGCATATATTTATAGCCAGTCATCTTGGCCTCACCCCTATATG GCAATAAACTGCCTAAGCACTCAGGCTCCCACTCATCAACCCCTTTGACCAGAGAAAGCACTCTGGTTCTCTATCCCTTGTACATAGAGAGTTTGTGATGGGGCTCTGGCTGTCAGTTCTAGTCTCTGCGGGCCACACAGAAACTCTTTTTGGGCTCT[C/T]TTTTCTCCCTCTGGATCA AAGTAGGCAGGACCATGGGACCAGGCTTGGAGCTGAGCCTCTCACCTGTACTCTTCGGAATAATCCTCTTCTGAGGCTGGATCCTAGCCTTATCCTCTGATCTCCATGGCTTCCTCTCCCTCTGCGGACTCCTGGTTGAGCTGTGCTCAGTCCCAACAGATGCTTTCTGTCTCTGTGACCAATTTATTTAGAGGTTTAACAATGGCCTGACTATCACCTGATGGTGGCCAGAATTTCTGTGACCAATGCTACCTGACTCTAACCAATGCTGCTGAGGGAGGCTCCCCCT[G/A]CCCTGATCATGCTACCTAAGCTGCTGACTGCTGAGGCTGCTGAGTGTATGGGATCCTAAGCCAAAAAGCTGAAATGAACATGTTCTAGCACTACAGAAATCCCATACTGCCCTCAGTAAAGGCAATTTTAAATCTCTTTGGATAACCCAGGGCACAT
WI-7322	275	A G	---	---	TCCTCAAAAGAGAAAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA[C/T]GGGATCATCAACAAGATTTCTTTGTGCAAAATATTTGACTATCTGTATCTTTTCATCCTTGACTAAATTCGTGATTTCAAGCAGCATCTTCTGGTTTAACTTTGCTGTGAACAATTTGCGAAAAAGAGTCTTCCAATTAATGCTTTTTATATCTAGGCTACCTGTGGTTAGATTCAAGGCCCGAGGCTTCTCCCGAAGCG

WI-931c	191	C A ---	---	GACCAGGGACACGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTCTTCTGCTGTGTCAAAATGATCCTTCT GTTGCTGCACTGTCACTTACTGTGTATGGATTATAATTATGTCCAAAAAGCC[C/A]GAGGCTGG TACAGAAAGGCATGGGAAAGATGTGTCAGA
WI-931b	81	A G ---	---	GACCAGGGACACGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCTCCCTA/GJCCCTCACCACACCTTCCAGTGTCTTCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCACTTACTGTGTATGGATTATAATTATGTCCAAAAAGCCCGAGCCTGG TACAGAAAGGCATGGGAAAGATGTGTCAGA
WI-931	31	A G ---	---	GACCAGGGACACGAAAGCCACGGAAGCCAC/GJGCCACTAGCCCTGAACCTTGCACACCCCTGGA GTTCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTCTTCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCACTTACTGTGTATGGATTATAATTATGTCCAAAAAGCCCGAGCCTGG TACAGAAAGGCATGGGAAAGATGTGTCAGA
WI-10870b	91	C T ---	---	GGATGACTTACCCCAATAGCAGGGTGGGTACATTCATGGGTAAACACACCCCTGGAGTGGCAGA GACATCCACCTTAGCAAAGTGGG[C/J]ACCTACTTAGAGCAGTGGAGTACCCCTGAGTACGACCC TTAGCAGCAGAAATACAAGAAATCTTGGGACCTGTACTCTCTGATACAAAATAAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAACGTTGCCCC
WI-10870	103	G A ---	---	GGATGACTTACCCCAATAGCAGGGTGGGTACATTCATGGGTAAACACACCCCTGGAGTGGCAGA GACATCCACCTTAGCAAAGTGGGACCTACTTAGA/GAJCAGTGGAGTACCCCTGAGTACGACCC TTAGCAGCAGAAATACAAGAAATCTTGGGACCTGTACTCTCTGATACAAAATAAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAACGTTGCCCC
WI-7719b	281	T C ---	---	AGTTTATCTTCCAGATGACCAAGTAGACAAATGGATACTAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGGCATTGGTCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTTCTGGACATTGCCCATGTATAATCTCTCACTGATGATTTCAAGCTAAAGCAA
WI-7719	163	A G ---	---	AGTTTATCTTCCAGATGACCAAGTAGACAAATGGATACTAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGGCATTGGTCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCC/JGTTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTGCCCATGTATAATCTCTCACTGATGATTTCAAGCTAAA
WI-10396	72	C A ---	---	GCCTTGGAGTATCTAAACTGTGGCCTCCACTTCTCATTTTCTTGAACATGTCTATCAACTGGGAA GAGT[C/A]GTGACTTTATGCCCAGTTCCCTCTCAGATTTTATGACGGTTGTTTTCTTTTGTTA TGCCATTTGAGGGATTGATGTTTCTTAAACTATGAAGTACTTGGCTGTCTCTCTCCATTGCTTCAGG TTAACAGCCACCATTTGTAAACACTTTGT

WI-10673	94 C G ---			TCCCTTTATGACCCCAAGAGATATTTATTAAACACCAATTACGTAGCAGGCCATGGCTCATGGGACC CACCCCGGTGGCACTCATGGAGGGG[C/G]TCAGGTTGAACTATGCAGTGTCTCCGGCCACACA TCCTGCTGGGCCCCCTACCTGCCCAATTCATCTCCCAATTAATCTGTCTTATTGTTTCATCCTG GAGAAITGAAGGGGAGGTCAGGTTGTTGTCATGATTGTCAGAGAACCT
WI-7842	57 T C ---			CACAGCCATGCCCTTGAGGAGCCGCCACAGATGCTGAATCCCTATCCCATCTGT[C/G]ATGAG TCCCAITTCCTTGCAATTAGCAATCTGTCTCCCCCAAAAGAAATGCTATGAAGCTTTCTTCCT ACACACTCTGAGTCTCTGAATGAAGCTGAAGTCTTAGTACCAGAGCTAGTTTCAGCTGCTCAGAAT TCATCTGAAGAGAGACTTAAGATGAAGCAATGATTCAGCTCCCTTATA
WI-7721	145 A C ---			CTGCCCTCATCAGCCCACTGGAGTCCACACTTGAATTTGGGCAGCTACCACGGGTCTGCCATGCTCTGG AGGAGCAAGGGGGCCACATCCCCACCCAGCTGTACCCAGCCGGGCAGGTGCAGCCCTTCCTCCG TGTCTCTGC[C/G]TCTGACTCTCTTTGAGGTCCTGTATGCTACCTCTGACTCTGTGGTCCCTCTG TGTCTGCTCTCATCCATCCTCTTACTGGGGCTGGGGCTCTAGCCCAA
WI-4767b	173 C A ---			TTTCCAGTCTGTTTATCCTTTTCATTGTCAAAAGATGCTCTTAGACTGA[A/G]ATTCATAAAGAGTT CAGGCTCGGTAATCCTAGATCTTCTATATCCATTGAGTGTGATGGAGTGGAGAGAGGGTATGTT CTTGCTTGAGAAATCCTAGAAAGCACAGGATGACA[C/A]AATCACTAAGGAATCCCACTAAGA CTCCTCTAACCCAGAGATTTTAACT
WI-4767	50 A G ---			TTTCCAGTCTGTTTATCCTTTTCATTGTCAAAAGATGCTCTTAGACTGA[A/G]ATTCATAAAGAGTT CCTCAGGCTGGTAATCCTAGATCTTCTATATCCATTGAGTGTGATGGAGTGGAGAGAGGGTATG TTTCTTGCTTGAGAAATCCTAGAAAGCACAGGATGACACAAATCACTAAGGAATCCCACTAAGAC TCCCTAACCCAGAGATTTTAACT
WI-7718f	222 C T ---			ATTGCACTGAAGTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAGTG ACTTTGCAGATGGAAAGAGGTGAAATGAAGAGGAGCTGTGTTGAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAA[C/T]CATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718e	60 T C ---			ATTGCACTGAAGTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGA[T/C]GCAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGAAAGAGGTGAAAAATGAAGAGGAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718d	31 G A ---			ATTGCACTGAAGTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGA[T/C]GCAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGAAAGAGGTGAAAAATGAAGAGGAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT

WI-7718c	91	C G	---	---	ATTGCACTGAAGTTTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGG[C/G]TGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGAGATGGAAAGAGGTGAAATGAAGAAAGGAGCTGTGTTGAACACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718b	248	A G	---	---	ATTGCACTGAAGTTTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAGATG ACTTTGCAGATGGAAAGAGGTGAAATGAAGAAAGGAGCTGTGTTGAACACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATT[A/G]AT
WI-7718a	42	A T	---	---	ATTGCACTGAAGTTTTTGAATAACCTTTGTAGTTACTCAAGC[A/C]TGTTACTCCCTACACTGATGC AAGGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGAT AGATGACTTTGAGATGGAAAGAGGTGAAATGAAGAAAGGAGCTGTGTTGAACACAGAAAAATAAG TCAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAA
WI-7227d	99	G C	---	---	AGGGAATTGTTGCTCCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTACCTGGCTTC CGTGACCAATTATCTTTAGACAAGCTTTA[G/C]AGAAATGGACTCAGGGAAGAGACTCACATGC TTTGTTAGTATCTGTGTTCCGGTGGTGTAAATAGGGGATTAGCCCCAGAGGGACTGAGCTAAACA GTGTTATTATGGAAAGGAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227c	291	G A	---	---	AGGGAATTGTTGCTCCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTACCTGGCTTC CGTGACCAATTATCTTTAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGCTTT GGTAGTATCTGTGTTCCGGTGGTGTAAATAGGGGATTAGCCCCAGAGGGACTGAGCTAAACAGTG TTATTATGGAAAGGAATGGCATTGCTGCTTTCAACCAGCGACTAATGCAAT
WI-7227b	93	G T	---	---	AGGGAATTGTTGCTCCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTACCTGGCTTC CGTGACCAATTATCTTTAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGTTAGTATCTGTGTTCCGGTGGTGTAAATAGGGGATTAGCCCCAGAGGGACTGAGCTAAACA GTGTTATTATGGAAAGGAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227a	24	A G	---	---	AGGGAATTGTTGCTCCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTACCTGGCTTC TTCCGTGGACCAATTATCTTTAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGTTAGTATCTGTGTTCCGGTGGTGTAAATAGGGGATTAGCCCCAGAGGGACTGAGCTAAACA GTGTTATTATGGAAAGGAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7310b	234	A C	---	---	CCACAATGCCTCTCCACGATGTCAAGGACTCCTGTCTGCTCTGGAGGTGGGAGACAAGAACCTCCG AAGAGGAAGCAAGAAAGCCGTACTGTCTATGTTGTGATCCTTCATCGAACAACTGATCGGAAAACT TGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAACCTGAGCCAAACACACTGTAAAT ATCCACAGACTCCCTCCCTGCCCCCATCCCA[A/C]ATGATCTTGAGATTTC

WI-7310a	64	T A	---	---	CCACAATGCCTCTCCACGATGTCAGGACTCCTGTCTGTCTGGAGGTGGGAGACAAGAACCTT/A JCCGAAGAGGAAGCAAGAAAGCCGTACTGTCTATGTTGTGATCTTCATCGAACAACTGATCGGAA AATTTGAATCTGTTACTGAAATGAGGAGAGAGACATGTGCTATTGAAGTGAAGCCAAACACACTGT AAATATCCACAGACTCCCTCCCTGCCCTCCATCCCAATGATCTTGAGATTTC
WI-7878b	162	A G	---	---	CCAGCAACACCTACACCTTGTACCTGCCTGGACTCCTATGATGGCTGCTGGTTGATAATAATCA GATCATGCCAAGACGGCCCTCTGATAATCGTCTGGGATGATTGCAATGGAGGGCAAAATGCGTCC CTGAGGAGAAATCTGGGAGGAGCTG/GGTGTGATGAAGGTGTATGTTGGGAGGAGCACAGTGT CTGTGGGAGCCCAGGAAGCTGTCAACCAAGATTGGTGCAGGAAACTA
WI-7878a	51	C G	---	---	CCAGCAACACCTACACCTTGTACCTGCCTGGACTCCTATGATGGCTGCTGGTTGATAATAA TCAGATCATGCCAAGACGGCCCTCTGATAATCGTCTGGGATGATTGCAATGGAGGGCAAAATGC GTCCCTGAGGAGAAATCTGGGAGGAGCTGATGATGAAGGTGTATGTTGGGAGGAGCACAGTG TCGTGGGAGCCCAGGAAGCTGTCAACCAAGATTGGTGCAGGAAACTA
WI-7381c	213	C T	---	---	CTCCACATTCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTTTCTTTCTACC AGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTCTGCTATGTTGAGATC AGATGTGCCAAGGAAGGAGCTCTGTTCCAGAGAAATTCACAAAGTTCCCTCTGTACAGAGACA AAACGGCTC/TGGCTCTCAGAGCATAATCCTTGGCAGGCTCAGCAGG
WI-7381b	54	C G	---	---	CTCCACATTCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTGCTTTCTTTCT ACCAGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTCTGCTATGTTGAG ATCAGATGTGCCAAGGAAGGAGCTCTGTTCCAGAGAAATTCACAAAGTTCCCTCTGTACAGAG ACAAAACGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGCTCAGCAGG
WI-7381a	53	C G	---	---	CTCCACATTCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTGCTTTCTTTCT ACCAGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTCTGCTATGTTGAG ATCAGATGTGCCAAGGAAGGAGCTCTGTTCCAGAGAAATTCACAAAGTTCCCTCTGTACAGAG ACAAAACGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGCTCAGCAGG
WI-1017b	93	G A	---	---	AAATTGCTCTATTCCGACCCCTCATATTAATAGAGCAATGAGAGCGGAGGAAATTTGAACCTCTC AGGTACTGACTGTGGACCCAGACAAG[G/A]GATGTAGATTGTACATTCAATCCCTGAAACAAACCTG CCAGGCAAGTCTTCTCCCATTTTACAAATAGGAGACAAAAATAGGAGATTAAATAACTCATCAC TGTTTCAAAATAAGGAGTGTGAGGTTTGTCCC
WI-1017a	92	G A	---	---	AAATTGCTCTATTCCGACCCCTCATATTAATAGAGCAATGAGAGCGGAGGAAATTTGAACCTCTC AGGTACTGACTGTGGACCCAGACAAG[G/A]GATGTAGATTGTACATTCAATCCCTGAAACAAACCTG CCAGGCAAGTCTTCTCCCATTTTACAAATAGGAGACAAAAATAGGAGATTAAATAACTCATCAC TGTTTCAAAATAAGGAGTGTGAGGTTTGTCCC

WI-1795b	130 T C ---	---	GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGTCTGGGTTCTTCCAGACTCCTACGATTA AATTGTATGCATGTGAACAACATGATGAGGTACTTAGATCTCAGTGTCTTGCAGAAAGAAAGT[C/C] GTCTACCATTTTACCAGAAATTCGTAGTACAAATTTAAGTATCTCTTGTATCTCCCTAGGAGTCTAA AGTGAGCTGGGAAGGCAGGATT
WI-1795a	47 T C ---	---	GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGTCTGGGTT[C/C]TTCAGACTCCTACGA TTAAATTGTATGCATGTGAACAACATGATGAGGTACTTAGATCTCAGTGTCTTGCAGAAAGAAAGT[C GTCTACCATTTTACCAGAAATTCGTAGTACAAATTTAAGTATCTCTTGTATCTCCCTAGGAGTCTAA AGTGAGCTGGGAAGGCAGGATT
WI-10616d	136 G A ---	---	CACACAAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGCTCTCCATACGTTAGGTCCTGGTCTCTATCACAATTGCCA C[G/A]TAGCCCTCCCTTCCCTTCCCTACAGGCCCTTTCAGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCAATTCCTGTTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-10616c	136 G A ---	---	CACACAAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGCTCTCCATACGTTAGTCTCTGGTCTCTATCACAATTGCCA C[G/A]TAGCCCTCCCTTCCCTTCCCTACAGGCCCTTTCAGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCAATTCCTGTTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-10616b	141 C T ---	---	CACACAAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGCTCTCCATACGTTAGTCTCTGGTCTCTATCACAATTGCCA CGTAGC[C/T]CTCCCTTCCCTTCCCTACAGGCCCTTTCAGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCAATTCCTGTTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-10616a	116 G C ---	---	CACACAAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGCTCTCCATACGTTAGTCTCTGGTCTCTATCACAATTG CCAGGTAGCCCTCCCTTCCCTTCCCTACAGGCCCTTTCAGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCAATTCCTGTTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-1126c	52 G A ---	---	CTCTTATTTCTCTGGGCACTGCTTTCTTTGGGGCAAACTTCCAGTATCACT[G/A]TACTAATAATAA AAACCCCTGTAAGTCTGCTTGCAATTTTCAAGATTCAATATATATATCCAGATTGTTTCCCAGCAAGAA AATTTTATTTCTCAAGATATAAAAAATAAATATTTAAATTCAGTTTCCCTCAAAAGGAATATGAAATT TGTTAAATGCAAAATCCAGCTGTAACTTTTTTGGACTTGCTTTTATTTCTT
WI-1126b	230 T C ---	---	CTCTTATTTCTCTGGGCACTGCTTTCTTTGGGGCAAACTTCCAGTATCACTGATACTAATAATAAAA CCCTGTAAGTCTGCTTGCAATTTTCAAGATTCAATATATATATCCAGATTGTTTCCCAGCAAGAAAT TTATTTCTCAAGATATAAAAAATAAATATTTAAATTCAGTTTCCCTCAAAAGGAATATGAAATTGTT AAATGCAAAATCCAGCTGTAACTTTTTT[C/GG]ACTTGTCTTTTATTTCTT

WI-1126a	97 T C ---	---	CTCTATTCTCTGGGCACTGCTTCTTTGGGGCAAACTCCAGTATCACTACTAATAATAAAA CCCTGTAAGTCTGCTTGCATTTCAAGATTC/CAATATATATCCAGATTGTTTCCAGCAAGAAA ATTTTATTCTCAAGATATAAAAAATAATATTTAAATTTTCAGTTTCTCAAAAGGAATATGAATTT GTTAAATGCAATCCAGCTGAACCTTTTGGACTTGCTTTATTCTT
WI-11183c	124 C T ---	---	TAGTGCTAATTTTGGAAAAGTTTGCCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGCTCACTAAGATTT TTTATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAATATTTGGT ATGGTGCTAGAGTTAGTAATGGAA
WI-11183b	192 T C ---	---	TAGTGCTAATTTTGGAAAAGTTTGCCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGCTCACTAAGATTT ATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAATTTAAATTC/ATTTGGT ATGGTGCTAGAGTTAGTAATGGAA
WI-11183a	118 C T ---	---	TAGTGCTAATTTTGGAAAAGTTTGCCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGCTCACTAAGATTT TTTATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAATATTTGGT ATGGTGCTAGAGTTAGTAATGGAA
WI-10770b	174 G A ---	---	GCTTGGTTTGCCTTATGCTTATGCTCAGTCTGAGTCTCCCTTCTGCCCTTTTGTATTCA CCCATACCTCTATGCCCTGCTCAGACCATTTCCCTATCTGGAGCGCTTCTCTGACTTTCTCTC TTCACCAACCTCTTTTATTTCTTCAGGACACTCA[G/A]TTCACATGCCACTCTCGTGACACTGCTCT TTCACATCTTTCTGTGTCCTTTCC
WI-10770a	49 G T ---	---	GCTTGGTTTGCCTTATGCTTATGCTCAGTCTGAGTCTCCCTTCTGCCCTTTTGTATTCA TCACCATACCTCTATGCCCTGCTCAGACCATTTCCCTATCTGGAGCGCTTCTCTGACTTTCTC CTGTTCCACCAACCTCTTTTATTTCTTCAGGACACTCA[G/A]TTCACATGCCACTCTCGTGACACTGCTCT TTCACATCTTTCTGTGTCCTTTCC
WI-9667b	82 C T ---	---	GATGACAACTTCTGCTGTGACCCCTTAGTCTTGTCTATGACACTTTCAATCTGCTGTATCATGG TTATCACTGGACA[C/T]AGCCACCTCCCAGCAGGCTTAGAACTCCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCTTATGGTATTACACACAGTATAGGCATGGTGAACATAATGGATCTTGGCT GTTAAACCTTTTCTGTACCCAGTACCTAAGTCCAACTTGCAATCT
WI-9667a	68 G C ---	---	GATGACAACTTCTGCTGTGACCCCTTAGTCTTGTCTATGACACTTTCAATCTGCTGTATCATG G/C/TTATCACTGGACACAGCCACCTCCCAGCAGGCTTAGAACTCCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCTTATGGTATTACACACAGTATAGGCATGGTGAACATAATGGATCTTGGCT GTTAAACCTTTTCTGTACCCAGTACCTAAGTCCAACTTGCAATCT

WI-10400d	189 A G ---			ACATTTATTAGCAACAAATCAGCAAAATAATAAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAAGCACTTACTAACACAATATTTATTCTAAATTT TCITTCCTTACCTTTACTCTCCCAACCAAAATAACGTAAGTACCTATGTC/A/GJTGCCATGTAG TTTTTGGTTTCATTTACTTGCAAAATTAATCAAGGGCGTTAATGCATTATG
WI-10400c	166 A C ---			ACATTTATTAGCAACAAATCAGCAAAATAATAAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAAGCACTTACTAACACAATATTTATTCTAAATTT TCITTCCTTACCTTTACTCTCCCAACCAAAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTTCATTTACTTGCAAAATTAATCAAGGGCGTTAATGCATTATG
WI-10400b	165 A G ---			ACATTTATTAGCAACAAATCAGCAAAATAATAAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAAGCACTTACTAACACAATATTTATTCTAAATTT TCITTCCTTACCTTTACTCTCCCAACCAAAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTTCATTTACTTGCAAAATTAATCAAGGGCGTTAATGCATTATG
WI-10400a	46 T C ---			ACATTTATTAGCAACAAATCAGCAAAATAATAAGAAAGTAATTGCAATTCAGACATCT GCTGGTTAACTGTTATAAGATGGTTTAGCACACATGTAAGCACTTACTAACACAATATTTATTCTA ATTTTCITTCCTTACCTTTACTCTCCCAACCAAAATAACGTAAGTACCTATGTCATGCCATGT AGTTTTTGGTTTCATTTACTTGCAAAATTAATCAAGGGCGTTAATGCATTATG
WI-10809b	78 C T ---			AAAGGGCTACAAACTAAGGCCAAAAACCATGAACGGTATAAGGAGGTAATGCAAGGGAGACCC CACCTCTACCA/C/TTAGAAAGGGCATTTCAAGCACATTCATGAGGCTTCATATACTGGTTAG CAACAAATGGAATGTATTAGCCCAAGGCAAGGGTATGGACCAAAAGTGCCCAAGTATGAGGCCACA GTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-10809a	33 C T ---			AAAGGGCTACAAACTAAGGCCAAAAACCATGAACGGTATAAGGAGGTAATGCAAGGGAGAGA CCCCACCTCTACCACTTAGAAAGGGCATTTCAAGCACATTCATGAGGCTTCATATACTGGTTAGC AAACAAATGGAATGTATTAGCCCAAGGCAAGGGTATGGACCAAAAGTGCCCAAGTATGAGGCCACAG TGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-7038c	266 T C ---			CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAAATACTGAGATGCTGGGCTGTCTCTCCCTCCAGGAATGCTGGCCCCCAGCCTGGCCAGAC AAGAAGACTGTGAGGAAAGGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATTGAT CATTTTATATGAAATAAAAGATCCTGCATTTATGGTGTAGTCTGAGTCC
WI-7038b	140 A C ---			CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAAATACTGAGATGCTGGGCTGTCTCTCCCTCCAGGAATGCTGGCCCCCAGCCTGGCCAGAC AAGA/C/JGACTGTGAGGAAAGGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAAATAAAAGATCCTGCATTTATGGTGTAGTCTGATCTGA

WI-7038a	31	G A ---	---	---	CGAGCTTGGGATAAGCAAGGGGACCTTGGC[G/A]CTCTCAGCTTCCCTGCCACAICCCAGCTTGTTG TCCCAATGAATACAGATGCTGGGCTGCTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCA GACAAGAACTGTCAGGAAGGTCGGAGTCTGTAAACCAGCATACAGTTGGCTTTTTCACATT GATCATTTTATATGAATAAAGATCCTGCATTTATGGTGAGTTCTGA
WI-3429b	64	G T ---	---	---	ATACGCTTCTGCTGTCCACAGTGAACCAAGCAGCCAGGTCGGGTCGGGCTCCACACA[G/T] CCCTCAGCCCTTCAGCTTTCAGCTTTCAGTGTCTCCATCGGTGACTCAGACAGAGTTTCCAACTCATGTGA CAAAAATACAGATCCCAAGTCTCTCTCTGGATTGGATCTAGCAAGACCAGAGACGGTCTCTAGAA TCCTGACTGTTAACAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
WI-3429a	62	C T ---	---	---	ATACGCTTCTGCTGTCCACAGTGAACCAAGCAGCCAGGTCGGGTCGGGCTCCACACA[C/T]AG CCCTCAGCCCTTCAGCTTTCAGCTTTCAGTGTCTCCATCGGTGACTCAGACAGAGTTTCCAACTCATGTGA CAAAAATACAGATCCCAAGTCTCTCTCTGGATTGGATCTAGCAAGACCAGAGACGGTCTCTAGAA TCCTGACTGTTAACAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
WI-6786c	151	G A ---	---	---	ATTTAGGACAGTGAAAAAAGGGATTTATAAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTGGCGAAAGGATAAAGAAAGTGAGTGACGGTGACCT GTAGCCCCATCTCT[G/A]TGGGATAAGGTGCCATTGTTCTTGGAGGGTGAAAATGCCACATTC TTTTGGCAGGGGACACTCCTCTGGGTGCTCTATTGCTCAGTTTCAICATT
WI-6786b	111	A T ---	---	---	ATTTAGGACAGTGAAAAAAGGGATTTATAAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTGGCGAAAGGATAAAGAAAGTGAGTGACGGTGGA CCTGTGAGCCCCATCTCTGTGGGATAAGGTGCCATTGTTCTTGGAGGGTGAAAATGCCACATTC TTTTGGCAGGGGACACTCCTCTGGGTGCTCTATTGCTCAGTTTCAICATT
WI-6786a	106	A T ---	---	---	ATTTAGGACAGTGAAAAAAGGGATTTATAAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTGGCGAAAGGATAAAGAAAGTGAGTGACGGTGGA CCTGTGAGCCCCATCTCTGTGGGATAAGGTGCCATTGTTCTTGGAGGGTGAAAATGCCACATTC TTTTGGCAGGGGACACTCCTCTGGGTGCTCTATTGCTCAGTTTCAICATT
WI-6711b	226	G T ---	---	---	GGCTATTTGTAATGCTTGGTTATTGACTCCAAAATTAATAAGTATTGGGGAAGAATCCCTCACCT ACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCCTAAACCTTCAGTTCCAACTCACTCTGAAT TTCATATACCTCCATTATTAAATCAATACATCATTCAGAGAAAGACACGGTGCCAACTGGGTT TGGTTGGTGGCTGCACACCCACAG[G/T]TGGCACTAAGTGTAATCTCTAAA
WI-6711a	36	T C ---	---	---	GGCTATTTGTAATGCTTGGTTATTGACTCCAAAATTAATAAGTATTGGGGAAGAATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCCTAAACCTTCAGTTCCAACTCACTCT GAATTCATATACCTCCATTATTAAATCAATACATCATTCAGAGAAAGACACGGTGCCAACTG GGTTTGGTTGGTGGCTGCACACCCACAGTGCGCAACTAAGTGAATCTCTAAA

WI-10613b	172 A C ---	---	---	ATTGTATGCCAAAATCATAATACCCTGCATTCTAGAACATACAGTGAATAGAAATTTGAGCCATA TGGTGAATAATTTAGAAGTATTTCTCTATATATATACTACGTTTAACATCAATGAATGTGATTT TTTGTCAACTTTTGACAGGCCAGGCAATTTTATTG A G C C C TAGGAGGTTACTATAATTTAGA AAGGCTTACCTTCCACTCTATAATTTTAAAGTCTCGGACTTAGGATGTAG
WI-10613a	44 G A ---	---	---	ATTGTATGCCAAAATCATAATACCCTGCATTCTAGAACATACAGTGAATAGAAATTTGAGCC ATATGGTGAATAATTTAGAAGTATTTCTCTATATATATACTACGTTTAACATCAATGAATGTG ATTTTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTGAGCCCTAGGAGGTTACTATAATTTAG AAAGGCTTACCTTCCACTCTATAATTTTAAAGTCTCGGACTTAGGATGTAG
WI-7587c	133 A T ---	---	---	GCTCTAGTGGGAAACCTCAGGTAGCTCCGGAAGATCTGTGCTTTCCAAAGTGACTACCCTTGAAGC ACATCCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA A TJGGAATGAACCACTCCCTGCCCATTTCCCTATAAGATATCCCAAGACCCAGGCAATTTTGCCCTCT TTCCACATGCCCCCATATGTCTGAGCCAACTGCAGTGGGGCTGCCCTC
WI-7587b	81 G A ---	---	---	GCTCTAGTGGGAAACCTCAGGTAGCTCCGGAAGATCTGTGCTTTCCAAAGTGACTACCCTTGA AGCACATCCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCCATTTCCCTATAAGATATCCCAAGACCCAGGCAATTTTGCCCTCT TCCACATGCCCCCATATGTCTGAGCCAACTGCAGTGGGGCTGCCCTC
WI-7587a	28 C T ---	---	---	ATGACTCAGGTGACAAAAGAGCATGTCTAGACCCCATTTGACTTACGCAAACTCAATCAGCCAACC ACAGAAAAGCTAAAGACATCCTTTTAA A A A G C C T A A A G A C A G C C A T T T A A T C C T A A T T C G TAGTTTATGATTTTCTCAAAATTTCCCAACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGTCTTTGGAGAAGGAGGTGACGCTCTGTTAAAG
WI-10681b	103 T A ---	---	---	ATGACTCAGGTGACAAAAGAGCATGTCTAGACCCCATTTGACTTACGCAAACTCAATCAGCCA ACCACAGAAAAGCTAAAGACATCCTTTTAA A A A G C C T A A A G C C T A A A G C C A T T T A A T C C T A A T T C G TAGTTTATGATTTTCTCAAAATTTCCCAACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGTCTTTGGAGAAGGAGGTGACGCTCTGTTAAAG
WI-10681a	41 A T ---	---	---	GCCTCTCCTCAACTGTCTGGACCCAAAGGCTAGGAAAGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGTCAAGGTGTCACCCCTGTTCTCAAGTTGGGGATGGG G T A A T A A AGGAGGGGAATCCCTTGAACAAGAAAGAACTGGGGATAGTTATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGGTGTGTTTCAAGGACTCGAATTCATTTT
WI-7222c	126 G T ---	---	---	

WI-7222b	255	G A ---	---	---	GCCTCTCTCAACTGTCTGGACCCCAAGGCTAGAAAGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCGAGTGAGCTCAGGTGTCACCCCTGTTCTCAAGTTGGGGATGGGAATAAAGG AGGGGGAATCCCTTGAACAAGAAGAACTGGGGATAGTTATATTCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGTGAAGTTGTATTTCAAAGACTCGAATTCATTTCTCA
WI-7222a	126	G T ---	---	---	GCCTCTCTCAACTGTCTGGACCCCAAGGCTAGAAAGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCGAGTGAGCTCAGGTGTCACCCCTGTTCTCAAGTTGGGGATGGG[GT]AATAA AGAGGGGGAATCCCTTGAACAAGAAGAACTGGGGATAGTTATATTCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGAAGTTGTATTTCAAAGACTCGAATTCATTTT
WI-8054d	41	C A ---	---	---	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTCTCTTC[C/A]TTATCTCTCCCAAGTCAAAATG CTTGCACTCTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCA CAATCTCTTTGTAGTTTGTAGCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCT TCCTGTCTATAAGCGCGCTTCCCTGGCGGTACAGAGAACTCCTTGGCCCTT
WI-8054c	237	G T ---	---	---	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTCTCTTCCTTATCTCTCCCAAGTCAAAATGCTT GCATCTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCACAA TCTCTTTGTAGTTTGTAGCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCTTCC TGTCTAACGCGCGCTTCCCTGGCGGTACAGAGAACTCCTTGGCCCTT
WI-8054b	148	T C ---	---	---	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTCTCTTCCTTATCTCTCCCAAGTCAAAATGCTT GCATCTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAG[C/G]A CAATCTCTTTGTAGTTTGTAGCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCT TCCTGTCTATAAGCGCGCTTCCCTGGCGGTACAGAGAACTCCTTGGCCCTT
WI-8054a	131	C G ---	---	---	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTCTCTTCCTTATCTCTCCCAAGTCAAAATGCTT GCATCTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAG[C/G]A CAATCTCTTTGTAGTTTGTAGCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCT TCCTGTCTATAAGCGCGCTTCCCTGGCGGTACAGAGAACTCCTTGGCCCTT
WI-10854b	152	G T ---	---	---	TTCCACAAAACCTTCCCTGGCGGGGTGACTAAGATGAGAACTGGGAGAACTGGATAGTTTAAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAAACACGACGATAGTTAACGCTGTTAGTTTAT ACGGTGTGCGAGGCAAC[GT]GGAGAGGTACGGGAATAGTTCTACTTCTTTTATTTCTTGTG TTTTAGACACAGGGTCTGCTGTGTG
WI-10854a	102	C T ---	---	---	TTCCACAAAACCTTCCCTGGCGGGGTGACTAAGATGAGAACTGGGAGAACTGGATAGTTTAAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAAACA[C/T]GAAGACGATAGTTAACGCTGTTAGTT TATACGGTGTGCGAGGCAACAGGGAGAGGTACGGGAATAGTTCTACTTCTTTTATTTCTTGTG TTTTAGACACAGGGTCTGCTGTGTG

WI-9826b	127	G A ---	---	---	AATTTATATGTGAAGGGTTAGCAAACTATGGCCACAGGCCCAATTCAGCCATGCCATATTTTGTG TGCTGATGGCTGTTGGTGTGTTTGACACGAGTTGAGCCATTGTACAGAGGCTGTATG/AGCCTT CAAAGCCAAAAAATAATTTACTCTCGGCTTGACGGGAAAGTTTGCTGATCTAGATAATTTAAA GGCAGAGAAGATCAGAAGTGTGAA
WI-9826	125	A T ---	---	---	AATTTATATGTGAAGGGTTAGCAAACTATGGCCACAGGCCCAATTCAGCCATGCCATATTTTGTG TGCTGATGGCTGTTGGTGTGTTTGACACGAGTTGAGCCATTGTACAGAGGCTGTATG/AGCCTT AAAGCCAAAAAATAATTTACTCTCGGCTTGACGGGAAAGTTTGCTGATCTAGATAATTTAAA GCAGAGAAGATCAGAAGTGTGAA
WI-15986	60	T G G T G G T T T T	T T G T T T G T G T	T G A C A T T A T A T	CGGACACGTGTATACAAATACAGATCGTATGGGTTTGTGTTGGGTTTGTGTTGGGTTTGTGTTGGTAC ATTTCTTTTACGTTTATATAATGTCAGCATTTCAA
WI-8655	29	A G A G	A A C T G C A A A T	C C A C T G G G G C	TTCAAGTAACTGCAATAGGAAACCAGAG/AG/AGGGAGCCCCAGGTGGGACAAATCATGGCTACCCC TCCCCAACAGAACAGGGGAGGAGGTGGCCCCCTACACCCITTTAT
WI-8170b	259	G A ---	---	---	GCACTTCTCTCTGAGCAACAGGTACACTTTTTCTCTAACATTGATCTATAACACACCAGAACCCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTTGGTGAGAGATTTACAAGGTTAAGATCATGTGTCCTCAAAAGTGAATCTCATCAATCAGAA ATAAAGGTAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACACAAGA
WI-8170a	204	T A ---	C C T T A T T A A A	G A A G A G A A A T	GCACTTCTCTCTGAGCAACAGGTACACTTTTTCTCTAACATTGATCTATAACACACCAGAACCCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTTGGTGAGAGATTTACAAGGTTAAGATCATGTGTCCTCAAAAGTGAATCTCATCAATCAGAA A/T/A/AAAGGTAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACACA
WI-8172	136	C G G A C A	A T G T T T C T T	G T A A T A C C T G T	CAGGATTCCTTAAGTCATCTCCAATACTCCAGGTCAACATGGTGAAGAGTCACCTGTTAAACACGAA ATCTAACCATTAACAAGCTTTTAAATCCTTCGGTAACTCCTTTTATAAAATGTTTCTTGACAT A/C/G/AGTACCTTTACAGGTATTACATTTCTCTCACCGTTTACA
WI-8183	56	G A T G C	T G A A A T A A A A	T G T G T T G A A A T	AGCAGGGTTGAAATGATCCCTTATTTACATGAAATAAAAAACAATTTCTGTGCG/AG/AGCAGGTT TGATTTCAACACAGATTGAATCTGTAAAAACCAAGCTCGTTTCTGATGCAGGACAAATATCCACAAT ATTTAAACTGCAAGCACCATGC
WI-14149	83	C T ---	---	---	GCTTTATTGGGATTGCAAGCGTTACAAGGTTAAAGACAAAACCCCAAGCATGGGATTTTGCCCGAAAT ATTAGCGTTAAAGGAG/C/T/GAGTTGAGTCAACACAGGGG
WI-8712	44	G A G	C A C A G G G A A G	C A G A A G C C T G	TCAACAATGACACTGTGTAACAGCACAGGGGAAGAGGTAGTGGAG/G/AGATGGTCAGGCTTCCTG TTCTTAACCCAGAGAGCCCCAGCAACCTAGAGCGCCTCACCTAGCCCTTAAT

WI-8827	22 C T	TCCCTGGGAG C	GGGATTAGGAT TTTAGTGTTCAC	GGTGCCCTGGGAGACTATGG[C]/JAGTGAACACTAAATCCTAATCGCCATGCATTGGAAATTATT CCGACTATTACTTCTTAGTCTCTTCTTATCCACCAGCTTCT
WI-8833	51 A T	TCCTCCATGCC ATCTCTG	CCTCACACATT ATAGGGGCA	CTCCGGCCTCTTAAAGCTCTGTAGACTGTCTCTCCATGCCATTCTCTG[A]/JTGCCCTTATAATGT GTGAGGGIATTACATAAGTCCCTATTCAAAGTCCCTTGTCATAAAAGGTCAGCTATGT
WI-8377	63 A G	---	---	ATTTTATGCCATGTTGGTAAAGTTCAATTTTCAGTACATGGGTAACACCCAGGCCCTTCCC[A]/GJT TATATCCAGTATGCTACAAAGTCTTTTAACTCTTATCAGAAGTTATTAATTACTGTTTCTTAGAGAG GCTACAGGCTAAATTCAGTTAGTTGGTTGCTAATGTCTCATTATTTATCCTGAAGCTCGTG
WI-8850	21 A G	GGGACTTAAC CTTTGGCCT	CAACACAGCCA GGCAGG	GAGGGACTTAACCTTTGGCCT[A]/GJCTGCCTGGCTGTTGGCTCTGCGCTTGCTGTTTGGTTTCTT TCTCTTACTGGTCTTCTTTGCTTTGCCAGCCACCTATGCTGCTGT
WI-8853	79 C T	CCGGGGCATTG AGGATA	AGTCTTCTGA GCCTTCCAT	ACTTTCTTGAGCTGAGCAACCTCATCTCTTAGCTCTGGTTGATAACGCTGGTTAATCCCGGG CATTGAGGATA[C]/JATGGAAGGCTCAGGAAGACTTCAATCTCAA
WI-8865b	52 A G	---	---	AGGGTGAAGTGAATCACAGGCACAGACTGAGGAAGACAGTCAATGGTGAACAC[A]/GJACAAACATGCT TCGGACTTACCAAAGGAGAGTCGAGCTTCCATATAAA
WI-8865a	42 T C	CACAGACTGA GGAAGACAGT CA	GGTAAGTCCGA AGCATGTTG	AGGGTGAAGTGAATCACAGGCACAGACTGAGGAAGACAGTCAATGGTGAACAAACAAACATGCT TCGGACTTACCAAAGGAGAGTCGAGCTTCCATATAAA
WI-8895	32 A C	---	---	GTGCCACAAACCTGGACACCACCAACAGAAAT[A]/CJCTCCGCTCTTGGAAATTTCCATTAAAGAGCA CAATGGGGTAATTATACCAGGGATGCTCCAATCGCTCTTTC
WI-8456	93 G C	---	---	CCTTTAAAGTCACAGTCAACTCGACTGTGGACTGATATATTTTGAAATATAATAAACTCTTTTCC AAGGCTCCCATGCTTGGATGTCACA[G]/JTTATGTCAAGTTAATAATAACATTTCTAAGTCTCACTC TCAACTTCTGTGTTATCTTGCCATGGTCCAGTAACAGTTTACACGGCAGACCAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACCTCCCGTCTGCGTCTCAGTCACCCAC
WI-8496b	157 A G	---	---	TTTTCATCATCAAAAGTTTCTTTCCATAGAAGAAATGGTAATGTTGTATCATGATGCTATTTCTATGGAAA ATTTCATATCTCAAGTAAGTAACTAGCCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAAGTCA AAGACACAATGCTGCCAATGCA[A]/GJTATAGTATAGAAATAATACGCAGCTGTTAGAAAAAGTCT GTGGCCAAAGTGGGATAAAACAGTAGCAGTGCAC
WI-8496	41 G A	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGAAATGGTAATGTTGTATCATGATGCTATTTCTATGG AAAATTTCATATCTCAAGTAAGTAACTAGCCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAAG GTCAAAGACACAATGCTGCCAATGCAATTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAGTC TGTGGCCAAAGTGGGATAAAACAGTAGCAGTGCAC
WI-14153	28 A G	GTGCAGGAAG GCCAGC	AACGGCAGGA GGGGA	CTGCAGGTCTATGTGCAGGAAGGCCAGC[A]/JTCCTCTCTGCGCTTGTACCCACATCCACAGAGCA GOCCTAGTGCCAGGTGCAGCCACTGCCACCCACAGGCAACAGGACCCATGCTGTC

WI-12108	40	C T A T A	TGAAAAGGG TTAAACTCAA	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTATTACTTTCTGGAAAAGGGTTAACTCAAATATC[C/T]GAAATACTTTCATTATACCAGGT CAAGAAAATGCCACAGCCAGAAAATTTATTTTAA
WI-5989	29	G A C A G G C A	CCACAAAGGT CACAGGCA	GGGTATAACAG AACCGTATGTA CG	CAGGCAACGTCACAAAGGTCACAGGCA[G/A]CGTACATACGGTTCGTATACCCCATATATTAC CCCTTCATGTCCTAAAGAAGACATTTCTCTTAGAGATTTTCATTTAGTGTATCTTTAAAAAAAAT CTTGTGTTAACTTGCCTCCATCTTTTCTGGGTGAGGACACC
WI-12201	61	C T C T G C A T G	CCCACTGATCA CCTGCA	CCGACCACATA CCTGGC	ATAGCTTTTAGCCTTTTCTGGAGTGTATGTCCCAAGCCACCTGATCACCTGCATG[C/T]GCCA GGTATGGTGGTGGGGTGTGATGGACGTGGTTCAGCCCTCCACTGCTCGATAAAAGGC
WI-12018	31	A T T C T G A C T T	GGCAGGCAGC TCTGACTT	GGAGATGAC AGAAACAGAG AG	TTTTATCTGTCAGGCAAGCCTGACTT[A/T]CTCTCTGTTTCTGTCATCTCTCCCCACATACCA ACTTCTCACCATGATGATTATACCAATAATACAGTTCTTATATGAGGGCTCTGGAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57	A G C C T C	TGGCCTCGCTG CCTC	AGGGATCAAA GAGAAAAGGC	TTTTTCGTTTGTAAATGATCCGAATGCTTGAGAGAAGAACCTGGCTCGCTGCCTC[A/G]GOCCTTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAAGATGAGGTCCCAAATGAGAGCTACCAAGATGTAGTCG AGCGG
WI-15407	92	A G T T	CATGCCCTTTA AGGATTAAGT	TCCTTCTCTTT TGGTAGTGGG	AGCATGTAAAGGAGCAGTTTTATTGATTGGTATATTCAGGTTCTAACCCAGCTGAAAAATTCAAATA CATGCCCTTTAAGGATTAAGTTTAA[G/C]CCACACTACCAAAAAGAGAAATTTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109	T C A A T T	GTTGAGTATT GTTCTGCTCAT	GGGAAGTCTG GTACATATTGG	TCTGATGTCATTTATTGGCACAAAAATTATTCTGATACAACATGGTGTCTAGACATGGCTACACTTTA TACTTTGTGCATTTAGTTGAGTATTGTTCTGCTCATAATTT[C]CCCAATATGTACCAGACCTTCCC
WI-12326	25	G A C A	GACAGACTTC AAAAGCAATT	AGGTTTGAAAA TATGTATTAAAG TACTTTGT	CTGACAGACTTCAAAAAGCAATTCAC[G/A]CTTCCAGAATACAAAAGTACTTTAATACATATTTTCAAAC CTGTTTGCACTTCAAAACAAAGTTAGCGTTTGTAAATCAAATTTGATAACCCGACTAAAAAT
WI-12361	63	C T	---	---	TTAAATCCACACTGAAGATCTGGAGTATGGGGGGATATAGGAATTTGAGCATATGTATTAT[C/T] TGAACATAAATTTACAAAAGTGGAAACAGTTGGAAGGTACTTATAGGTAGACCTGAGGGTCTGTTAOC
WI-11305	87	C T A T C A C A C C A	CAGACACAGC ATCACACCA	GACCTCCCGT GGC	ATACTGGTTTAAATCCATGTCAAATGTAGTTTACAAAGGGAAGGACAAAGTACCTTTGTATAGAATAT ACAGACACAGCATCACACCA[C/T]AGGGCCCCACGGGAGGGTGGGGGAGACACACTTTTCCCTGGG AAAGG
WI-11321	67	A G T T T T	GGGAGGAAAA TCCAATAAAT	CATTGGGGAAT AGCTAAACCTT	ATTTTATATGAAGGTTTCTGGTGAATCTTTTAAGCAGGAGGAGGAAAAATCCAAATAAATTTTAA A/GAAGGTTTAGCTATTTCCCAATGCTATTTAATACAATGAGGTAGGACGTTAAGTCTTATCAGA CTGTGACTGGAGCCCCG
WI-11324	40	C G T G T G C C C C A	GGATAAATCA TGTGCCCA	ATCAAGCTTTG GGGCTCT	AGCATACTGCATCTCCTTTATGGATAAATCATGTGCCCA[C/G]AGAGCCCCAAAGCTTTGATGACAT TCGTAAAGTTACACAAATGATCTGAAGAAGTTATCTGTTCTGTC

WI-11352a	69	T C G	AGCACAGCAC ATAGTGGAAA	GACCTCTCGTA GGACACTTAGC	TGACACATGGTTCTGTTTCCAGAAGGAGAGAGAAGTCATCTACATAAGCACAGCACATAGTGGAA AGT/CJGCTAAGTGTCTACGAGAGGTCAGATCATATCCATAGAAAACAGCTCTCTTTTACTTGCA CACTTA
WI-11371	84	C T G	CAGCTGGAG ATTCTGATTCA	GCCCCGCCTGA GCAC	TTAGCCCATGCTGTTCATTGCAATCACCTGTGAAACCTATGAAACCTATACCTGCCAGGCTCAGCTT GGAGATTCTGATTGAGT/CJGCTGCTCAGCGGGGCTGGACATCCATGTTTGGGAAGAGTTGGCGCGGT GATTTCGATGCGTATAT
WI-11385	75	T C G T T T T	ACAGAAGACT TTCATATCTT	GATTCATATCT AGTCATGGTCA TATTTT	CTTAAAGCATTATAGTTGGCCTGATGGTGGACACAGAGACTTTCATATCTTGTTTTTTAAAGTC TCTTCAGT/CJAGGAAAAGCTACAGATTTAAAAATATGACCATGACTAGAAATAGAAATCAGC
WI-11388	88	C A A A G T T C	TGTTTGAAAT ACACGTAAC	TGCCTTGTATC CAAGTTAAAAT T	TCATGTGCCAGTTAGCTCAGTTGTTAGAGTGTGGAGCTATAAAAAATTAAGAATGAATGTTTG AAATTACACGTAACCTAAGTTC/CJATATAATTTTAACTTGGATACAAGGCATTGTTATGCTAAT
WI-11392	55	T G A T A A T A C	GGTATGTT CTTGAACCTTA	GTACATTCAG TGTTTTGTAAA AAG	TTCTATCATTTCCATTAAAAATGGCAGGTTATGTGTTCTTGAACCTTAAATAAATAC/T/GJCTTTTACA AAACACGTGAATGTACTTTCTTGTGAGAAGGGGAACACTGAGTCTCCGCTCTAGATCCATTAACTGT CATACTCTTCCCCAGA
WI-11396	52	A T T	TTTTGTTTTG AAATGGTGTTT	AGCTTATTTTC ATATTCACCCA TC	AAAGAATAAGATGGCATTTGTTTCAGTTAATTTTGTTTTGAATGGTGTTTTAT/GATGGGTGAATA TGAAAATAAGCTTACCTCATCCCACTCTAAAGGTAGTTGGTGATTTTGAACCGTTGTCAAT
WI-11441	100	C A C A G C	TCCCCACCAAC CAGC	TGCCAGGGCCT TATTTG	CTGTGAGTCTTTCCCAACTAAACCGTGAGTCCAGTATGTCTGGAGCAGCTGTGCTTGTCTTGGTG TATCCCACTTACTGAATCCCCACCAACCAGC/CJCAAAATAAGGCCCTGGCACAAAGTAAGCTCTCC ATTTTGTAGATGAAT
WI-11466	26	C T T T A T T T T G C A	TGAGAAGCCA TTTATTTTGGCA	GTTTATTTGTA TAAAAATGAC CTACAACCT	ACTTTGAGAAGCCCATTTATTTTGCAG/CJCTTCAGTCCAAAAAAGTCAACATTTTCAGAAATTTT TATATAAGTTGTAGGTCAATTTTATAACAATAAACTTCTATTATCTATTATCTCTCACATACATTT CATGTATCCCTG
WI-13364	35	A G ---	---	---	TTTTCTTTTGTGCTCTTTTATAGTAGAAGC/JGJGGAACAGTTGTCAATACTACCTTCTGTGG TCCCCGTAGACAACATACCTTTCTTTGAAATGTAAATGTCA
WI-11276	41	A G A G A G A C	GGCAGOCAGG AGCAGAC	TGTACTGAGGA GOOGGTG	AGGCAACACTGCTTTATTAGCCGGGAGCCAGGAGCAGAC/JGJACCCGGCTCCTCAGTACACATT CCCCACCCCTGCCCTGGTCTCCCCACTCAGGGCTGGCATGGAGGGGCGCAGCTAGGTCTGGAA
WI-12210	76	A G A	ACTGGGAAAA CAACTATTGC	TGCTAGTTTGC ATAATGTTTTCC	ATTGGAAACAACCTTAATAATTGTCATCTCTACATATAGAAAGCTGCTTTGAATAACTGGGAAAAACA CTATTGCAT/JGJGGAACAACATATGCAAACTAGCATCAATGCTCTAGA
WI-14186b	88	A G ---	---	---	AATGGTCTGGTTTTATTGAGAAGCTGTGGTCAATTTGATGGAAAGACACATACGGGTACAAAATTACA GGTGGTTAGTTTCAATACATG/JGJACAAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT

WI-14186a	52 C T A	GGTCATTGAT GGAAAGACAC	AATAAACCA CCTGTAATTT GTACC	AATGGTCGGTTTATTGAGAAGCTGTTGGTCATTTGATGGAAGACACATAC/C/TJGGTACAAAT ACAGGTGGTTTAGTTTCATTACATGATACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66 A G	GAGAACACTT GTGGGGCTT	GGACCTATCAG TCCATGTTGA	ATTTTGTGGCTATAGGTCAGTGGTTCTAAACCTTGAGCTTGCAAGAGAACACTTGTTGGGCTT[A/ GTTCAACATGGACTGATAGTCCACCCAGATTCTAAGTGGTAGGCTGGGGTG
WI-12345	37 C A	GTGGCAGGAA AAAGAGGAA	TTCAGAGGG TTCAGG	GGAAACAGACCTGATCCACGTGGCAGGAAAGAGGAA[C/A]CCTGAACCCCTCTGCAAGTATTCTCT TTCTGACCAGCTGGGCTTGGCACTTTGTGAGATTGCAAAA
WI-13416	71 C A	AAATTTTGG AAGTTTTCAG	AGTGTATTAG TTCAATGAATA ATTCAA	GAAAAGGCTGTAATTTTATTTCAAAATTTTGAAGTTTTCAGAAAAAATAAAATGACAAGAACA CATA[C/A]AAATATTGAAATTTATTCATTGAACCTATAACACTTAGCAGAGGAAGGACTTTTGAT
WI-12310	46 G A	TTATCCCAAG TATAATTTA	TGTTTAAATAT GTTTGGTGCT AAA	TTTGAAAAGATGCTGAATTTATCCCAAGTATAATTTTAAAAAGCT[G/A]TTTAGGACCCCAACATA TTTAAACATCTCTACACATACAGAAATTTTCAGTTTACAAATATCCAGAAGGCATTTTCTTAAGCAG T
WI-12086	72 C T	CCGGGAAAC TTGGATT	GGAGTCTCGG GTCTGG	GAACCGAGCTTATTGGAGCAAGAGTGTGGACACTGTTTACAAACAAACGTTTCCGGGAAACTTG GATTT[C/T]CAGACCCGAGACTCTCCAAAGTCTCAGTGTAGTAAGGTCAATTTGGGGGCAGA ACAGGAACATGCCTTAGCT
WI-11549	102 T G	GGCATAAAGT TCATAATATTC	GGAAAGTCTGT ACAAATCCCC	ATGTCTTCACAGGTTGATTTTGTGAAGAGTTTGTCTATCTATAATTTTATATTATTGGCATAAAGT TCATAATATCTTTTATGATCTTTTAAATATCTG[T/G]GGGATTTGTACAGACTTTTCCCTC
WI-11585	79 T C	TGGGTTTGCAA AAACAAAA	CCATGCTTCAC TGATACTCC	TTAGAAGGAAAGAAATAAACACGGTAATGGGAAATCAGTTCAGAGGTAGGAAGGAGCTGGGTT TGCAAAACAAAA[T/C]GGAAAGTATCAGTGAAGCATGGCCTAGAAATCCAAAGAGCAGGGGTAGAGT TT
WI-11604	68 G C	---	---	TTAGTTGGTTTCCCTGAAACTTTATGCTGTTTATTTTAAACCAATAGGATGTTCCAGTTACCAGCATTT G/C]AGAACTAGGGACTTTTCCATGAAAAATAATTAAGAGCTAAGGAATTCAGCGCTCACCATTTTTC TTGTACTCTGCAGTT
WI-11614c	108 C A	---	---	CAAAATCAAAAATTGAGGAGGCAAGAACAGAAAGTAAAAATCCAGAAAGACTCAGCTGCTTGAGGCAT GTTCCACCCCTGGACTTGCCAACCTTCACTGTGAAACTGCA[C/A]ATATTAAAGTATTCGTCAGCTAC GGACTTCGT
WI-11614a	60 A G	CCAGAAGACT CAGCTGCTTG	AGGGTGGGAAAC ATGCC	CAAAATCAAAAATTGAGGAGGCAAGAACAGAAAGTAAAAATCCAGAAAGACTCAGCTGCTTG[A/G]GG CATGTTCCACCCCTGGACTTGCCAACCTTCACTGTGAAACTGCAACATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11626b	83 T C	---	---	TTGATTTTACTAAGGCTTCCACTGGAACATGAAGGTAGGGATAAGTGTACAGGATAATATACCTCAG ATATTTTAAAAATAAA[T/C]TACTTAATAAAGAAATTAGCCATACCACATTTGTTCCATTTGCTAC AAGAACAAATTGGCAATGA

WI-11626a	39	G A G	TCCACTGGAA CATGAAGGTA	GTGGTATGGCT AATTTCTTATT ATTAAGT	TTGATTTTACTAAGGCTCTCCACTGGAACATGAAGGTAG[G/A]GATAAGTGTACAGGATAATATACT CAGATATTTTAAATAAAATTAACCTTAATAATAAGAAATAGCCATACCACATTTGCCATTTGGCTAG AAGAACAATTTGGCAATGA
WI-11627	23	T C	CCTTCCCTCC ATTGCTCTC	CATTTGCAACC CACTCAAG	ACCCCTTTCCCTCCATTGTCCCTC[G/C]CTTGAGATGGGTGCAATGGGAAGTAAAGCAAAAAGGG AGATGAGAAATAGTATGCTTTTGTCTGGCTTACTTCCATTCGCATGTCAAGTCCATCCATG
WI-11636	61	A G	GGACTTAAAA AGATCTGCTTA	AGAACTTTGCT AAATATTTTAT GTAACACT	TCAGAAATGTTGCAAGCAAACTACTATTGTAAGGTGGACTTAAAAAGATCTGCTTATCC[T/A]GJTA TATCCACATACTCTAGTGTACATAAAATATTAGCAAGTTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCCCTTTTGGTA
WI-11537	119	C G T	ATTGCTCATCT TACTCTGACCA	GACCCAGCAA AAAGAATGAT T	GTACCAATTTCTTATGGTGGCAATAAGCAAACTGTGAGTAAACGAGGGCAGCTGAATAAATTTACAG TATACAATATTAGAGAATATTATGTTGCAATTTGCTCATCTTACTCTGACCATC[G]JATAATCATTTCTT TTTGCTGGGTCCAGGACC
WI-11654	37	G C	GCCAAAGAC TATTCAGCAA	GGCTCTCCAG GACAGTTT	AGTAGAACATCAGTGCCAAAGACTATTACAGCAACTG[G/C]JAAACTGTCTGGGAGAGCCACTCCAG AGCTATTTCTAAGACTTCTGTGGTGTTCATACCTACTCAGAGTTTCACACTCATATTTTCATATTTT ATTTTGGGTGTTGGGT
WI-11656	28	G A A	ATTGATTTTAG AAGGAAGTGC	CAAGGCTTTGT CCTCAAGTAA	ACCTGATTTGATTTTAGAAGGAAGTCAAG[G/A]CTTTTACTTGAGGACAAAGCCTTGCCCTGCAGTTGTTT AAATGTCTGAAACAATCAGATTCCCAGCCTGGAT
WI-11680	55	T C	TTATCAGAGC AGGGGACAG	---	ACAGATACTTTTCCACGCAACATTTCTGAAATGAAAGCTTTGATTCCTCCCTTTT[G/C]JTGCCATAAA GGCTGGGAAGGTGGTTTGGCCAGACCGTACATCTTTT
WI-11696	47	T C	TTATCAGAGC AGGGGACAG	GGCATTAGAGA AGCCAACCTT	GTCCAAGAACAAAGATACTTTGACATCTTTATCAGACAGCAGGGGACAG[G/C]JAGGTTGGCTTCTCTA ATGCCCAACCATCTTGTGTTTTCAGAACTTTTCCACTTCGCC
WI-11702	69	C T	GAATAATACT GAAATAACCA	AGAACAACCTT AAGCAAATTTAT ACTGAAA	TTACATGTGGTCAATGGTGACATACCTTCAATAATTAAAAATCGAATAATACTGAAATAACCCACAGC AG[C/TT]TTCAGTATAATTGCTTAAGTTGTTCTAGAAAACACTGCTAATTTTGTTCCTGCAGA
WI-11706	60	C T	TGGCTGGAATT TTCTCTTCTT	ATCACCAGAG AACAAATTCCA	TGCTGATTCATCGCTTCTACCATCTGGCTGGAAATTTCTCTTCTTGTAACAATTTATTTGGCTG GAAITTTGTTCTTTGGTGAATTTGCTCCCTTTGCTGCT
WI-11709	105	T A	AGAAGCTTGC TTCAGTTTGC	TCATTTCTTCT AATTTTACGGG A	AATATCATCACTCATATCAGGCATGTTTATAAAAATGAGAGATTATGTCCTTTTTGGCATACTTCATC TTCTTCAGGACACAGAGAGAGCTTGTCTCAGTTTGC[T/A]GTCCCGTAAAAATTAGAGAAATGAAT GGCCAGATGGATGGAAAA
WI-11710	103	C A	GCACCTAGCCT CAGTCTTCA	GTGTGGAGGAG GGAGGAG	TTATTACCATCAACCTGTCCCCAGCTTTCCAGCAACAACAGCCACACTCTAGACACGCCCTTCAC TCCAGTCCATTTCTGGCACCTAGCCTCAGTCTTTCAG[C/A]CTCCCTCCCTCCTCCACACACTCCTTC

WI-11715b	123 C T	AGCT	AGGCTGGCTGC	TCCCATCCTG TGGCT	AGAATGGAGCTGTTGGGAGGGACATGCACACAATGTAAACACAGACAAAATGCAATACAACTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTC/TAAGCCAC AGGATGGGACTGGGGAAGA
WI-11715a	49 A C AAA	AAA	GCACACAATG TAAACAGAC	CATTACACCAC AGTTGTAATGC A	AGAAATGGAGCTGTTGGGAGGGACATGCACACAATGTAAACACAGACAAA/AC/ATGCAATACAACTG TGGTGAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCAGCCAC AGGATGGGACTGGGGAAGA
WI-11727	43 G C TCAACA	TCAACA	AACAATCCTT AAAACAACATA	CCTGTGGTTTG TGTTGCAG	CTGGATTTCTATACCTAACAAATCCTTAAACAACTATCAACA/G/C/CTGCAACACAAAACCCACAGGC AAATGAAAACACAGATGCCCCAGACAGCACCCACCCACACATGGCACACAC
WI-11728	16 C G ---	---	---	---	TTTTATTATCAAACTC/G/CAATTCATTTACAAATGTAAATATCATCAGCTCCCATCCACTTT CTCCCATCTCTATCTCTTTCCACCCCTACACTTTCTCTCCCTACAAACCCGGGTTCCAAA
WI-11758	61 A G TCGCTG	TCGCTG	ATCTGTGGTTT	TGATTGGCCT GTGGTCTA	TTTTCTCTTTTATTAAAGTCGCTATACCTAACTAGAAAGGAGAACTGTGGTTTTCGCCCTG/AG/ATAG ACCACAGGGCCAAITCACCACAGCTCTTGTAGAGAACATGGAGAGTGCCAAAGATCACCATCA
WI-11295	37 A G AATATAA	AATATAA	GCCTCACAAA GTAFTTTCTAA	AAAAGTGCTCA TCTGTGAACCTC T	CCGGCCTCACAAAGTATTTTCTAAATATAATTTGCT/AG/ATAGATTACAGATGAGCACTTTTCA CATTAGGTGATATGCAACAAATCACTATTGGCTCAGCAGGAAACAGACTTTT
WI-11773	93 T C ---	---	---	---	AGCATGATATTCGCTGGAGTTTCTGTGAGCTCAGCAACAGCAGAGTCAGAGATTAAAGAATT ATTATTGCCTCCTTTTTCCTCCCTC/CTGTGATTGTTAATAGGAGTCAAGGCCAAGTTA/C
WI-11282	42 C G GCAAGGAA	GCAAGGAA	GGCTCAGAGA	AAAACTCAGA CTGTAAATTTT GTGTG	CATGACAACCTCTTTTATTAAATGGGCTCAGAGAGCAAGGAA/C/G/ACACAAAATTTACAGTCTGA GTTTGGCGGCAGAGACCCCTCTCCACCTTTTCATGCCTGTGTGTACACACACACTGTCCAAAGCCTC AGA
WI-11790	28 A G AAACCTCTG	AAACCTCTG	CCCAACTTACC	CGGTAGGCGAG GCTAAGC	TAATTCACCCCAACTTACCAACCTCTGT/AG/CTTAGCCCTCGCTACCGTACACATGCTCAGAGCAC TTACATTAACTACAAATGGGCAAAATCATCTAACACAAAGC
WI-11879	61 C A AGTATACA	AGTATACA	TCATCTAATCT GTGAGGTATTT	GATAGTTGAAC CTCTTCACITTT ATAAAA	TTTTAATCCCAAAGCTTACAACCATCTTTTCATCTAATCTGTGAGGTATTTAGTATACAG/C/A/AGT GATTTCTCCTCTTTTATAAAGTGAAAGGTTCAACTATCCAGACAGTCCCATCTA
WI-12469b	91 C T AAGTTTAA	AAGTTTAA	GTTTTAATGT GGTATTAGAA	CAATTTTCAGA TTGTCTATAGC AAAC	TTTACTAATTTTCCATTTCCCTCTTTTATAGTTTTTAATGTGGTATTAGAAAAGTTTAAATTACAT ATGTGGCTTATATCTATTTCTA/C/TTTGACAGCACAGTCTTCAAGTTTGTCTATAGACAATCTGA AAATTGGGTTCTGAACT
WI-11906	52 A G ATCTGAA	ATCTGAA	TGTTATAACAT CAAGAAAGA	TAAATTTCTGC AGTTCCCTCA	ACATTTGAGTAGGAATGACTTTGTGTTATAACATCAAGAAAGAAATCTGAAT/AG/ATGAGGGAACTG CAGAAATTAACCTTCAGTCTAATTTCTCAGAATGCCAGAGTAAGATGAACCTTTACAG

WI-11909	78 A G	TTTGTTGGG TGGTCAAG	CCTCCTCTGAG ATTTTCTGAAT AG	GCAGTTCTCTGAAAGACAATGAGATTGTGGAGCATACTGAAGACTATTCTCTAAATGGCTATTTGTGTG GGTGTCAAG/A/GCTATTAGAAATCTCAGAGGAGGACAAATGATAGTCACTGCAGCCAGCTCG GACTGGCTTGCAGAGTC
WI-11806	60 T G	CATGAAGAGT GGGCAGTTCA	TCCTGTAAAGC CAATTTTATAT ACTAATAA	AAAAATACCATTTAGCATCAATTTGCCCAAGTTTGGCAGGCATGAAGAGTGGCAGTTCA/T/G/GTT TTATTAGTATATAAAATTTGGCTTTACAGGAAGCATTTATGG
WI-11946	31 C A	---	---	CCCTAGTGAATACAACCTTTGTCTCTGGAGAC/C/ACAGCTAGTCTAAGAAAACTTCTTAGGCTGAG CTCTCTTGGGAATCTAAGATAAAGAACTGAGATCCTTGGGAAGAGGGAA
WI-11965	65 T G	TGAAGATCAG ATCTCTGGTTT GATT	CAGCTGTGGTG AATGTTGAT	ACAAAAATCACAAGTACAACACTGCTTATTTCTTGCTTGAAGATCAGATCTCTGGTTTATTTAA/T/ GATCAACATTCACCACAGCTGAAGGAAATTAACITGAACCT
WI-11027	90 T A A	TGCCCTACTAC GCTTTTAAA A	TGAGGAAATGT GTTACAGTATT TTTATT	ACCTATTTTGAACCTGCAGAAAGGGCAGGACAAAACAAATCACTTCATAGATTTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAAAT/AJAATAAAATAGTGTAAACACATTTCTCATTTCTCTTACGA ATACCTTCTTTTGATATTGCAATTTCTATGGCATAACAGAGGCACCTCTCTCAATGCCCTG
WI-11049	95 C T	---	---	TTCTGCTGAAGATCACAAAACAATTTCAACCTCTGTGGTTCAAAATAAATTAAGGATCTTGTACCTTT GTGTTATTTTCTGTTTCAACTAAGGA/C/JAGACTTCAGAAGGCATAGCTTCCCTTGTAAACGTTTTT AAACATCTTTTCAITTTGAGGAAGGAACATTTCAAAAGCCCAA
WI-15488	69 C T	AAAAGGACAG CCAGATATCA AC	TTTCCATCTTA TTTCATTTCTG TAAC	CAACATTTATCAACATGGTAGGGAAAAAGTTCTCACTCTGCACATATAAAAAGGACAGCCAGATATCA AC/C/T/GTTACAGAAATGAATAAGATGGAAAATTTTAAACAAATTG
WI-13654	49 A G	AACAGTTAAT GAAACACATC CGT	GGCTGGTGAAA TGATGTCAT	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAACACATCCGT/A/G/GTATGACATCATTT CACCAGCCAGCTACTTCATGTGGCAGAAAAGGTAACTTTTCCCAATTTACAGACAAAACCCAGT
WI-11070b	135 C T	---	---	ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATAATGAAAAGGAGCTAGGACAATTTCTTGCTT TCAAGTAAAAATTTGACTGAGCAGAAAATCAGCCAGCTATCTTGGTGCAGAGAGGTACTCCAAAGTA C/C/T/GTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAAACAGAAAGGAA
WI-11070a	110 G T	CAGAAAATCA GCCAGTATCT T	TTGGAGTACCT CTCTGCACC	ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATAATGAAAAGGAGCTAGGACAATTTCTTGCTT TCAAGTAAAAATTTGACTGAGCAGAAAATCAGCCAGCTATCTTGGTGCAGAGAGGTACTCCAA GTACCGTGGGGTTCTGATGACTTCCACGGTCACTGGGATCCAAACAGAAAGGAA
WI-12020	121 T C	---	---	AATCTTTTATATTTCCAGCTGTGAGACAGTATTTTGAGGGCTGATGTTACCTCTAGCGGCGAAACC AGAGCCAGCTATTAAGCGAGCCAGAAAGCTACAGTAATTAATACATGACCATTT/C/C/CTCTTTTAGC ACGTTCTTTGTTCTCCTG

WI-11076b	142	G A	---	---	CATGGTCTGCCAGCTTACAGGAAGCATGGTGTGGCATCGGCTTATCTTCTTGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCATGTCACATACCCAGAGCAGGAGAGAG AAAGAGAG[G/A]AAGTGCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCAT
WI-11076a	106	T C	AGGCA	AAGGGGAGC	G TCTGCTCTGG GTATGTGAC GGTATTCAAA AATTAGTATGG GACA
WI-14263	49	T C	GGCATTCA	CGGAGAAAA	ACCTTTAAAGTTTCTCCCACTACTCCCGCAGAAAAAGGCATATTCAA[T/C]TGTGCCATACTAATT TTTGAATAACCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTTCTTTTGGCTACAAGTAACA AATTATTGCTGAATTAGGAAGGGAGCAT[C/T]GAAATGGGAAGGGGAGGTAGAGAAGACAGAG ATTTAAAGAAAGCAAGTACCATTTTCCAAGTATAAAACTCGTA
WI-14267	28	T C	---	CTTTTCATTT	GATTGTTTTATTCAATCTCGCTTTTCATTTTGTCTTTTAAATAGAACA[G/A]CTTTGATTTTAGTA TATGACATCATCATGAATTTTCTCTTACTTTGTATTTAGGCTCCACCTCAGTAGTTTGACAA AGTGAATGAGTTCA
WI-13892	50	G A	TAGAAC	TGCTTTTAAA	ACCTCTTCTGATGACACTGTACCTGTAAAGGGGTCTAGAGAGAAAGAGTAGTAGCTCTACTTTTGC TACAATTCAGGATGCAGGGCATGAGAGGATTCCTCTCTC[G/T]CCAAAGGAAAGAGCTTTTGGC AATAAATGGAAGAAGGAGTGAACAAAGTAATGAACAAACAGACCCAGATCAGAGGAAGAGATG GCTTCTGTGTAATTCTGGAGCA[G/C]ATTCAAGCAGCAATATTTACTGAACACTTGCTAIGTCTG
WI-13951b	88	G C	---	GGAGTGAACA	G AATAAATGGAAGAAGGAGTGAACAAAGTAATGAACAAAA[C/T]AGACCCAGATCAGAGGAAGAG ATGGCTTCTTGTTAATTCTGGAGCAGATTCAAGCAGCAAAATATTTACTGAACACTTGCTATGTGCTG
WI-13951a	39	C T	CAAAA	AAGTAATGAA	G GAGACCAAAAAAGGCTCTGCCCAT[G/A]ATTCCCGTCTCTCCCTCTGACTGACCCAGTGTTCTT ACAAATGAACATCCCTCAGCCCCATGGCATGGTGCATCCCTTCTCTTGGGATCTGTGAATATAACCA ACTGCTTGCTCAATGGC
WI-13264	25	G A	TTGCCAT	AAAAAGGCTC	TTATTTGTCATTAGCAAAAGGAAGTTAAATACTGATAGA[C/G]ATGCAAAATTTGTCTTTCATGCA TTTGTGAGCAAAGTACTAATCTGCTCACTGTCATTTCCCTCACAAGGAGTTGAGCCCTAGATGAC
WI-13960	39	A C	TGATAGA	AGCAAAAGGA	AACCTTTATTGTTTAGCTAGCCCCAGTGACTTTATGCATCTTATAACCAAGAGCCTTCAG[C/T]AG AGCAAGCTGAGCCAGGTTTTATCACACTTTGCTCAGGGTCCACCAGGAACCCAGGCTTGGCT
WI-15843	62	C T	CAG	ATCCTTAACC	

WI-13983	52 G A	TCCTCCCACT CCTTAAACCT	CAATACTCTCT TAGCCCACTGG	TTGTGTATCTGATTTCCGAAACATAGAAATCTCTCTCCCACTCTCTAAACCT[G/A]CCACTGGGCTAA GAGAGTATTGTACAGAAATATGCACTCACTGACTTAACAGAAATTAGAACATCCAGGCACCTCACTGAGA
WI-13850	51 A G TT	AATCTCAGGG TCACAGCTTTA	TGTTCCCTGAC AATGTTGTAA	CATGAATCTCAGGGTCACAGCTTTATTTATAGATTTTTTAACACACAGCCAT[G/G]TTACAAACATTGT CAGGGAACATTTACAAGAAATAAATAGATGGACTTGACGGGTGTAAGAAATTACACTTCA
WI-15295	27 G C A	TGTCAGTTTGA ATGTATTCTTG	TGAATAGTTGG CAAGGAAAA	AGATGTCAGTTTGAATGTATTCCTGAT[G/C]TTTCCCTTGCCAACTATTCAATTATTGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATCAAGAAAGGCCGCCGAAATATGAGTGAGACTCA
WI-14284	55 C T ---	CCGCTGCTATT CCCAGAT	---	ATTTCAACAAATCCAGAACAGGTTCTCACACITTTGAGCCCTTAGTGCAAAAACA[C/T]TATGCCAT GCGGGAATAAATGCTTATCCAGTGAGGCTCCCTGATGCAATTGA
WI-14288	85 G C	CCGCTGCTATT CCCAGAT	GGTCTCTCTC ACCAAACTCT	ATGACCAGACCAGAAAGCCCTGTTCTATATGAAGACAAACAGGTGCCATACTTTGGTGGAGGGGATA CCGCTGCTATTCCAGAT[G/C]AAGATTTGGTGGAGGAGACCATGACAGATGACAAACGG
WI-13522	33 C T	CCCACTAAT ACAAC	AAGTCAGTGGT TCTC	TTTATTTGTAGTTACCCCACTAATACAAC[C/T]GAGAACCACTGACTTCAATATTATGAGAG AAATTTACTCCAGGGAATTTTGACAGAGAATAATA
WI-13529	42 T C TTACCA	CACAAACATT TATTGAACAG	TCTATACACTT CTCACTCTCTT GCTT	AAATATGATTCCATCCACAACATTTATTGAACAGTTTACCAT[C/JAAGCAAGAGAGTGAGAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGCTCGAGGGGTTTATAGTCTAACAGGGGAACAACCTCTC A
WI-13859	84 G A ---	---	---	TTATTTGTCAGAAATTTCCAGAAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAAGTTTACTAC TTTGAAAAAGGAAACTAT[G/A]ACAAACAAGTATATATTGAGGAAAGGACTCCTAGAACTTGAGCA ACA
WI-13536	29 T C ---	---	---	TGAAAGGATACAGAAAAAATCAGCGAAG[T/C]GAAAAAGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCACCAGCTTCCAGTTGTCTCTCCAGTGCCATTACATGGAGTACACTTAATTTCTCAGCA
WI-13373	52 G A ---	---	---	TTTATTGTTTGGTAGAAAAACAGGCTCTTTAACACTGAATAAACATCTCAC[G/A]AACTGTGCTC CTAGATTACAAAAAGTCAAAACCAATTTCCCTTGACGCGGGCCCTTGAATCTGACATTTCAAGTCAC CGTAATAGAAACCAGAGCT
WI-13477b	61 A G ---	---	---	TTGGTTTTTAATACCTCTTGTGGATAAAAGGACATTGTTTTTCAATAGCTTGTCTTCAAA[G/G]GAC AGAGAAATAAGATAAAATTAACCTTAAAGAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCTCTCAGTT
WI-13477a	32 A G AAG	TTAATACCTCT TGTTGGATAA	GAAGACAAGC TAATGAAAAA CAATG	TTGGTTTTTAATACCTCTTGTGGATAAAAGG[G/G]CATTGTTTTTCAATAGCTTGTCTTCAAAAGAC AGAGAAATAAGATAAAATTAACCTTAAAGAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCTCTCAGTT

WI-14297	86 A T G	AATGTTGGGT ACTTTTCCAA	TGTGCACATTC AGAAACATTTT	CTGACITTTATTAGCATGCAATGCAATTTATTCTGGCAATAAATTAATATGTGCAGTTATAAAAAAT GTTGGGTACTTTTCCAAAG[A/T]AAAAATGTTTCTGAATGTGCACACTAGAATATATGCAGAAATCCTTTT AAACAGTCGACT
WI-12229	89 T G AAA	CATGTGCACA AAAAGAGTAA	ACATGTGAATT GTCCCAAAAA	TCCATGTAATATTCTCAACAGAGAACACTATCTTTAAATGAAGGATTACCATTAAGAAATCAACA TGTGCACAAAAAGAGTAAAAAT[T/G]ACCAAAAAATTAAGATTTTTGGGACAAATTCACATGTTG AAAAAT
WI-13582	43 C A	TGCAATCTAG AGACTGGGA	TCTGCGCAGTT AGATTCCA	AAGGCTGCCCTTACTGGACCAATGCAATCTAGAGACTGGGA[C/A]TGGAAATCAACTGCGCAGAG AAATCAAGACOGATGGTGAAATCTGGGCGAGCTTCAAAATTTCTGCCTCCTAAAAACATTTTCAG CCAAATTTTCATTATTGCC
WI-13857	28 A G ---	---	---	TCTGAGTTGATAAAATGCTTTTCTGAAC[A/G]TACATTTTAGGTATCTGGCACAAATTAACCAATGT CTGCCAATTTTGTGTAGCTTTTCATACAGTACAGATTTTCATTGATGTGCTGCCACATCTG
WI-15809	77 T G	TGTTTCTGT TGTAATGCC	TAAGTAGCTA ATTCAATGTTT GTAAA	GTTTAAAGTTCAGAGATGTGAATGGTTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTCTGTT GTAATGCC[T/G]TTTACAAACATTGAATTAGTACCTTAAGTATTGAAGAGCTTCCATT
WI-15801a	81 T G AA	CTAGTCCACT CTAGTGCAGT	AGAAAGATGG ATGGGATGC	TAAATCAGTCTGTGTCAAGAAAGAACAGGACTTGAATCAAGCTTCCAGCCCTCACCACCTATCAGCA TAGCAATTTTAAAGATCAGAGCTTTGTTTACATTTGTCTAAAAACCAAGAGAAAGAA[A/T]GGAATCA ACTCCACAGATCAACATGT
WI-15801b	123 A T ---	CATACTCCACT CTAGTGCAGT	---	TCCTTTATTCCAAAGATGGGAAGCGCATTTTCATTGGCTTGAATGAGAAAGCTTCATCTCCACTCTA GCTGCAGTAATAC[T/G]GCATCCCATCCACTCTCTCTCTCTTTTGTGACTGAAACTCTTCAAGAACT
WI-15801a	24 G A	TTTATTCCAAG AATGGGAAGC	TCATTCAAGCC AATGAAAATG	GCTGAATGTCCTCTCTC
WI-13763	59 T C	GGCTGGACACT GCAGTGAT	CCACACCTGC OCT	GCTCGTAATGAGACAGAACGCTACATCTGTTCAACACTGGGCTGGACACTGCAGTGAT[T/C]AGGG GCAGGTGTGGGCGAGGTGGGGCTCTGAGCCGAGGACAAATGTCCATGGCAGAGCTTCCAGAA
WI-13578	48 T A AACC	TCAATAAAGA GCAGAAAGAA	CAGTGTGAAG AACATCTTTT GTC	TTTTTTTTTGGTGAGTGTGTTGCTTCAATAAAGAGCAGAAAGAAACCC[T/A]AGACAAAAAGATGTT CTTACACACTGAGCTTTACACAGTCAACCAACATTGATATTTTGTCTTTTCCCGAGGGCAAAAAAGA GAGTCTCCCAAGAAACCTC
WI-13789	62 G A AGGGAG	TTGGATGGCTG	CAGTGGCTTC CTCTGTTT	TCCAAGGAAAAAGAAAGAAACCAATCAGTGAGAAAACTCAAGAAATTTGGATGGCTGAGGGAG[G/A] GAACAGAGGAAGCGCACTGGGGCTGGGACTGAATATGGACAGTGGATGGTAGGGTCCCTCACTCTCTT GAGGTCCCT
WI-13594	66 G A AAGC	TTTTTAACACA GATCACA AAA	CCTTGGCGCA GTACTTTT	AATAACAAGTTTAAAGTTCGAGCTGCAATGTTGGCAATGCAGGTTTTTAAACACAGATCACA AAAAGC[G/A]TGCAAAAAAGTACTGGCGCAAGGACAAAAATATGCTAAGAAATTAGGCCAAACAGCTGC

WI-15625	40	C T ---	---	GTCTCCCACTACTCCCGGAGAAAAAGGCATATTCAAC[CT]GTCCCATATAATTTTGAATAA CCTAACTCTCCCTTGTCTTACTAAGAGAGGTTCTTTTGGCTACAAGTAACA
WI-13367	84	C G A	CCACTGAA GACTCACAG CCCT	GTCTCACTTCTTGCTAGGCTGTAAATTTTCAGTTTAAACAAGTTCTTATGTGATTTGTGGCCACACT GAAGACTCACAGAA[CTG]AGGGTGGGTGGGAATACTTAATCAATATTTGTGGAATTTACCCGAT GAAATCCAGTTATTCCT
WI-13600	26	G T	TTAATGAGCC AAGCATCCAT	CTCACITTTAATGAGCCAAAGCATCCAT[GT]CCATCATCTAGTAACAATTTTCAATATGCACATTATAT TATACTGGAACAACAAGAAATACGGATTGTGTAGGGAAGAGCATAGAGGACCACCATCAGCAACCCCTCT TGATCCCTTCTCTACCC
WI-13602	89	G T	TCCATTCTGGA GACAACACA ATATTAAT	GATAGGAAAGAAGAATGAAGTCAATAGTCTTTAGCAAGCCAACTAGCTCAAGGAATAGACAGCCC CTTCCATTCTGGAGACAACACA[GT]AAATCTATTAATATTGAATTTGTCTGAGGTATGCACCT GCCC
WI-13650	76	A T	AAAGATTAC AATATTTCACT TTTAAAC	GCATTAAACATTTAAAAATCTGAGGGATATTGATGAGAACTATGATGAAAGATTCAACAATTTTCAC TTTTAAAC[AT]TAAAAACTACTCTTCATATCCTAGCCTGATGACTTAAAGTTACCCGG
WI-14319	83	C T A	CAATCAAGG CACAAAGCTA TG	TGTTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAAAGGAATAGCAATT CAAGGCACAAAGCTAAG[CT]ACATGCAACAATATAGATGATTTGGGGTGGACAGTACAGAATT
WI-13528	80	A G AAAA	CAATACATTT GCATTTTCTCTA AA	ATTGGATACATGCTTTTAAAAATGGTAGCTTTTAACTGTAACTCAATACATTTGCATTTTCCATAAA AAAGAAGACATTT[GT]TCAGAGAAAACTGGGTATCATGCGAGGAAAGCAGAAAAAATTT
WI-13909c	93	A T ---	---	ACTTAACTGGCTTATCTTCACGGTAATCTATTCTGTATTTCCAGTGAAGTTTCATCTTCCACACT CTCTTCAAACTCGAATATCTTTTCT[AT]GAGATGTCTAGCTAGTACCCACTGCAACATCTCTCAA
WI-13909b	80	G A C	TTCTCACACT CTCTTCAAACT CTC	ACTTAACTGGCTTATCTTCACGGTAATCTATTCTGTATTTCCAGTGAAGTTTCATCTTCCACACT CTCTTCAAACTC[GT]AATATCTTTTTCAGAGATGTCTAGCTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86	C A ---	---	TTTTTATTGAATCCAAATGTAGCAAAATCATTAAAACAAATTATAAAAGGGACAGAAAAATTAAG AATCAAACTCATCTGGAC[CT]ATGGGAACCTTGAAAAGGCATGGCAGTGGAGACCAGTAACATA
WI-14323a	78	T C ACATCA	ACAGAAAAAT TAAGAATCAA GTTCCCAT	TTTTTATTGAATCCAAATGTAGCAAAATCATTAAAACAAATTATAAAAGGGACAGAAAAATTAAG AATCAAACTCATCTGGACCATGGGAACCTTGAAAAGGCATGGCAGTGGAGACCAGTAACATA
WI-15389b	104	G A AAA	AGATAATGAA ACATCTGCGA TCCCACACTT	AAAATTGACAAATCAACTAGCTTGTCTTTTGTGCTTTTGGAGACTACCATATTCAAAATTTATTATGT AATACACTCATCCAGATAATGAAACATCTCGGAAA[GT]AAGTGGGAAATCACCTCATCTGTGC

WI-15389a	33	GA TC	AATCAACTAG CTTGCTTTTG	TTTGAATAATG GTAGTCTCCA AA	AAATTGACAAATCAACTAGCTTGCTTTTTC[G/A]TTTGGAAAGACTACCATTAATTCAAATTTATT ATGTAATACACTCATCCAGATAATGAAACATCTCGAAAGAAAGTGTGGAAATCACCTCATCTGTGTC
WI-15747	88	TC AGTGTT	TGCTTCATTT AAACTAAAT	CATAATTCACC AAAAGTTTCATA TAATTT	TGTAATCTGCTTACAGTCCCTTTGCAAGACAGACATATGTTTTGCATAAAGATATAAATTTGCTTCAT TTTAAACTAATTTAGTGTTT[C]TTTAAATATATGAACCTTTTGGTGAATATGAACCTGTACCAAAAC C
WI-13752b	117	CT ---		---	AAGAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTCGGATGAGTTCTCTCGTTAAGTGCTGGATATACCTGGCTTGAC[C/T]GGACACCTTTTACG GAGGATTCGGACAAC
WI-13752a	106	TC AGTGCTGA	CCTCTCGTTA	CCCTCCGTAAA AGGTGTCC	AAGAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTCGGATGAGTTCTCTCGTTAAGTGCTGGATATAC[C]TGGCTTGACCCGGACACCTTTTACG GAGGATTCGGACAAC
WI-14339	102	TG TTAG	CCCAATCAAA CAGTACATGA	TCCAGATTTCT GGAAACCG	AATCATTAAATGAATGTTCCAAACACACCCCTCACTGGGCTACAGGTAAATTTCACTGGGATGGAAG CAGATGAACCCACCCCAATCAACAGTACATGATTAC[T/G]CGGTTCCAGAAATCTGGATAC
WI-13744	115	CT T AAACTGAA	TGGTGCTGAAC	AATCAGGAAA GATAAGCACA GC	TGGATGGATGGATGAGGCCACCTGTGTTCAACAAAACACACGTAAATGGAACCTTCATGCAGCTTTAGAT TTCCCTTGCCAGCTAGGAGCTTGTTGTTGCTGAACAAAACCTGA[C/T]GCTGTGCTTATCTTTC CTGATTCT
WI-14061	68	CT ---		---	CCTTGACTATATTGTTTTTCCAAAATAGGACTATGTAGAGAGAGAGCCCGGTACATACCTTAT [C/T]AACCATTTCAATCCACCATTTGTAAAATCTCATCTTCTGGGCTGGATACCTCAAAAACAGAT
WI-15719	69	AC CATTACGC	ACCTTTTCATC CATTACGC	TGATACTTGGC AAGAGTTTTTAA ATT	TTACAGTTGGATTAACTACACACTGAATATACCTGAATTAACCTTCAACCCCTTTCATCCATTACG C[A/C]AATTTAAACTCTTGCCAAAGTATCATGAACCTACGAAGAGGAGATAAGAGATCTGATC
WI-13810	106	TC AACTT	CTCTAAATCG ATACATCCAA	GAACTGATGCT TGCTGCTAACT	TAATCCATCAATCTAAAATCACACATACATAGATCAAAACAGAAAGTACCACAGTATGCTTTATTTGCA GGTATTAAATGGTTCTCTAAATCGATACATCCAAAACCTT[C]AGTTAGCAGCAAGCATCAGTTCTTC
WI-15736a	27	GT CACA	ATTTATTACAC ATTAACCTTG	GTTCTTTGATA TGTTGCTTAGT TTT	GGATTTATTACATTAACCTTGACA[G/T]TAGCAAAAAAATCAAAACATAAAACATAAGCCACA TATCAAGAACAATATACAATAGAGATTGAAATTTCTCAATAGCATTTGGAAGGTATTTCCATAAATA
WI-13785d	72	GA ---		---	TCAAAACGTCACACTATAAAAGTGCTTTAAAATGCAGCAGCAGGAGATGTGAAGACACAAAATGAAC AAGTG[C/G]ATTAGTGACACATAGCTGTGCACAACACAGTG
WI-13785c	56	AC ---		---	TCAAACTGCACACTATAAAAGTGCTTTAAAATGCAGCAGCAGGAGATGTGAAGAC[A/C]CAAAATG AACAAAGTCGTAGTGACACATAGCTGTGCACAACACAGTG

-59-

WI-13785b	40 C G ---	---	---	TCAAAAGTGCACACTATAAAAGTGCCTTTAAATGCAGCAG[C/G]AGGAGATGTGAAGACACAAAATG AACAAAGTGCCTAGTGACACATAGCTGTGCACAAACACAGTG
WI-13785a	27 T C TGCTT	AAAAGTGCAC ACTATAAAAG	TGTTGTGACAG CTATGTGTAC T	TCAAAAGTGCACACTATAAAAGTGCCTTT[C/J]AAATGCAGCAGCAGGAGATGTGAAGACACAAAATG AACAAAGTGCCTAGTGACACATAGCTGTGCACAAACACAGTG
WI-13793	88 C G ATAGG	GGATTTTACAT TCAGCCTAGAT	GGCAGGAGGA TTTGTTACT	AGAAACCAAGTATATCATAGGCCAAATAAAAATAGTTTTACCCCAATTGATACAACATAAGGGATTT TACATTGAGCCTAGATATAGG[C/G]AGTAACAAATCCTCTGCCCAATAATCTATGACTTG
WI-13794	52 A G TTTCTTCTC	TTCTCACCCCT TTTCTTCTC	AGAATGGGCTC TTAACCTTGTA	TAGTCTCCTACAAATTCCTTCAATCCATTTTCTTCTCACCCCTTTTCTTCTC[A/G]TACAAGGTTAAGA GCCCATTTCTTCAACAAACAAAACACATAGAGCAAT
WI-15729	35 A G GTGTAGACTGC	CTTTGAACCAT GTGTAGACTGC	CTCAGCTTCTT TCTAAAGTGCC	TCATTTAAGTGCACCTTTGAACCATGTGTAGACTGC[J/G]GGGACCTTTAGAAAGAAAGCTGAGACTGAA AAGTCTGCTTGACTTCCAAGGAAGGTAAAGTCCCTGTTTGCAGCCCCGGGCTGCTCATTTGTTA
WI-13424	66 G A C	TGAGGTTTTTC ACGCTATTCTT	TTTTTCTCCCC AGGGTCTA	GTCCCTTGCACAAAGTCTCCCAACTGGTTTGGAGTTTCCCTTCTGAGGTTTTCACCCCTATTCTTC[G/A] JTAGACCCCTGGGGAGAAAACACATGTGTAAAGTGCTCAGGACATGAGGCGCCGTTTCAACAAGAT GCTGGCTAAGCGGCTTC
WI-14065	29 T C AATT	TCTTATAAAA GGTCAGAGGC	CAAGCTGAATC TGGGATCTC	AACTGTCTTATAAAAGGTCAGAGGCAATTT[C/G]AGATCCCAGATTCAGCTTGTCTCATAAAAAGAT TCAACTTCAAGTAGCACAATTTCTTGCTGCTTTTAAATCCTGAACATTTCTGAAGCACGAA
WI-13446	22 G C TCACTCATCA	GCCATGTTCTT TCACTCATCA	AAGGGAAATCA AAATCAGAAG G	TGCCATGTTCTTCACTCATCA[G/C]CCTTCTGATTTTGATTCCTTCTGCTCTGTAATTTTCTTC TTCCCTTTTGTAGGGCCTAGTCTGTTAGAAATTTCTGGTTTTTGAGAGTAGTGAGCCCTTTTACTTTTTT CTGACTGCCTAAT
WI-13725	56 A C TGGGTGOC	TGAGCACATA TGGGTGOC	CCTGCTGTCTC GGGC	TCACACAAAGGCATTTGGAAATGTCACCTTACACATGGTGAGCACATATGGGTGCC[J/C]GCCCGAG ACAGCAGGATAAGTTTCACAAAACCTTGACCAGGCAGGTTAGAGCAAGGCATGGTTCAAGGATG
WI-15702d	107 T C ---	---	---	CAAATGTTTTATGAAGAGACTCCGAAACAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCCCTGTAAACAAATCTAAAT[C/J]GGGTTCTTTGAACAAATAGTTT TGA
WI-15702c	101 T C ---	---	---	CAAATGTTTTATGAAGAGACTCCGAAACAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAACT[C/J]CTGTAAACAAATACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702b	90 C T ---	---	---	CAAATGTTTTATGAAGAGACTCCGAAACAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAACT[C/J]CTGTAAACAAATACTAATGGGTTCTTTGAACAAATAGTTT TGA

WI-15702a	48 G C A A A G	A A C A A A A T A A A G C T T T C A A	C C T C A C C C C T T T A C C C C	C A A A T G T T T A T G A A G A G A C T C C G A A C A A A A T A A A G G C T T T C A A A A A G [G/C] G G G T A A A G G G G T G A G G A A A G C A T G T G A G A A A C T G T A A C C C T G T A A C A A T A C T A A T G G G T C T T T G A A C A A A T A G T T T T G A
WI-13831b	113 T C ---	---	---	T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A G C G A A G G T G A C T T G G A A A A [G/C] G A G A T T C A A C T T C C A C T G A T C C T C G G G T A A G T T T C C T C T C T C T G T A G A T [C] G T C T C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13831a	56 G C ---	---	---	T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A G C G A A G G T G A C T T G G A A A A [G/C] G A G A T T C A C A T A C T C C A C T G A T C C T C G G G T A A G T T T C C T C T C T C T G T A G A T G T C C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13806	62 G A ---	---	---	T G A T T G A G C T T A G A A A G G A G T C A T G T T G A A T C A G A G A G G C C A A A A C T A G G C C T C A G G T [G/A] C C C A T T A A G C A T G C T G T G A A T G C A A A G G A A A G C T T A A A A A A T T T T T A A G G G T G A C T C C A G T A A A C A T
WI-14372	86 A G ---	---	---	C A C A T T T C A G C A A A C A A A T C G A G G T G C A A A C A G G G T T A T T T C A C A T T A A T A T A T A A C T G G A T T T T T T G C A A A T A A A T A G G G A [A/G] T T C T C T T T A A A T A A C C A T C C T C A C T T C A T G G C C A G T
WI-14373	95 A G ---	---	---	A G G C T G T T T T T G A G G C C T G A G G C C C C A C A C A T G A C A C G T A A G A C T G T A A C C A T G G T C A T G T A G T T A T G A G C T A G G A A C C C T G G A C G A A A C C A [A/G] C A C A T A T A C A A T C A T C T C C A C C T C C C A A C G C C T T T A C T T T C A C A G C C T C T G C A
WI-14078	61 C T G C A A G	A A A G A A G T A A A T T A G G A A G A	T G T G T G C A T G T C T C T T A C T G C	A G A A C C G A G A A C T C A A A G A A C C A C A T G G T G T A T C A A A A G T A A A T T A G G A A G A C A A G A [C/T] G C A G T A A G A G A C A T G C A C A C A A A T C G A A C A A G G G C A T G G A G G A A G G A C T T T A G A T G G T C A C G
WI-14083	47 C T A C A C T	A G A C T T G A G A G C T T A A A A C A A C A C T	G C C T A C T G G A C C T C T A A A C T A C T G A	T T G C T A C A T A A C A C A T T A C T C C A G A C T T G A G A G C T T A A A A C A A C A C T [C/T] A T T T G T T A T T T C A C A G C T C A G T A G T T A G A G G T C C A G T A G G C T T G G C T G A G T T G T T G C T T A A G G T C T T A C A A G G C C A A
WI-14085	31 A G A G A A A A	C A T T T A T T T C A T G T G T A A G A A G A A A A A	C A G T C A T G T T C A C G T G C T A G T T	T G C A T T T A T T T C A T G T G T A A G A A A A A A C [A/G] T A A C T A G C A C G T G A A C A T G A C T G C A T C G A T A C A C G G C T C A G C A C G A G G C T A A A G T C A G A A G T G A G T G A A A A C A A A A T A G C A T G T T G A T T T A A G T G A A A T A A C A G A A C A G G A G G C C T T
WI-12169	121 G C T T G C T T	A A T A A A A C T T C C T A T T T C T T T T G C T T	G G G T T C T G A G G T G A A A G A A A A A	G T C A A A G G T T G C A A A T T T A T T T C C A C T T A T C A A G A A C T T A C A A A A T A T T T T G T T T C A T T T C T A A A T T T T C A C C T T T A T T G C T A G T T A T A A A T A A A A C T C C T A T T T C T T T T G C T T [G/C] J T T T T T C T T T C A C C T C A G A A C C C C C T T A
WI-15705	50 A G A T C	G G A G G G A G A T T T T A G A C T G A	A G C T G T A G T C G T C A A A T A C T C T A G A A	T T G T T T T A T T T G G G G A G A T G A A G A G G A G G A G A T T T T A G A C T G A A T C [A/G] T T C T A G A G A T T T T G A C G A C T A C A G C T C C T C T C T T T G T A C T A C G G A G A C C C T G C T T A T A G C C C C A A C A G A A A T C C T C A T C T G C G T T G C C A G A C A G

WI-14379	102 C T	TCTATTAACA GGGTATGTCA CACC	ATCATCTGTT TGAGGTGACA ---	TTTATGCTGTTGTTTCTACTGGTGGTCTGGCTCACTAATATCAATCCTAGTAGTATTTCTTT TACTTGGTCTATTACAGGGTTATGTCACACC[C/T]GTCAACCTCAAAACAGATGATACT TAAATAAAACAAGCAGAAA[C/A]CCACCAATTAAACAAGAGGACACTGCAGAGGCTTATGTACA ACACGTGTCGCGAGGCTGGCGCAGGACTGCCACTCACTCCAAAATTTCTTGGAGCAGAG
WI-14102	22 C A ---	CGCAGAGCTG CTGTATTTAAA	GCAGAGATCCA GACGCTTGT	ACCGCAGAGCTGCTGTATTTAAA[A/G]JACAAGCGTCTGGATCTCTGCAGGGCTGGGACCAGCTGC AGTGGGGCTCCGGCACTGCTCTCTCCAGGACTCTTCCACACCCCC
WI-15937	24 A G A	AAACTGAAAC GTATTTCTCTC	GGCCTTTAAGT TTCTACGGTG	TGAAACTGAAACGTATTTCTCTCA[A/C]JACACCGTAGAAACTTAAAGGCCGCAAAAGACTCACACCC ACCACCTAGCGCGGAAAAAGGAAGTTTCAGGTGATACAAGATGTCCTGCCATCACACCTGAAGGAT GGTT
WI-15944	24 A C A			ATGTTTATGATCAATTCAAACATACAGTACAGGGAAGGTGAATGAGTAAGAAAAAATCAT ATTTAAGTCCCCGTTAACACTAAGCC[A/G]TATTATTCAAATGTGTTTCAAATACTCAGCCAGAT CACCAAAGCTCAGTCACTAC
WI-14124	92 A G ---		---	GACAAAGAGGCGAGTTTCTGTAGTTCACAGAGGGCCAGAGCAGTTATCAGAACGGTGGTTGACCT GCATAGATTTTGTGACGACT[A/C]TGTGGCCATGCCATTCTGTAAAGTGAAATTAATGAACA
WI-14125	88 C T	GGTTGACCTG CATAGATTTT	GGAATGGCATG GOCAC	GTTTATTTCTCACAGTTCTGGAGGTTAGAAGCTGAGATGAGGATATCACAGCATGGTTAGGTTCT GGTGAGGACTCTCTGGCTTACAGCTGGCTGCTTTCTCACCATGTCTTCACAT[G/A]GCCCAAAGAGAC AGAACAAAGCTCTCTGGT
WI-14136	120 G A	ATGTCTTCACA	CAGTATGTACA GTGACATAACA	TTGTTGTTGGCACCAGAAAAGCT[C/T]ATGTTCTATGTATTGTCACCTGTACATACTGTAAACAAGACT GCATTAAATATGTTTCTTATGATTGTTTCAATG
WI-14138	23 C T	TGTTGGCACCA GAAAAGCT	TAGAACCA	GGCAGGTTTATTCATAATTTCAAACITGGAAGCAACCAAGATGTCCTTCAGTAGTAGTATTTCA GACAAATC[G/A]AATATTACTTAGCACTAAAGAAATGAGCTATCAAGTCATGAAAAGACATGCAGG AACCTTAAATGGATATTACT
WI-13551	74 G A	GACAAATC	TAATATT	TTTTTTAAGAGTGCTCTCACATCATTTATATTGATTGCACAAAACCTTTTTTAACCTC[C/T]GTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCCAGTGTCTTTTGAGATAGAAGCCTTCTTCAGAAATCA CCTOCC
WI-15953b	59 C T ---		---	TTTTTTAAGAGTGCTCTCACATCAT[T/G]TATTGTTATTCACACAAAACCTTTTTTAACCTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCCAGTGTCTTTTGAGATAGAAGCCTTCTTCAGAAATCA CCTOCC
WI-15953a	26 T G A T	TTTTAAGAGTG TCCTTCACATC	TCATCTGTTCT TGTTGTTTTTG A	TTTTTTAAGAGTGCTCTCACATCAT[T/G]TATTGTTATTCACACAAAACCTTTTTTAACCTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCCAGTGTCTTTTGAGATAGAAGCCTTCTTCAGAAATCA CCTOCC

WI-14631	82 G A ---	---	---	TGAATCAATGGACAGTTTGGCTCTGTTTAGTGAAACCCCTCACAAGCACCTCTGCATAGTCCGCTTT CTGTCTCTTTAAAC[G/A]TGCCCTGGTCCCTCTGCCAAACCTTTTAGGATTGGGCTCCTCAGGGGCTT GTCCTGA
WI-6053	24 A G ---	---	---	ATCACCCCGTGTCTAAGAACAAAC[G/A]GTCCTCATGTCCAACTCATATCCCGGGAGCTTTGTCAACTG CAGTACACTTCTCGCATTAACCTGGCTTCTGGAGGAAGCCTCCTAGAGGCCAGGTAAGGGGGTGC AGCAGTGAGGGGTATATCTGGCTGGCCAGTTGGAACCCAGGAG
WI-15964	99 T A CTGGAGGTA	GACTTCTCCAC OCTCTTGC	---	CAGAAACCTCTTCTGTGTTAAGCTGATGCTAAAGTCAGAGCAGTCCAAAGGCAGGAGGCTGCCTT GGGAGGTAGTAAGCTCTCTGCTCCCTGGAGGTA[T/A]GCAAGAGGGTGGAGAGTCTTGGCAAG
WI-12075	103 G A GGCAC	AGCAGCTGGG TCTTCTTC	---	CAGCTAAAGGATCACTGCAGCTAAATACAGATAGAGAAAGCAACAAAGCCAGGCAAAATACCCATCAG AGACAGTGACAAGAGCAGCTGGGGCACGGGGAGGC[G/A]GAAGGAAGAGAAAGAGGGGAGGAG OCT
WI-12179	96 G A TGGAGGTCA	TCGAAATGACCC TGTAAGTGC	---	TAATTTAAACACGCCCTTCCCACATAGTGGTGAGGCATCTGCACATTTCTCTAGAAGGACATGA ATAGTGATGTGGAGGTACGGTGGAGGTCA[G/A]GCACTCTACAGGGTCACTCGAGGAGGAACAG
WI-14651	49 C G ATTGT	CAAGAATCAT TCATTTTCTGA CTTATTT	---	CACAAATAGTGAAATTTATCTGAGCAAGAATCATTTCAATTTAAATTTGTC[G/A]AAATAAGTCAGAA AAAGATCAATATCTCCCTGCTTCAAAATGACACTCCCAATTTTACAGGTAACTGTTA
WI-14666	105 T A ---	---	---	AATGTGGACTTCAACAAGGGTTTAAACCTAATCTAATAACAACCTCTACAACACATTTCCAGAGCAT TATAACAAGAATTATTTACAGGCAGCTAATGTATTAAAT[A/A]AACCATGAAAAGAAAACCTTG
WI-13473	31 C T ---	---	---	ATCTAGATGTCAGCAATGGCTGAGACTGTC/TGTGCTGGTAGAGTGTGTTGTATGTTTCTAC TCTATTACAAAATTAACAGAAATATGGCTTCGCTTTTGCAATGTTTATATACAGTC
WI-13967	103 A C AAATAAAAA	AAAAGACTAC AGATACAAAG TG	TTGTGTTTCA TCTCCTAAAAG	AAATTAATAGCAGCTCTGTGTGTGATTTTAAAGAACAAAGATAAAATAIGTCATTCAGCAGTCATTT AAAAAATAAAGACTACAGATACAAGGAAATAAAA[A/C]ACTTTTAGGAGATGAAAACACAAA
WI-14408	60 T A G	GCAGACACAC TATTACAGGCT	TTAATTGTGTA AAACTCATTTG TTACTTT	TTAATATTTAGCAAAAGTTATTGCAACAGGTTGAAAATGCAGACACACTATTACAGGCTG[T/A]AA GTAACAAATGAGTTTACACAATTAATAATTAACACATACTTATGGGATTTGTTGAATGA
WI-13683	47 C G ---	---	---	TTTTGTGTTAAGAACAGCATTTTGAAAATAAAACCTATCTGCCCATG[C/G]TTTACAGCCTTTTAAAT TTGTAATATTTATAGTCGTTTATGGTACATATTGATTGTC
WI-13910b	63 C T CGTCT	CACCATGGCA CAC	CATTGAGATAA AGCACACTTAT	TTAGAAAACCTGATAAAAGCAACAACTTTTGGGAAAGCACCATGGCAGCTCCTTTGTGCTA[C/T] GTGATAAGTGTCTTTATCTCAATGAAGCAACCCCA
WI-14635	22 G A ---	---	---	ACATGGCAGATACAGAGCTG[C/G]ATCTTGAAGACCACTGACCAGGAAATGCCACTTTTACAA AATCATCCCCCTTTTCATGATTGGAACAGTTTCTGACCGTCTGGGAGCGTTGAAGGGGTGACCCAGC ACATTTGCACATGCAAAA

WI-16002	59	T C	GATAACATAA AATGATCATG AGAATTTC	GCCATCTCCTC TTTGACTTTT	CCAACATTTTAAACCCTATGACTGGTCATTGATAACATAAAATGATCATGAGAAATTTCA[T/C]GTTA AAAGTCAAAGAGGAGATGGCTAATGCAIGCTGGGCT
WI-15361b	101	A G A	CCCACTTGAAC TCAAGTCATC	AAACTAAAC CTTTGTGCTA AAA	GTGGAATTTTATTAAAGCCATCAAAATTTCTTCACACTCAATACTGTTGAACAACAAGATAACACAT CTTCTTGCTCATCCCACTTGAACCTCAAGTCATCA[A/G]TTTAGGCACAAGGTTTGTAGTTTCTCGG GAAATCAAGTTTAAACCA
WI-14759	73	T C	GGGTTTGACTT GTGGG	TCCCACACTGC OCCC	TGAGTTACAACAATGAGCAACAAGTTAGAAAAATGGTTTTTATTCAAACCTCCTAGCGTTTGACTT GTGCGG[T/C]GTACTCAATGGGGGCGAGTGTGGACGGGAGGATTGCAACCCAGAGTTTCATACTG CAA
WI-12535	50	A T T A T	CTAGGAGGGTT GAGGTGTAGA	GCTCCACGAGA AGAGAGGAA	TCCTAACATTTATTCAGGTGGTACTAGGAGGGTTGAGGTGTAGATAT[A/T]CTTCTCTCTCTC GTGAGCCTTACTGAAGACAGGATGCCGTTCTTGTGTTTATCAGCTGAGAAGGGCAGTCTCGCCATC TTAAAGACCTGCCCTCC
WI-13805a	112	G A	AAAGGCACAC GGGAA	CTCAGCCTGOC TTGACC	TTCCATTCAATTATGCTTGGCTTTACCAATTTTATAGCTATTGGGAGGCAGGAAAGGAAATTGTGGC CCAGAAACCATGAGATTTGGGTGAGAAAAAGGCACACGGGAA[G/A]GGGTCAAGGCAGCTGAG AGTCACATTTCCAGACCTC
WI-12340	18	T C	---	---	ACACAATAAATCCATT[T/C]CGAGTGATTAAAAACCTATTGTTGTTTAGAACCAAAACAAACTAC AAGAAACATTTTCAAAACCTTTTTTTTCAGGCTGA
WI-14808	52	T A	ACCCACCACA CTACCCTGT	GAGGCATCACA ATGTTAAGATT TT	CTTTGAAACACTTTAAGCAACAGTTAAAAAGTACCCACCACACTACCCTGT[T/A]AAAACTCTTAAC ATTGTGATGCCTCTGCATCAATTTTAGAAAAACAAGAAAAACAACAACCTGAAGGCCCATGTA AGTTAAAAAAATCGAGTCAGCATTTATTT[A/T]AAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAAATGCATTTATTTTGTATCCCAAGCCCTGAAACATGAAAAAATATTTACTAAAGGAATGTTG ATTACCAAGCTACGACTTC
WI-14816	29	A T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG[G/T]TAGGTGATTGATACAAATACGATCCATAA
12542c	71	G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC AT[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-12542b	70	G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC AT[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-12542a	45	C T	GCTATTAGGC AAACTGAACA TTTAAA	TCTAGAGCCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATG[T/C]TATCCATGTGAGGGCTCTAG ATCATGGTAGGTGATTGATACAAATACGATCCATAA
WI-12173	57	C T	GGATACAGCA GTAAAGAATA CAAAA	CCACCTCTAGA ATGATGCTCT ATAA	CACCTAAATCATCTAGAAACTGGGGATACAGCAGTAAAGAATACAAAAATCCTG[C/T]CTTATA GAGCATACATCTAGAGGIGGGAAAGAGGCAATAAATA

WI-14836	28 T C ---			TC TTG GAG GGA TAG AGG ACAG AGT GTT C/GTT GAT TTT CG TTT CGG TTT CAG TTT GGT TGT CATT GG TTT TGT TTT TGT AAT TTT GCC CAC CCT AT AAA AAG CAG TGC CAC CCG AGG CAG
WI-14856	60 A T AA		TGG TGACACG GAAAATACTT	ACATTCC TTAGATAGCAACAAC TAAATATGATGGATGGTGACACGGAAAA TACTTAATATATTA AGTTGTAA AAGTAGCAAAACAAAAT TGGATATACTATAAGTGATAGGATGATATGAAAAA GGCTATAAAAAGCTCCAAAA
WI-14863	61 G A ---			ATGGCAATTTACTTTATAGCAATGAACAATATTTGTCAAAGGGCAAAATATTTTGTCTG[G/A]AG TTAATAAAGTTAATATCTTTTACCACAAAGCTAGAGGTCAACAGTACCAC TATTATTGATTGCCACT ACCTGGC
WI-14867	46 T C A		GACATTCCAA GGCTCTCTAAC	TTTTAATTAACGTAA AAGGACAGACATTTCCAAGGCTCTCTAACA TTTTGGTGTCTGCAGCCCCA TTGGCTTTGAGATGTGAATGTGTTAACCCAGGGTGA
WI-14733	98 G A A		CCAAATTGAC AGATATTCTGC	ACGGAGTCGTCTCTGATGATTTCTTTGTCAA AAAAATGTTTGCCTGATTCTTAATCATGAAAGAACAAATT AGAAAAAATCCAAAATTGACAGATATTTCTGCA[G/A]AATAAATGGCCTGACCTCATCAAAAAACATCA ATGTCATGAAAAACACAAAA
WI-14898b	79 A C ---			TTTTGACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCATAGAAGTGTGCCACTAAGGAAA ACTTCTCCATG/AAGCTGCCTGCTGTGCACGTTGCCCTGGGCTTTGCTAACCCCTGGTGTGCATCT GCCTGTGTTCTGCTT
WI-14898a	50 A C CA		CATGTACAGG AAGAGTTGTCTT	TTTTGACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCATATCAGGTGCCACTAAGG AAAAC TTTCTCCATAAAGCTGCCTGCTGTGCACGTTGCCCTGGGCTTTGCTAACCCCTGGTGTGCATC TGCTGTGTTCTGCTT
WI-14907	48 G A GGACTCTGAC		GGCACACATT GGACTCTGAC	TGGTATTTATTTCCGACATTACTGTAGAGGCACACATTGGACTCTGAC[G/A]ATTCCCTTGCAGCAG ACATTTGTGAAGCTGCTGGTGGCACACACCCATCAATCAGTGACTCCTGCAC TGCAGAGGGGCCACATG CACGATGCTCACGTGTG
WI-14911	52 G A C		CCAATACATT CAGTTCCTGGT	CTAGAACTCTGGGAAGTCCAAGCTCAGTGCACCAATACATTTCAGTTCTCTGGT[G/A]AAGGTCTTTTC CTGGTTTGCAGACAGATACCTTGTCTGTATCTCTCACATGGCAGAGAAAGAGGAAAGTAATCT
WI-14913	88 C A ---			CTGATGCTTTGACATCTGGGGCATTGCTGTCTCTAGAGAGACTACTTCTCTGGGACAGCAATTC TAGTGATAGTAGAGGACTCA[C/A]CCTGCACGTGCACCTTTTCATATACAGATCAACCAATCCAAAC CTACACCTCCAACCACT
WI-14914	66 G C A		CTGGACACAG TTTTCTCTAGC	ATTTCCTTGATTTGGCTGTCTGTAAGCCTGTGAAGTCATGCACATCTGGACACAGTTTCTCTAGCA[G/ C]GAATTTATTTGCTCTGGGCTTGTGATGGCTTTTCACAGC
WI-14926	49 T C ---			GTTTATTTCAAATGACACATCCAGATTGAAATGGGCACCTAGCGAA TTTCTCTGTTGGACCACA AGACTGTCTGAGAACATGTTCAAAGACAGTTTTCAAAATAAAAATTTTCTTAATCAGGTCCA

WI-16083	89	C T	ATGTTTAAACA CAAACATATC AAGGAT	TGGAAAGATT CCAGCCC	GCATCTTTATTACCAGAAACTCATTTAIGTCCTTAATCATGTTTAAATATAATATAAGCATGTT TAACACAAACATATCAAGGATC/TJGGGCTGGAATCTTTTCCATCTATAGAAAAGCACAACCATC CATTAAGGCAG
WI-14930	55	C T	GGAGGAGTCC CTCATGGAT	CACAACCAACC AATACCGC	CAGTCTGTGTTCTGGAACAGCTCTCCTTTCCACAGGAGGAGTCCCTCATGGATC/TJGGCGTATTG GTTGGTTGGTGATTGGGGAGCACGAGGGAGAGCAA
WI-14946	47	T C	---	---	TCAATACTGAAGGTGTCAAAGTGGTCTATTTGCCCCAGACATAACA/TJCTCTAAATCATCCTCTTA GATCAGGGAGTCATAAGGACCATTAAGGCTCATTAACACAGACTCTTTATGGAAGGATT
WI-15987b	80	A G	---	---	ACATTAACACAGCACAAATTAAGGGGTCCCAACGAGGTTGGTAGTGCCCTCCACTATGTGAGGACAC TAAGAAGATGGTC/TJCTATGAACCAAGCTGCCGGTGCCATGCTCTTAACCTCTCAGC
WI-15987a	32	C T	CACAAATTAA GGGTCCCA	GGAAGGCACTA CCAACCTC	ACATTAACACAGCACAAATTAAGGGGTCCCA/TJGAGGTTGGTAGTGCCCTCCACTATGTGAGGA CACTAAGAAGATGGTCACTATGAACCAAGCTGCCGGTGCCATGCTCTTAACCTCTCAGC
WI-14948	56	T C G	AGGGAACCTG CTAATTGTCA	GATGATCTTAC ATCAGTTGTTG GA	GAATAAAGTCTTATTGCCGTTCTTCAGGGGAACAGGGAAACTGCTAACTTGTGAG/TJCTCCAACA ACTGATGTAAGATCATCTCTGACCATAGCGAACCTGTAAAGGCTTGCTGTTCCCTCCAGCTGA
WI-16100	52	A G	TTGA	ATATTAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAGCTATTTTCTACACTTGAC/TJGTAATATACTG TTTTCTGACATCTCTTATCAACTCCTCTGAAAATC
WI-14958	83	A G	CAAGGG	TTGGGTTTT	GTGATTGATCTGTAATTATTGGGATTATTTATCAACTCTAAAATTCGAAGATGAAAATAATTTATCT CTTCTTTCAAGGG/TJGAAAAAACCCAAATGAATGCAATTTTCAAGTTCTCCAGGCCCTTTGAAGCTGC AGCAGAAAATTCAGGA
WI-14976	35	C T	GTGATTGCT TCGTTCAAAG	TCAAACATAAT CTTCCATTCTA AGC	TATTTTTTAATTGGTTGATTGCTTCGTCAAAG/TJGCTTAGAATGGAAGATTTAGTTTGAGGAG GGGCAGGTTTGGGGTAGGCTCAGCGGGCATAGTGGCCACAAAGAAGATGCCCATCTCACACCTGGAG ACGTCCATGAGCACTCG
WI-14981	31	G T	TCAGTGGTGT TATTGGATTT	CACCTCTGACA TAATACTTAGC ATAAA	TAATTGATTCAGTGGTGTATTGGATTTT/TJGTTTATGCTAAGTATTATGTGAGAGGTGGAGAT AAAGAGGAAAAAGAAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTTGTACAGGAAGTTTTTGA GAGCTCACAAA
WI-14992	80	C T	TGCATTAAAT GAAGCTGCAG	GCTATGTGCTC AGCTTTCTC	TGATTACATTTTTTAAATCATGCCTACCAGCCCATCTAAGCCAAATTCAAACACCACTCTGCATTA AATGAAGCTGCAG/TJAGGAAAGCTGAGCACATAGCACCCTAAGTATGCGGAAAGAAAACGTA
WI-15002	72	T A	---	---	AAATCTCTCTTTCACACACAGATGAACCTTTAATAATTACAAATGCACCTGAAAATGCCTCTTGA TTTCC/TJATTCAGTTTAGCCCTCAATGGGCTCTCCTCAAGGCTGGACCTCAAAGGCCCAGTT
WI-15000	90	G A	GACAGAAAA GACTCAGACT GTCTAA	GTTTCTAGTTC TGCACAAACTT CA	TCAAGCCAAATATCTGCAACAATAACATGTATTGAAAGGTATAGAAAATAAACAGATGGATAGACAG AAAAAGACTCAGACTGTCTAAGTA/TJGTAAGTTTGTGCAGAACTAGAAAACAAAAATCCACCT

WI-12323	68	G A	CACAATACTT CATGTACCTAT GAAATAA	CACTGGACATA TTCCCTACCTG	ATTTTGTGATGTTGTTAAATCTTATCTCTTTTATACACAATACTTCACTGACCTATGAAATAA G/AJACAGGTAGGGAATATGTCAGTGCAAAACAGAGGACTCACACCTGTGCATAGACAGCACC
WI-14683	91	A T	AAGGACGAT TTAGTATCTAA AAACA	GGCATGTCCCA GTGTTTT	CATAAGTTGCATTATTCACGTCCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTAGTATCTAAAAACA/AJTCAAAAAAACACTGGGACATGCCCTGAAATTGCAAGT TGGAGTTCGTAAAGATCTAC
WI-13470	100	C A T	CCTGCCCTTAT ATTGGAATTC	GGGAGACCATG GGTCTCT	ATTTTGTGTTTATTTAGCACCTGAATTTAGGCAAGAGAAACATTTCTACCTGAAGACTCCATGCAGT CAAAATTCCTGCTTATATTGGAATTTCTA/C/AJAGAGACCCATGGTCTCCCCAAGTGAGGAAGCC AGGGCACTCAGOCCTTC
WI-14712	38	T A C A	TGAATGCTTCC AAGTACAAAT CA	TGAAAGTATGT TGTATATGGTA TTGGA	TTTGGTGCTACTTTGTGAATGCTTCCAAAGTACAAATCA/AJCTACAATACCATATACAACATACT TTCAATCACAACCTCAAATATAAAATAACCTACAAAATCACAATTGC
WI-13712	40	A C T C T A T T G	TTTACTTTGTT GTCAATTTTAT TCTATTG	CCATAAGGTCT CACACTTTTCT TAT	TGGGATACCCCTTTACTTTTGTGTCATTTTATTTCTATTG/AJCTAATAAGAAAAAGTGTGAGACCTT ATGGCTCTGCTTATTTGGCAATATGCAATATAATTTGTGTTGTTAAAAATTTATGCAT
WI-16163	35	C T A	TCTGGTGATGC AATTGAAATA A	GCTGCCAATTA CATTAACTTAC AA	TCTAAGATTTTACTCTGTGTGATGCAATTGAAATAA/CJATTGTAAGTTAATGTAATTGGCAGCATT GCCCAAAGTTAAGAGGACTATTTCTTTAAACAAAGACAGTGTGACATTTATTTTCAGGT
WI-13453	88	T A T C	AATGCACAAA ATCTTGCTCT TC	TCAGATTTTAA CATCTCTTCT AGCA	TTTTTTTATTGTCATTTGAGTGTCTTATTATATTGGGAATTTGCGAGTATTAACATTTGTACAAT GCACAAAATCTTGCTCTCTC/T/AJTGCTAGAAAGAGATGTAAAAATCTGACCTAGTTGAACAGTCTT AATGAACCTATTGTCCAT
WI-16167	58	T C G A T T T T	CGCACTCTAA ATTAGAGATA G A T T T T	TGCTCGTGGTG AATAAGATG	CGGATATAATTATGTACCGCACTCTAAATTAGAGATAGATTTTTTCTGATATACATTT/CJCATCTT ATTCACCACGAGCACACCACCGCACAGTAGAACAGTTCCACACCTGATAAAATTGCACAAGATG
WI-14482	17	G A ---	---	---	GCAGAACCAATTAAATG/AJAATCTGCAAGTTTTCCCAAGAAACTCTGGAAACCATAGTGCCTAAT GCCCTTTAAATCGATACTAAGGAGAGAGAAATAAAGGACTGCTTGATGTGACAGTCACTGGT
WI-15069	81	T C ---	---	---	TGTAGTCTTCAAAAGACATGTTGGCAGATAGCCAGGCCATACTATGTGATTTCCAGTATCATGTAC GCACTAAAAAAAAT/CJGTGTGCTGTGCTGCTGTGAGTGAACCATTTGCTTAAGATAAA
WI-16156	97	A C C C A G A T C G C	TGAAGATTAA CCAGAGTCGC GCAGCAAGAT TACATCAGTA	AATTGTGIGA TTTTGAAGAGA CTCCAAATAGC CTAGAGTATAG TAAGGT	ATCTGGTATTGTGATCCCAACAAGTATACAGAACTCTATAAAACCAACCCCAACCCCTTCAATA TTACACTAATGAAGATTAAACCCAGAGTCGC/AJCTCTTCAAAAATGCACACAATTAAGACG
WI-15012	59	G T A T G T	---	---	CATGGCAGCAAGATTACATCAGTAATGTAATATAATACAGCTTTTTTTCATTGAAGCTTTGTTTACCTT TACTATACTCTAGGCTATTGGAGTGTCCCCAC

WI-15100	74 G A ---			TCCTATTACAGGCCAAGAAAAATACCCAAATTATTTCCAAATAAAGCAAAAAATTTGGAACAGACTGGA GTGAGAA[C/G]AGTTCCACCACCAAGCCCTCAAGACAAGATGGACACGGCAGCTGGTTCTGGGGT GCATTTCTAGTGGACTTAT
WI-14492	92 A T AATTACT		CCTTTATTTTC CCAAATATAA TAAGAC	TGGTACAGAAATGTTTAATTACAGCAGGCGAGTGATTCAGTTAAATAAAATTAATAAAACCTTTATTTT CCCAAAATATAAAATTAATAATTAA[A/T]GTCTTAAAGAAAATATAACATGGTGACAGCTTT TCCTTAATTTTATCGGAATCCAGGACACAAAGAAAAACACCCAAAAACCATGGAGACAGAAG ACGAGACACAACCTCTCCCCAC[T/C]GCCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGTGAGAC AG
WI-12002c	89 T C ---		---	TCCTTAATTTTATCGGAATCCAGGACACAAAGAAAAACACCCAAAAACCATGGAGACAGAAG AC[G/A]GACACAACCTCTCCCCACTGCCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGTGAGAC AG
WI-12002b	68 G A ---		---	TCCTTAATTTTATCGGAATCCAGGACACAA[C/G]AAGAAAAACACCCAAAAACCATGGAGACAG AAGACGAGACACAACCTCTCCCCACTGCCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGTGAGAC AG
WI-12002a	30 C G GGACACAA		TCGGAATCCA GGAGCCCTA GGGAGCCCTA GTTGCAGTAA	TTTTCAATTTATTTCCAGAAAAAGAAATCACATTTTCAGTAACAACATTACATATAGAAATTAACCTTTG TTCTGGAATGGAGCCCTAGTTGCAGTAA[C/T]GTGTCATAATAATAATTGCATATTCAGGATTTTG TGAATAGGTGATTGGGA
WI-15116	96 C T GTTGCAGTAA		ATGACA	GCAAAAGCAAGCTATGGAGCCCTAAAGGAATGGAA[C/T]GTGTGGTGGTCGCTTGATACCTTGGT GCTTGTGTGCATGGAGCAGAAAGTCTCTGCTCCATGCAGGGCGTCACATATTTAACTGCACATAAT TTGGCNAACCTGTCATTC
WI-12578	37 C T AATGGGAA		TCAAGCGACCA CCAACAC	ATTTACAGTTGGCCCAAGATCTCCCTTATGTGGCATTGCA[G/J]AGACACTGCACCTTATCTGAGGTTA GAAAAATGTAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAAATACCATTTCCCTAA
WI-15153	40 A G GCATTGCA		TGGCTTTAGAA TCAAAATGGG AAAAGTCA	CCCTTGTCTCTGAACTGGGACAGGATGTGAATAATTTTGAATCTGATGCAGGTCGAGGTATGGC TTTGAATCAAAATGGG[G/C]TGACCTTTTCCCTGTGGTGGAAAACTCTGTGAGGGTTGGCA
WI-15215	84 G C TCAAAATGGG		CTTGAGGACCT AGAAAGCAAA TAATCACTCC	AGGAAAAGTGTTAAAGCAAGGCGATCATTTGGATGGAATGATTATGTGTACGAGCACTTGAGGAC CTAGAAAAGCAAA[C/T]GGAGTGATTATGCCAATCAAAATTCGAAGGTTGGAGATATGCTAAAA
WI-15225	80 C T C		---	AAATTTGCTAGTGCAAAATGGACCAGAAATTTGGAAGGGCTATGTAACTACACA[G/A]TATGCACACCAC AGCCATGTCAAGTGTACAGATCCTCTGTGCTTCTTCTTAAACACATCAAAAGGCTGCA
WI-15152	51 G A ---		---	TGACTGTATACCAAAATGCTGTGCTTAATGTTAGTGACAGACAGATAAATAGGATG[C/T]GTCTGTTT GCCCTTAAGCAATTTACAACCTCACTGGGGAAGAAACAGACATGCAACACAGATAAAACACAAT
WI-15123	55 C T TAGGATG		TGTTAGTGACA GACAGATAAA CAACAGAC	

WI-15182	49 C A	GCACAACAG GGCAAAATA	GCATGGGTTAA TCCAGCA	GAGACTGCCCTGTGACACAACACTAGCTAGCTGCACAACACCGGGCAAAATA[C/A]TGTCTGGATTAAACCC ATGCTAATGGGTTACCTTTATTTAGTAATCATGGTCCCTCATAGCATGGTCCAGATCCG
WI-15198	38 T C	GGGCGCTGGC ACTATG	ACTTATCCGTC AGGCAGAGTAG	GTGGACCTCTACAAGTACCATGGGCCCTTGGCACTATG[T/C]TACTCTGCCTGACGGATAAGTTGGC ATATGGTTCCAGATTGCTTGTCTACACAGTCCAGTTCCCTAGAGACTAGTCCGACTCTCT
WI-12601	42 T C	TGAT	GTGTAGTCTT ACATGCTTACG TAGAC	TCAAGTGGTAAATAGCCATTTATTGAGTATTCCTGCTTGTATG[T/C]GTCTACGTAAAGATGTAAGACT ACAACTTACGACCCCATCTCTTCAAGAGGAAGTCTGGTATTATGGAACAAATTTTGTCAATTCAGAT T
WI-14510	104 A T	TGCAAAATA TGCAATAACA AA	TTGAAAATGGT TAACTGGCA	ATGTTGAGAGTAATAATGCCCTACATATTTAGTGTAGTACACCCCCAGATATTTTGGGAGAAGAG TTGTTTGTCTTTTGGGCAAAATATGCATAACAAAAT[A/T]TGGCAGTTTAAACCATTTTCAAGAGT
WI-15239	57 T C	CATTGCAAT AAACACCATC CA	GGACCTTATCT GTGGACTCAGG	CAGTGTGATGACATTTCAATGGGAAAAGATTGTGCATTTGCAATAAACACCATCAT[T/C]CCTGAG TCCACAGATAAGGTCCCGGAGAAGGGCTTCCCTCTCTCTCGCTGGTTGACGTTCCCGAGCGAGT GAAGCCTTTCTGGAATG
WI-12634	52 T C	GCATCATATG AAGTGTCTAGC AGT	GGACAAAATTGT AAACATAGCT AATAGC	ATGAGTTTATAAACTGGAGACAGCGCATCATATGAACCTGTCTAGCAGTATTAT[T/C]GTATTAGCTA TGTTTACAAATTTGTCTGAAGGGGTCTAGATGTGTACACCCAGAAAGTGGTATTCTCTGA
WI-15249	34 T C	GGCTTGACAC AAAGTTCTAA AA	GGAAAGCCAG AGATTTTAAAC AA	TTTGCTGAAGGGCTTGACACAAAGTTCTAACTTT[C/T]TTGTTAAAACTCTCTGGCTTTCCCTGGCTGG TGAGGAGCAGAGGTGGGTCTTCAGGTATCCACTGGTGGCCCGCATCTGTTCCTCCACTCCCGAG CCCACATCTCTGGCTCT
WI-12159	28 C T	AAGACACCGT GCAAATGC	CCCTCTCCTCA GTGCACITT	CTGTCCGGGAAGACACCGTGGCAATGC[C/TA]AAGTGCACCTGAGGAGGGGGGCTGTGACTC CCAAACCCCTCGAATATTTTATGAATCTAAGAGTCCAGCGCATCTCCACGGAGATCTGC
WI-12648	41 A G	OCTAGTGGCAT TAAGGATGC	TTGCTACTAAA AGTGGACATCC T	TCCCCAGATTGTATGGAATGCCTAGTGGCATTAAAGGATGC[A/G]GTAGGATGTCCACTTTTAGTAGC AACCGATGTTAATTCACACTCCCATGTTAGGTGCTTTACTTGGATTATCTCACTTAAAAACACA
WI-12684	64 G T	CATGCTGTAA ACAGCTGTGC	GGAACAACAA AGCCTAAATGG	ATGAGAGGTAAGTGTCAACAGTAGGCTTAAATATTCAGTAAACCATGCTGTAAACAGCTGTGC[G/ T]CCATTTAGGCTTTGTTTCCATTTAGAGAGGCACAGGAGGAAATTTAGCATAATCTT
WI-15260	75 G A	AAAGGATGAA GCTAATCATG GA	TCCTCCAGGG AGCTTGC	TTTATAAGCTGAATGAAAGAGGTGACACAGCGGACACTGTCTAAGTGGAAACAAGGATGAAGCT AATCATGGA[G/A]GCAAGCTCCCTGGAGAGACAGGACAAAATCAAGATGAGCTGGAGAAATTA TCCTG
WI-15325	39 T C	CATGTGGCTGG GAGG	CCTTCCACCAT GATTGTA	AAGGTTTAAATGGACTCACAGTTCCATGTGGCTGGAGGCT[C/TA]CACAATCATGTGTGGAAGGCAAAA GGCACATCTTACATGGTGGCAGTCAAGAGAGATGAGAGC
WI-13936	123 C T	AGTTGGCATTG AATAGCCTAT C	TGAAACTCCCA CATGGAGTT	TATTTAGTATTTTCCATGGCGCTTCTCACTCCCTATACATTTCCAGGGTTGAGGTAGTCTACCC CCATAGGTTCCAGAACCTATGACCTGTATCTTCAGTTGGCAATCAATAGCCTAT[C/TA]AATCTCATGT GGGAGTTTCATAATAA

WI-14528	62	T G	TTTAACTTTT TCTGGATGGTA TAAAT	CTCGATTAGCA CTTATTATAAA AATTAAAA	TATGCTTTATTGAAGAGAAATAGGCTATTAAATATTTTAACTTTTCTGGATGGTATAAAATTT/GTT GAATTATAAATTTTAAATTTTATAATAAGTCTAATCGAGACATCACCTGGGATATAATTGA
WI-15347	74	C T	GACTTCAAAG GAAAAGAACA AATTT	TCACCTCCCCA AGCTTTTG	TATTTCTTCGGTTTCGGATGCAAAACAAAAATTTTAAAGAAAAATGTGACTTCAAAGGAAAAAGA ACAAATTTTC/JCAAAGACTTGGGGGAGTGAAGGCAGAGCCTGGTGAGATGGACGAGGTCTGCAGA GG
WI-14546	95	C A	CCAATTTCTAG TGATAGTAGA GGACTCA	AAGGTGCACGT GCAGG	GTATTTCTGATGCTTTGACATCTGGGGCATTTGCTGTCTAGAGAGACTACTTCTCTGGGACCAGC CAATTTCTAGTAGTAGAGGACTCA/C/JCCTGCACGTGCACCTTTCATATACAGATCA
WI-15353	37	G A	---	---	TTTATGGCTGTCTGTAAACAATGTGGTGAAC[C/GA/JCTTAAATCAGGACATCTCCACCTTG TTTGGCTTCCAGTTGACTGCAAGACCAGTGTGAGGCACATAGGCTGATTATCATGIGG
WI-14580	100	G A	CATCCCATCT GTCITGCA	CCGACCAAGAT COCTCC	AGAAATTTTTCCTTTTAAACAGGACAAAGTAACAGATTACATCAAACTTCAGAACTTCTCAAAATAC CTAGTTATTATACACATTCCTCATCTGTCTTGCA[G/A/JGGAGGGATCTTGGTGGCTTAAACA
WI-8540	73	T C	GGCTGCATTT GGCTTA	GGCTTCTTTT TCAGGCAC	CCAGCTGGAGGTGAATAAATGGGGCAACCAACAGAAAAAACACACAGCTACACACAGGCCTGCATT TGGCTTAT/C/JGTCCTGAAAAAGAGGGCCGACCTCTTGATAAAGAAATGTCT
WI-8039b	97	T C	---	---	AAGTAGAACACAATAGAAATGGCTCAAAAATATCAGAAATGCACACTCGGCACATCACGAGTAAATACTG TTTGGTAAAACTTGTTCAGTT/C/JAAATATGTATGTGTCCTGGCATGTGATTAATATCTCTCT TACCACAGTCACCTTAAAGAACCAAGCTTAGGACTAGGGACACAACTATGCAGAAAAAGCAGGGA GACCAGACACTCTGGGTTGAGATGATTTTAAATGCCGACGCCGACACCCACA
WI-8039a	87	T C	---	---	AAGTAGAACACAATAGAAATGGCTCAAAAATATCAGAAATGCACACTCGGCACATCACGAGTAAATACTG TTTGGTAAAACTTGTTCAGTT/C/JAAATATGTATGTGTCCTGGCATGTGATTAATATCTCTCT TACCACAGTCACCTTAAAGAACCAAGCTTAGGACTAGGGACACAACTATGCAGAAAAAGCAGGGA GACCAGACACTCTGGGTTGAGATGATTTTAAATGCCGACGCCGACACCCACA
WI-8044	107	C A	---	---	CACAACATTCAGAAAGTTTCTGCAATTTGCTCTCTGATGTCTAAAAAGATTGAGCTTTGACTAT ACGATTTCCACACTGAACGCAATTCATAAGGTTTCTCC[C/A/JAGTATGGATTCTCTGATGATTAATA AGCCCCGAATCTGGCTAAAGGCTTCCACATTCAGACATTTGTAAAGTTTTCTCCAGTGTGGAC TCTCTGGTTGCAAGAAATGGAACCTCGGCTGAATGCTTCCACACT
WI-8550	32	G A	GGGAACATCA ATGCAACAAG	AGTTTACAAAT T	CTTACTACATGGGAACATCAATGCAACAAGTA[G/A/JAATTTGTAAACTCAAGCCACAACATTAGTTA ATAATCATGTTAAGGGACATTTGCCAAAAGAGCAACTGATGCCTCAGTGAA
WI-8057	87	T A	---	---	TATTAGATAAAACCCCTTGTCCCGATTCCAGGATGTTTAAATTTGCTCTCTTTAACTCTGTGACTTTT CCTGGTTCAAAGGACAGTTA/JGATGGACAGCAGCAGAGGAGTGGGGTCTGAAAAATGTAATCTTT GTGTCAAGGCACCTCTGTGGCTCACAACCTGCCCTGTGAGAGGATGCTGCCTTCCAGGCCCTAAAG ACACTAGGGCTTTTCAATGGACGGGTTGAAGCAGCCAGATGGTAAGG

[illegible]

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WI-6375	28 A	GGTTATTGCA TATGGAATC GAA	AATGTGAGATC TTTATTCTAAC CTTTTT	AAGGTTATTGTCATATGAAATCAATAG[A/G]TATCTTTTACAAAAAAGGTTAGAATAAAGATCTC ACATTTGTAAAGGCACATATGAAACAATTTTATAGCAAGCACAAAGGCGAGTGAGACATCAACAA TTGTGCTCAACAGATGAAATTCATAACCTTTTCTGATAAGACAATTCAAACATACAAATCAAT TACAACAATGTGCTTATCAGCTCCCTCCACCCCTATATTTAA[T/A]GCAACTGACAGTTTGAAG GACACCAAGACAATAGGGCT
WI-6409b	112 T	A ---	---	TTGTGTCACACAGATGAAATTCATAACCTTTTCTGATAAGACAATTCAAACATACAAATCAAT TACAAC[A/T]ATGTGCTTATCAGCTCCCTCCACCCCTATATTTTATGCAACTGACAGTTTGAAG GACACCAAGACAATAGGGCT
WI-6409a	73 A	T ---	---	CTAATATAATCCTGGGCACATGGATTCCAAAGAGAGATTTTCAGCAGATTTTATTATAGTTACTTAA CAGCTAAATAATAAGGGTGATTTAACTTACTTACAGAGTCACTAAATAATGGAGGGAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG[G/T]ATCAACCTTCCCTAAGCATCTGTCTGGTCCG CAGC
WI-6523	165 GT	GCTG	AGATGCTTAGG GAAGGTTGATA	TCCTAGCCCTATTAGGCTACACTGTAGTCACCTTCTATGAGAGCAAGGGAACAGGAAGATGGGC TCCTGGAGTCCAAACAGGATGTGGACGTCCTGGTAGTCTCTCTTTTACACAACCTTTTCCCTGAGA ACTGTCCAGTCAAGTGAGCTTCAACAACACGACGCTAAACTCTGAGAGAAAAAC[C/G]CTG ACTTTGAGAAAGCATAAAGCTGAGAAAAA
WI-6554	195 C	G ---	---	ATTGTAATTAATAATTACATGGGCCTATTATTAAAGGACATTGTTAATGTTTCCACTTTGTTTAA [C/T]AATTAACAAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGCG
WI-6558b	68 C	T ---	---	ATTGTAATTAATAATTACATGGGCCTATTATTAAAGGACATT[G/C]GTAAATGTTTCCACTTTGTTT AAACAATTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGCG
WI-6558a	42 G	C ---	---	AACCAACAAAACTAAGAAATGGGAAAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGAAATAA AGTTGTCATA[T/C]AGCAATGGATGCTGTGTCAGAACATCTGCCAATAAACTTTAAGAAAAAAGGA ACTCAATGAAGTTACTGTTATATAAAACAGGAGCTCACAGCGGATGTAAAGAGTTAATGGAAGAT ATCGTGAGCCAAAAAC
WI-6629	75 T	C GTCATA	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTTAGTTTAAATCAATCAATCAAACTCCAGCTGTTCTCTTGCTTT TTACTTAGCAAGGAAAACTTTAGTGAATGCTACTTGACAAGAAAGAAAGTCAATTTCTCAAGCACA T/C]ACCCAACTTGAAGGTGATTGAACCCAAATAATGGTGGGAAACACCAAAATGAGGTGGAGGA ATGAGAAAGATGTGTGGGCCAAAGCTATCTGTTATATTTTGATGTTGCCAAT
WI-6644	134 T	C ---	---	TGCTAAACACACCATTATTAAAGGAGAGTACTAGGAAAACTACCAACACAGCATGTGAAAAACAGT TGGGCACGGTGGTAAAGGGCACAGACTCTGGAGCCACAGC[C/T]GGCTAATACACTGCAATATTTTA TGTTAGCAAAATTATAGCTGGTCTGTGTATACCAGAGAGCGGTACTGG
WI-6690b	106 C	T AGCCACAGC	ACATAAAATA TTGCAGTGTAT TAGCC	

WI-6690a	28 T C	AAACACCACC ATTATTAAGG AGAG	GCCTGTTTGG TAGTTTTTCT GCTTTTGGAGT GTATAATAGTA TGAATAA	TGCTAAACACCACCATTTATTAAGGAGAGT[C]ACTAGGAAAACTACCAACACACAGCATGTGAAAC AGTTGGGACGCGGTGTAAGGGACAGACTCTGGAGCCACAGCCGGCTAATACACTGCAATATTTTA TGTTTAGCAAAATTATAGCTGGTCTGTGTATAACCAGAGAGGGTATCTGG
WI-6770	53 A G	CAACCCCAA AACATCACA	GTATAATAGTA TGAATAA	GATGTTTAAATGACACAGATCTTCCAAAGTAATCCAAACCCCAAAACATCACA[A/G]AATTATTTCAT ACTATTATACACTCCAAAGCAAAATACITCAACTGCAATCC
WI-6686	151 A G A	GCAATCTTCCA AAACAAAAGA	CCTTGTAAGTG ACTATTCCAAT GTT	ATTCTGTAGGCAAGGTTACGAAATCAGTAGACTAATCTTGACCAATGGGTGAGTCAGCCTCA TCACAGAGATTTTTTTTTTAATTTAGATGAAATTCACATTTAAACATGGTAACCTCAAGCATTTCT TCCAAAACAAAGAAT[A/G]AACATTGGAATAGTCACITACAAAGGAC
WI-6761	32 C A G	GATCTAACAG CTGCAGAATG	AAAAGCTGGG AAGGAAGAAG	CCTGAGAGGCAGATCTAACAGCTGCAGAATGG[C/A]CTTCTCCTCCAGCTTTTGTGAACAAAAC AATTCCTAAGGCATCAGAAAGCACTGAGTGCAAAATGGTTGTTCAGGTACAAGGCTC
WI-6814	225 T C	---	---	TAAATACTGCCAACTAGCATTACGTCCTCTTGCACTATTGCACTATTAAAAACAAAGGGTATTTCCCTTG GTATTTTCAATGATGCATTATACAATAAACGAAGTTAGAACTTAAATGCACCTGATTAATTATG TAACTGGTAATTTGTTTAAAGCATATAATTTGGTCTCTTCATATAAATGGAAATTTAAA TATTTCTTCTGATAGCTTGAGGTT[C]ATCATTATGAGTAGTGCAAGTG
WI-6824	112 A G	---	---	CGGTTTGTCTACACTTAATGGGTTTTTTTTTAAGGGATTTTTTTCAGGCTTGTGCAACATCAA ACAAAAGGTACTGAGTACTCCACAGGGTACAGAGTGTGCCAA[A/G]ACCTTAGAAAAATTTACAT GACACGGAGAAATGCGCTCTTGCTCCTTGAAGAGCTTACAGTCTAGGGATTTGACAACTCACAGT CTTAGGAACTGGGCAAGTAAGGCAAAATCTTCATCCCTAGAGCTATTGTG
WI-6889	139 T C AATC	GAAAAATGAG ATGCAGTTAA	TCACITTTGTGG CTTTTAATTAT TCT	GTACAAAAAGCTGAGAAGAGCCCAACATGGAAGTGTCAAGAAAAACATCTGATAGGTACGGACAA AAGAGCTCCTTCAATCAAAAGGAGTTACATATTAGTTCTCACCATGCTAGAAAAATGAGATGCAGTTA AAATTC[T/C]JAGATAATTAAAGCCACAAAGTGAAACTGTGTCTCGGGGCCCTATGTTGTAGATT CTCT
WI-6911	216 T C	---	---	TCCCAGCTCATATTTATTTGGGCACAGAGTGGGCACCTCAAATATCTGATGAACCTGAACTGAA AAGAGGTCTCCTTAAACAAGATATCATCTCCCGAAGAGAGAGTCCCAACCATATAAAATGTATGAT CAAGTCCAGAAAACCTTGGCTTCCCAAGGAATGTGTTTCTAATTTGGTTTCAAGCACACTGGTTCC CACTTTTACCACIT[T/C]CATGACATTGGACAATAGTACTCTTTTCTAC
WI-9413	112 G C	---	---	GCCAGTCTCTAGTAAGTCTAGGGACATGACCAGACCAAGCCCTGTTCTATATGAAGACAAAAC AGGTGGCCATACTTGGGTGAGGGATACCGCTGCTATTTCCAGATG[C]AAGATTTGGTGAAGGAG ACCATGACAGATGACAAACGGAACAGTTTCTCAAAAACAGAGGTATGA
WI-9557	74 C T	---	---	AAAAAGCTTTAAAAAAAAGTGGTGTCTATCTTAGAAAACACTTTACGCAAGATCAAGTAGCCAGCT ACAGCC[T/C]TGGTGCATCTTAACCCCTCTCTCTTT

WI-9617	37	G T ---	---		TGCTCTTTTATTTACAGTTCACAACACACGCCGTG[G/T]GGCACAGTCTACCAAAAGTGCCCGCAG CGCCACGCTGGCCGGAAGTCTCATCTGTCGTCCTATGGACTGATGAATTTGGGATGGCCAG CTCCAGAATGTTCCACGTGGGGCACTCTGTGGCAGAGAGGCTGAGCCCTTGCCCCACACTGGCACCA AAGAGTTGCACGATGCAGCTGCAGTGGGTCGAAGCCGGGTGCTGTG
WI-9657	121	T G ---	---		AATGCTGGAGAAAACATCAACATTGAGTTGACATTTGTTTTGCTGAAATAGCTACCATCCACTAT CATGAATTTTGTTCATTACAAATGATAGAAAAGCCAGATTCTCAAAATAAAGT[G/A]ATAATCTT TGTATTAATAAATGTTTATAAATGTTTATGAAGCTCATACATTATCTTTTTTAAAAAAGTAAAAA TTTTAGACATATGACGCTTTTCATAATTAATGCTTTTGATATAGATTTGAGG
WI-13119b	114	G C GCTGGGA	CCTCCCAAGTA T	AAAAATTAAAC CAGGTGTGGTG	CAGGCTTGCTGCTCTCCAGGCTAGAGTGAGGTGACACAATCAAGACTCACAGTAGCCTCAACCT CCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGT[G/C]ACACCACACCTGGTTAA TTTTTTAAATTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAACAAAACCACTAAG CAGGCTTGCTGCTCTCTCCAGGCTAGAGTGAGGTGACACAATCAAGACT[G/C]ACAGTAGCCTCA ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACCACACCTGGTTA ATTTTTTAATTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAACAAAACCACTAA C
WI-13119a	51	C G ---	---		ACAGGAATCTGAAAGTTACCAAGGCAATTTCCCTTTTAGGATCATAAAGACTACAGACTTAAGCTT TTTT[C/T]CTTTTCCATATAATACACAAAATTTCTAAATATCCTTAAAAAAGAAAATATAAATAGT TTCAGTATGTTATGATAGATCACATACTATGCGCAAAAATATTTTATTAAATTGAGGGAATAGGCCAAT TT
WI-13112	71	C T AGCTTTT	TTAGAAATTTT GTGTATTATAT GGAAAAAG		TGTTAACATTTTATTGGTACGTGCTCTCAGTACAA[C/A]AACAGCATCAGTAGGTACACTTTGAT AAAAAGGAATTTTATAGCTTAGTAGAAAAGAAAGCCCAAGGTCAGAAATATAATGAATATGTACAT CTTTATGGAAGTCTTTGTGTGACCATCTTTATCTTCCCTGTGGATGAGATGATGACACACAAGT AAA
WI-12988	36	C A CTCAGTACAA	TGTACGTGCT CTACTGATGCT GTTT	CAAAAGTGTACA	TGCTATTCATGACAGACACGTGAGACAAAATATCTTATTTTACAGATGGAATAGACCCAGACATTA TTCAGTACTTTAACCACTAATAGTGAACCCCTGAGACTTTA[G/A]ATCTGCAAGGGGTTTAAATAT GCAATATCACATATATTTCCATTTTAAACACCATATTTAAGTTTCCATTTTCTTAATAGAAAAATGA TAAAAATGTTTTCCCAATAT
WI-13020a	108	G A CTTT	CTAATAGTGG AACCCTGAGA CTTT	CATTATTAAAC CCCTTTCGAGA	TGTATAAAAAATCCAACCTGTTCCACAAGTACATATGTCCTATGATTTTATGCATACATCCATATAC ATATATCAAGGTAAAGTCCA[G/T]ACAAAAAACAGCAATTTCCCTATGGCCAGTGTCTACAGAAGT AAGACTGTGCAAACTTTATCGTATAGTCAATGAGATTGCACACTAAGGCAGGATGAGGCAGAAAGCA AGTTGTGTCCA
WI-12837	87	A G AAGTCCA	CCATATACAT ATATCAAGGT GCCATAGGAA ATGCTGTTTTT		

L42611b	50 GC ---				GTCTCAGGCCCTTCTGGCTGCAGAGCGGTCTCTCAGGTTGCCTGTG/CJCTCCCTGGCCCTCTAG TCTTCCCTGTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGGCCCTCAGCTCTCTCTGTCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATATGATTCACCA CTGGAGCTTCACITTTGTTAC
L42611	34 TC ---				GTCTCAGGCCCTTCTGGCTGCAGAGCGGTCTTC/CJCTCAGGTTGCCTGTGCTCTCCTGGCCCTCTAG TCTTCCCTGTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGGCCCTCAGCTCTCTCTGTCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATATGATTCACCA CTGGAGCTTCACITTTGTTAC
WI-1172b	179 C T A	TGAAGAAATG GCTGATACCA	ATGTGCATTTT TCACTGCAG		TGAACGTGTGGTTAAACTAGGCAATTGGTTAAATCAATTTAAAAACAGGCCTAGAAACAGTG ACCACACCTCAAGCAATGATATCCCTAGCAGCTCAGATTTGTTCTTGAATACCATTTTCTGCTTTC AAAAGAAAGACATGAGGCTTCTTGAAGAAATGGCTGATACCAAG[C/T]CTGCAGTGAAAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1172a	17 C A ---				TGAACGTGTGGTTAAAC[C/A]TAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCCTAGAAACA GTGACACACCTCAAGCAATGATATCCCTAGCAGCTCAGATTTGTTCTTGAATACCATTTTCTGCT TTCAAAAGAAAGACATGAGGCTTCTTGAAGAAATGGCTGATACCAAGCCTGCAGTGAAAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1177	35 G C A	GCAGATTGGA AGTGTGAAAA	CACCTACATTT CTGAATATTTA GACTCTTT		AGAGGCAGATTGGAAGTGTGAAAAAATGAAAGAA[G/C]AAGAAAAAAGAGTCTAAATATTTCAG AAATGTAAAGTGTGCCCCCAACTGTTCTTTACCCCACTTAAATCTGCAATTTTGAAGAACTAGATTGAAT TCCTTTGCAAAACCCCTTGCAATCATGGATACCCGAGTTAAACCGTTAATTAAAGACATTTAAACATGG CCTGGTG
WI-1231b	141 G A ---				TCCATGGTTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCCACTATGCATTGGAACATTCGCCATATTC CAACTAAGCAGGAGGTTCACAATAAACAACATAGGCTCTTTATTTCTCCTTCTTCAATTTTCTT TCAC[G/A]TTATCCCTCACCCCTGAACGCCCTTCTTCCCTCGTAGTGACATTTTAAATCCACITTTAC ACATTCGGACC
WI-1231a	126 T C A	GGCTCTTTATT CTCCTTCTTTTC	CGTTCAGGGTG AGGGAATAA		TCCATGGTTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCCACTATGCATTGGAACATTCGCCATATTC CAACTAAGCAGGAGGTTCACAATAAACAACATAGGCTCTTTATTTCTCCTTCTTCA[TC/TAATTTT CTTTCACGTTATCCCTCACCCCTGAACGCCCTTCTTCCCTCGTAGTGACATTTTAAATCCACITTTACA CATTCGGACC
WI-472	114 G C ACAGAAAAAG	ACATACATAT CCATTATACA	GACCTTTCTTT TCCAGGCC		GAAAGCAGGAGCTGTGTTTGGAGGACAAAAAGTAAATCTTTTATATCTTTATTTTAAATTTTATT TTTTTTCAGGCATATAGACATACATATCCATTATACAACAGAAAAAG[G/C]GGGCTGGAAAAAG GTCAAGTGAGATTTCAGATATTTCTTAAATGCAAGGCTGACAAATTTGGGCTTGATT

WI-478	46 C	GCATGCTGTG TTACTCTATTT TGTT	AAATGCCACAG GTGGCT	AAACCACTGCAACCTTCAAGCATGCTGCTGTTACTCTAATTTGTTCTC/TAAGCCACCTGTGGCATTTC CAAAATATGATAATCTCTGCCACCATACTGCTTTAAACACAAATAGAAATCTGGCAGCAAAATATAGC ATAAGCTTACTTCTAAATCAAAGGCTACCATCAGTACCTTAGCACATTTAAAAAATAAAAAACCAAC ACTGCCCA
WI-533	29 T	ATCACAGCAG AGTACCTTTCT AACT	CTTCCCAACCT CTACACAATCT T	AGCCATCACAGCAGAGTACCTTTCTAACTT/TAAGATTGTGTAGAGGTTGGAAGGAGGACAGGA CTGTTCTGTTGGTATAATGACCCCTGTGTCCAGTTAATCCA
WI-601b	112 T	---	---	TCACCTATCTCTTTTTTTGGTGAGAACACACTTAAATCTAAGAATGATCAATTTCAAATAAAGATGG TAGTGAGCGGAACAGAGAGGTTTCTATTGACTCTCTAACTGAGTAC/TA/CAAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-601a	74 C	---	---	TCACCTATCTCTTTTTTTGGTGAGAACACACTTAAATCTAAGAATGATCAATTTCAAATAAAGATGG TAGTGAG/TA/CAACAGAGAGGTTTCTATTGACTCTCTAACTGAGTACTCAAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-863	107 A	CTCCTTCACAA CCTCACCA	CTTCCCGGTAA GCCAAGT	AACAAAAACAGACACCCCTCGGCTTCTCTCACAGTCCACATGGGTGCCAAACAATCCACATTCCT ACATCTCTCCCACTGGCTGCTCTCTCACAACTCACCA/TA/TAAGTTGGCTTACCGGGAAGCATAAA GCCAAAGCATTTAGTCTTTTATTGCAACATGGTCTGGCTGCAATAC
WI-919	36 G	ACTGCTTGCTT GTTGATTTAAT C	TTATTCTAATC CCACATGACAG C	ACTCAGTCTGCTGTTGTTGATTTAATCAACCTAGCC/TA/TAAGTGTGATGTGGGATTAGAATAAAATA AACACAAAAATGAAAAACACACGATTGCTAACAAAGCAGATCTTTTCAAGGCACACGTAAGAT AATAACTTCA
WI-991	37 A	---	---	TGCATTCTATTGCAACCAATAATAACTTCTGTACAT/TA/TAAGTGTGATTTTATTATCACAATAAT TATGAGTGAGGGATGATTGTTATCCCTATTTTACAGATGAGAACACTGAGACTTAGAAGAAGTATCT TTCCAAAGTCACAAAGTTAGTGACAGAGCCGGGATTCGAATCCATCACTTGAATCCAGAGAAAAAT GTTCTGCATCACTGTACACACTGACTCTTTTCTCTTTGAAAAACAAGGC
WI-1011	70 G	CAGTATCTGA AGTTTTTGCT CCA	AGGAACACCTA CAAAATGACTT CT	CTTCTGACCTGTTTGCAGTGGATACTGTTTGAAGGCTCTGTCTCAGTATCTGAAGTTTGTCTCC A/GC/TAAGAGTCAATTTGTAGGTGTTCTGGCGTTTGTGTAAGTTTCTTCTTAATACACTGC CGTCTTAAGGGAGGCTTGCAGAGCAATTAATCAGATGGCTGTTTGTGCTGCTGCTGCACTGAAG
WI-5381	178 A	---	---	TTATGTCAGAAAGGTCCTAGTTTACAGATCTCAAGGAAGAAAGGCCCTAGAGATGACACCCAGAA ATGAGAGTGGCTGCTCATGAAAATTGGACAGCATGTTCCAAAGCAGAGGGAACAGCATGGAGAAGA AAAAATCATCTATCCACGTGCAGAAACTGGCAATAGTTTGT/TA/TAATAAAACACAAATGT TTAACTTGGGGTCCACAACAAGGATATGTTGGCAATGGTATTTCTGTGATG
WI-5791b	76 G	---	---	CTATGTAATTCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTCAAAAGATGAGAACAGGTCCTA GAACCTCAG/TA/TAAGAAAGGAAGTTTCATCTAGTCCATAGACCTATCTCACTGACCCAAAAGGTA AAAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCAATTTCTTATTTTGCCACCCCTGTTGT TAGGAA

WI-5791a	44 C G ---			CTATGTTATCCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTTC/GIACAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAAGTTTCATCTAGTCCATAGACCCTATCTCACTGACCCAAAAGGTA AAAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCATTTCTTATTTGCCACCCCTGTTGT TAGGAA
WI-5406c	120 C T ---			CACCTGCTGTTGTCCATGGGTGCCACAGACTCTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC/C/TTATGAGCCAC ACTTCTCATTTCCCTTAGAATTTCTTGGACTCTGTGAAGAGGAAGGAAAGGAAAGGAAAGAGAGGCAA GG
WI-5406b	118 C A A	CCAGGATGTC AAGGTGAGAA	AATGAGAAAGT GTGGGCTCAT	CACCTGCTGTTGTCCATGGGTGCCACAGACTCTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC/C/TTATGAGCCAC ACTTCTCATTTCCCTTAGAATTTCTTGGACTCTGTGAAGAGGAAGGAAAGGAAAGGAAAGAGAGGCAA GG
WI-5406a	42 A G ---			CACCTGCTGTTGTCCATGGGTGCCACAGACTCTCCAGAAGAGGCGCACTTCCACAGATGCAACAG GCCCTTTGAAGGAGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCCCTATGAGCCAC ACTTCTCATTTCCCTTAGAATTTCTTGGACTCTGTGAAGAGGAAGGAAAGGAAAGGAAAGAGAGGCAA GG
WI-5798	48 G C TG	TTTATCTCCC TTGTTTCTTT	ACTGTTAGAAA ACCAAGTATTT TCAAT	CCATTCCTTCTTCCCTCTCCCTTATCTCCCTTGTCTTTTG[G/C]ATTGAAAAATACTGGTT TTCTAACAGTGTGCTGGTATGGATCTATGTTATAACATGCATAGTTCTATATGGGTATCA
WI-5415	54 T A TTT	TCCTCATGAAT TCATCTTTCAG	GGACTAATTCA TGATCCGATCT	CCTGCTAATAATAATTAAAGCAGCAI TTGCTTCATGAATTCATCTTTCAGTTT/T/ATAGATCGGAT CATGAATTAGTCCAGGCTTTTAGTTGTAATCGAAATTGGA
WI-5437	41 C T G	TCCAGAGAA AAATCCAAGA	AGTTTCTAAAC ACAAAATATG GTTTAAG	TGTTTTAACCCAGGCAGACCTCCAGAGAGAAAAATCCAAAG[C/T]CTTAAACCATAATTTTGTGTTTA GAAACTCCTGTGCCAACCCACTCTTGATGTGAGTGAC
WI-5481b	131 A G CTGCAGTCG	TGTCATTATG CTGCAGTCG	TTACTTCCAGG CTCCAAGTAT	AAGCCAAATTCACATTAGTTGATGAATTTGAAATTTACAGTATCTAATGCATGGGCATCTGTTCAAC TCCTGTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTTGICATTTATGCTGCAGTCG[A/G]A ATACTTGGAGCCTGGAAAGTAAAGACTTGGCTATTTTTCACAATTA
WI-5481a	29 G A AATTT	CCAATTCAC ATTAGTTGATG	CCCATGCATTA GATACTGTAAA ATT	AAGCCAAATTCACATTAGTTGATGAATTTG/AJAATTTTACAGTATCTAATGCATGGGCATCTGTTTC AACTCTGTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTTGTCAATTTATGCTGCAGTCGAA ATACTTGGAGCCTGGAAAGTAAAGACTTGGCTATTTTTCACAATTA
WI-5492	38 T C ---			TCATGAGCTTTCTTCAAGATGCTTGTAAAGTCCCAT/C/CAAAAGAAAGGATCCCATGGCCTAAT GAAGATGTACCTCCACCTTAGGATATTTTGCAGACCAA

WI-5826	134 T C ---	CCCAATACTTT TTCAGGTGAA	---	TATTTT TTTTCTCAATTCTGGAGCACACCATGCTCTTCTATTTCTCATGCTTCACATTTATTTT TTTCACCTAGTTAAATGCTTTTCCCTTGATAGCAATGGCCAGTTTATACATATTTCTTTAGTC/C TTTCAAAATTAATGCCACCATAGAAATAATTTTCTAACCAACAGCCAAACAGCCTCACTCTTCCTT CCTGGTGCAATTTACTCTTTACAC
WI-5546	40 C T A	TTCAGGTGAA	CCTGTATTTTA GCAACATGGG	CCTTATAACCCAACTCTTTTCAGGTGAAANAAGGAAAA/C/TACCCCATGTTTGTCTAAAATACAGG AGTATAACAGCATGACATGTTAAGGGAAATTACAAATGCTTGAGTGAATTTCTGATGTGGGAAATAT TAGAAATTAAGCGAGAGAGGCA
WI-5552	97 C T TTTTAGGT	GGCACAGGCT	TGCACAAATTG OCCAGG	TGTTGTCTGACCTCCCAACAAGTGGTCAATGAGCCTCAAGGGTTTGTGAGCGGGTATGGGT GGGGCTATCGGCACAGGCTTTTATAGAT/C/TCTGGGCAATTTGTCAGTGTGTCAGA
WI-5836b	161 C T ---	---	---	TAAGTTGATTTAAACACTCTGTGCCCTCAATTTCTCACCTATAAAATAAAGATAATAGTATCTAAAA AAAAGAGAGAGAAATTAAGTGGATAGACATGAATAACTCTGATGATCTGTTGTATCCCTGAA TCCTGCAATATACACATGATTCATGAT/C/TCCATTTTGAAATTAAGCTTTTGAATTTGTTTCCCA ATG
WI-557	58 C T AGTGGGA	GTTATAAGG	TGAACAGTTGG AGAGTAATGTG TC	TCGGGTATTAGGATGCGTTCAACCTCGATGATGATGGCGTTTATAAGGAGGTGGGGA/C/TGACAC ATTACTCTCAACTGTTCAATCAGAACACTTCACAGCG
WI-5850b	134 G A ---	---	---	CAGGACCTTGGAGCCTTTGCTGTTTGTCTTCCACCCCTCACTCTTCTCTGCTGCCATGGGTGGAGC CTCTCTCAGGCTTCCCTATGACGCGTCTATCTTCTATATGGGCAATATCCAATGTCCCATTC/GA TTTTGGCATTTCCGTATATCAAAACAGAGAGAGGGTGG
WI-5850a	92 C T ---	---	---	CAGGACCTTGGAGCCTTTGCTGTTTGTCTTCCACCCCTCACTCTTCTCTGCTGCCATGGGTGGAGC CTCTCTCAGGCTTCCCTATGCA/C/TJCGGTCTATCTTCTATATGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCCGTATATCAAAACAGAGAGAGGGTGG
WI-5612b	125 A T TTC	CTATTAAATGA GCATCGTGTCA	TTCTCTTGAGA AACCTAAAAC ACTG	TGCCGTGATTGACACATAGTTATCTGACAGTAATCATCTAACATCACAATACTTATTTCTGCCTG TCACACTAATTGCAAGCAATTCATTTGATTGACTATTAAATGAGCATCGTGICATT/C/TJCAAGTGT TTAGGTTCTCAAGAGAAATTATGCTGTCTTCTCCGTAACTCAAGTA
WI-5612a	44 T A ---	---	---	TGCCGTGATTGACACATAGTTATCTGACAGTAAATCAATTCATAACA/TJACACAAATATCTTATTTCTGC CTGTACACTAATTTGCAAGCAATTCATTTGATTGACTATTAAATGAGCATCGTGTCAATTCACAGTGT TTAGGTTCTCAAGAGAAATTATGCTGTCTTCTCCGTAACTCAAGTA
WI-5636	26 A C CCGCAATAA	GCCAAATTTAT CCGCAATAA	CATCGAGGACT TTGGGA	TGAGAGCCAAATTTATCCGCAATAAA/C/TJTCCTCCAAAGTCTCGATGGAGGCATTCAGAAATCGGG GCAGGGGAGGCAGAGGTGAGACAGATGTGAAGAAC

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WI-5865c	103	C G ---	---	---	TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTAAAGAACTCTTTTTCATTATGCATTC ACTGACTCACTCACTTGTCTCTATCAAAAATTAAAC[C/G]AAATATTAATATTTTATTACAGAGGAA CTCAGAAAGCCAGAAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAGGTACACAGTCCCTTCA GAGAAGACAGACAACTAAATAAATCCAGG
WI-5865b	99	T A ---	---	---	TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTAAAGAACTCTTTTTCATTATGCATTC ACTGACTCACTCACTTGTCTCTATCAAAAATTAAACAAATATTAATATTTTATTACAGAGGAA CTCAGAAAGCCAGAAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAGGTACACAGTCCCTTCA GAGAAGACAGACAACTAAATAAATCCAGG
WI-5865	165	T A ---	---	---	TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTAAAGAACTCTTTTTCATTATGCATTC ACTGACTCACTCACTTGTCTCTATCAAAAATTAAACAAATATTAATATTTTATTACAGAGGAACTC AGAAGCCAGAAAAAATGACCAAGACACAGTAAACAGTCTCCATCTTCAAAGGTACACAGTCCCTTC AGAGAAGACAGACAACTAAATAAATCCAGG
WI-5874	76	T G ACAGAAAA	CATAGCATGG ATAATATTAT ACAGAAAA	CCTAGTAAGTT TCAGTCAATTG ATATGT	CTCAGACATTCATTTTCATTAGTTGTTAAATTTTGTGTTTTCATAGCAATGATAATATACAGAA AAAAAATTTG/TACATATCAATGACTGAAACCTTACTAGGTAGCAATTTGTTTGCAATTTGCT CATGGAGCCGACGTTCCAGCTCTCAGTTTTCATC[A/T]TTTTCATAATTTACTCTCTTTCTGTC ACAATGTTCTGCTGCTGTTTCAACTCTCATTTGCTGATTTGGATGGTAGTCATAAAATATGGGTGATTC AGAAAAATAAGTAAATG
WI-5752	36	A T TTTTCCATC	CAGCCTCTCAG AGAGTAAAT ATGAAAAA	GACAGAAAAAG AGAGTAAAT ATGAAAAA	TTAGCAGAAACAACAAAAATGTCACACACTGCAGTAAAGAAAGTGTTCCTCCGATAAAAT[C/G] CATTAGGTATTAGATAAGCATCCCATAAAAACATTTGTTGAAACGAAAGCCGAGTTTTCGATTACACACA GTTGCTGTTTAACTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGTCCACGAA CATTGTTGAAACGAAAGCCAGTTTCCGATTACACAGTTAGTTGCTGTT
WI-5760b	61	C G ---	---	---	TTAGCAGAAACAACAAAAATGTCACACACTGCAGTAAAGAAAGTGTTCCTCCGATAAAATACCCAT TAGGTATTAGATAAGCATCCCATAAAAACATTTGTTGAAACGAAAGCCGAGTTTTCGATTACACAGTT GTCTGTTTAACTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGTCCACGAA ACATTGTTGAAACGAAAGCCAGTTTCCGATTACACAGTTAGTTGCTGTT
WI-5760	187	G A ---	TTCTCACCATG TTCGAACTTG	GGTGGGATCT AATTTGCA	AATATCTGGCTTTTCTCTTAGGAGGAGATTCTCACCATGGGAATCTTG[A/G]TGCAAGTTAGAT CCCACCTCACTATTGAGAAGCTAAAGGTAAAGACTACTCATTTCTCAGTCTTCTTGCTG
WI-5944	52	A G GGAATCTTG	TTCTCACCATG TTCGAACTTG	GGTGGGATCT AATTTGCA	GAGTTTAAATGAATCCTGTTCCCTCTAAACCTCTGTTCCCTCAACTTCACATTCAGCAGATATT CTTTCATGGGTTATTTGCCCAAGTATGAGGAGATGATGATTAATTTGATCATTTTCAAGAGGTGAG TAATGCTTGGTA[C/T]TTGCTCTGTGCGGTATCTGCTCCAATCACCCATTCCTTATTTCTTATAT GCTGAATGAAACGGTTATATACAG
WI-5967b	148	C T ---	---	---	

WI-5967	165	C T	---	---	GAGTTAATGAATCCTGTTCCCTCCTAAACCTCCTGTTCCCTCCCACTTCACATTCAGCAGATATT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGCATGTAATTGTGATCATTTCAAGAGTGTGAG TAATGCTTGGTACTTGCTCTGTGCCGTATC/TJTGCTCCAATCACCCATTCACACTTTATTTCCCTATTAT GCTGAATGAAACGGTTATATTACAG
WI-6093	53	G C	---	---	GGTAAGATCCAGAGCCACAGGTGAACCTGCCGGTATTGAAGTCTTTGGCCA/GC/GTCTGTAATG ATCTGACTTCTCCAGAACCCCTCTCTCTGGAAGTCCAACTGTGCACGTAGCCCATTTGTAGGGA GCATTTGAACCAAAACCCAGCGACACTGCTGACATTTGACTTTTCAGCAAAACCTTGATTGACGGTGAC ACACCAATGCTTCGAGAGGAATGAGG
WI-6141	80	T C	AGGTACTT	CTTCTTAATTA AGCATCTACA	GACTCTGTCTCAAGAAAAAATAATGAAAAATGAATAATTAAAGCACCTCTTAATTAAGCAT CTACAAGGTACTTAT/CJCACTGTCTGGGGTTTCAATCCCTTCACCTTTTAGACTTCAGGAAAT CAGAAAAATGCATGAAACAGGATTGTTACATGCAGAGAAATAGGGGGAGATAAAATTTGTCITTT CTC
WI-6450	45	T G	TTGTCACA	TTGTTGAAAT GTGTGGTACTT CT	ATAGGACAGTTTTTCTTCCAATGACTTATTCTATATCTTGTACAT/GIAGAAGTACCACACATTTCA AACAAAGAGCCAGGCTATGCCAGGGTGGGATTATTTACGGTCATGGTAATATGCATGTAAGACTA TTTTACTGGCCTCTTTTATGCATAAAACAAGGATTGGTCTATTCAACAACATGTGTCAATACAG CAGTTGTCATGTCCTCTGGTACTAGAAATAGTCTTTATAGAATATGTGTTTAGAATAAAAGCCACA AATTATCTATAAAACAACA/CJJAAGGAACGAGGCTCAAAAGTGAACAAAAACGGCCTTAGTTTC TAAGTGAAGACTAAGCAGATATAGGAAATATAATCCGTGACCTCTTA
WI-6461	88	C T	---	---	GAAACTATCCTTTAGTGGTGCCACATTTTCTATTCTGATTTCTGGTCACACAGGACCTTTCTGGGCT ATGAAATAGTCTATTTCAGTGAAGTATGATCAATAAAGACATGCAAAAACCTTTTCACAGTCTTGT CCTGG/GJA/AAATATCTCACAAAATTAATTAATTAATGGCATGCGACTTTCTGATTTAGCCTGACAGG ATTGTTCCCTTT
WI-7466c	141	G A	TTTGTCCTGG	TTTTCACAGTC TTTGTCCTGG	GAAACTATCCTTTAGTGGTGCCACATTTTCTATTCTGATTTCTGGTCACACAGGACCTTTCTGGGCT ATGAAATAGTCT/CJATTTCAGTGAAGTATGATCAATAAAGACATGCAAAAACCTTTTCACAGTCTT TGTCCTGGGAATATCTCACAAAATTAATTAATTAATGGCATGCGACTTTCTGATTTAGCCTGACAGGA TTGTTCCCTTT
WI-7466b	80	T C	GTC	GACTTCTGGG CTATGAAATA ACTGAA	TGCTTTTTAAAAATAACAATGACCACCACCTGACACCATAGTGTCTCCATTTGCCACGCTTCCTC AGTAGAATAAGACAGGGACTTTGTGGTGTCTATCT/CJATTCTCCTCAGAGAGCAGCTTTGGCCCT CATAGGCATTCOCATAGATATTTGTTGAATGAATGTGCTTTTTCATATTGATTCCTACATTTGATACA TTCTCAGGAGGGACATTTGGCCTAT
WI-9814	104	C A	---	---	CCTCTAACCAAGAAAACTTGACTTCCTCAACTCAAAATACCCCTCTCTAATAATTTA/GJAGTAACCA AAATATTCTTCAATAAAATTAATCTTTTAATTAGAAGAACCAACAGTGTAGAGGTAGTACATTCA CCACC
WI-9720b	55	A G	---	---	

WI-9720a	47	A G	---			CCTCTAACAAAGAAAACCTTGACTTCTCCTCAACTCAAAATACCCCTCTCT[AG]ATAATTTAAGTAACCA AAATATTCCTTCAAAATAAATTAATCTTTTAAATTAGAAGAAGCAACAGTGTAGAGGTAGTACATTTCA CCACC
WI-9825	123	A T	---			CACGCTAAGGCAGGATGTGGCTTATGAGATACTTTGCATTGCTGTGTCACACCTTGAATCTGCC TGCTGGCTCCCTTACTTTACCTCTCTGTCATGTGCAGATGAAGGCTCAGGGTGT[AT]GAGGATTAG TAAGATCTCTTTCTAAGACAGAGAGAGATTATTTACAAGAAGAACTACCAGGGTTAGTTTGCATT TAAGAAITGCCAGTCTTTTGCTCTGCATCATCTTGAACATTAATCCACATG
WI-9748	74	C G	---			CCACTTCAGTAAATCAATTTGTAGCAGCTTATTTCTAAAGATTTCTAAITTTTATATGTTTACCCCTT GTCATT[C/G]TCAGACCAAGTACATGTTTTCACACAGCCATCTTTCTTCTGGAATCTTTTCAGAAT TACAGTTATGATGCTCTTTTATATTCCCCA
WI-9943	91	T C	---			TGAGGCTATGATTGCAGATTGTGTAGTGACTAATACTTATTAGCAATTTCAATGTTGTGGGCACTGTT CGTTGTGTTTTATATCCATCTCT[C/G]ATTTTAAATTTCTACTGAGCAGAAAAAATAATGTATACATT AACCTTGTCTCCCTATTGTACCTTTAATATTGCATTTACACCTTCTCTTTTGTCAATTAGGGA
WI-9891	39	T C	---			AGGGGCTTTCACAGATCCGTGAGCTCAACACTGCCTCCCTT[C/G]AGTGAGCCTGTGAACCCCAAGAC GGCTGGTCATCAGTGTCATCCCTCTCTTTCGGGACAACATCTTTTAAAGAAAAAAGAGAGTGT CTTTGAATGTATCCATTTATCCCCAAATAATCTTGTTTAATAATCTTATTAGGCCAAATCCAAT GTGCTGAATAATCTGCCAAGCATGTCTATCTACACAAAAGGATTGTGCAA
WI-9897b	84	C T	---			CTCAGAAATTATCAGATCTCCCCAAATGTCATGATTCTTGTCTCAACATCCTATTTTCTCTCAAAC ATTTATCTAGCCTGT[C/G]AAGTCATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9897a	83	A T	---			CTCAGAAATTATCAGATCTCCCCAAATGTCATGATTCTTGTCTCAACATCCTATTTTCTCTCAAAC ATTTATCTAGCCTGT[C/G]AAGTCATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9935b	115	C A	---			AGATAACCCCTGGAAAACCTAGAAGAAATTAATAACGTGTTGCACACCTACCAGAACTGGAAAGAGT CTGACTGTGTTCTTATGGGGTGTGACTGGCAGGGGGAGTTCAGACA[C/A]AGCCCAAGAAAAGCC TGATATTAAGAGGCACCTTGCAATTA
WI-9935a	42	C T	---			AGATAACCCCTGGAAAACCTAGAAGAAATTAATAACGTGTTGC[C/A]CTCACCAAGAACTGGAAGG AGTGTACTGTGTTCTTATGGGGTGTGACTGGCAGGGGGAGTTCAGACACAGCCCAAGAAAAGCC TGATATTAAGAGGCACCTTGCAATTA
WI-9983	146	C T	---			CCCTGTAGGTGCCAGAGTCCATGCTCTTGGCCACAATGTTAGGCTGCCTCCCCATTTCTCTTGTGA TTCCCCAAACCCCAAGGTTCTACCCCAATCTGATCAATGCTGACTAGGTCATGGCTGTCAGGGTAA AGCATTTATGA[C/G]TAGACACAAAGACAAAAGAGGTTAAAGTTGCTGTCTCTCAAGAGAGAGACATAA AAACAAATGGATCTGGAACCTAAGTAAGGCTTCGAGGAGGAGGTGAGCAAGG

WI-10019	139	A T	TGATGTAATGC TATGTAGCAA ATCT	TTGATTACTGT GCTTAGGGGA	ATATCAGTGGTTGAGTATACAGCAATCTATTTGTTTATTATGTGTCTATAAATCAATGGTTCTA ACATTCAAAATAAGATCTTTTTCCTCTCTCTCAGATGCTTTCAATGATGTAATGCTATGTAGCAAT CTAATTTCCCTAAGCACAGTAATCAAGGCCCTTCTACCCCA
WI-10020b	122	T A TTT	GCAGAGAAAG AAATCATGAC	GACTGTTAATT TATTTAATCAT TAGTCTGG	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTAATGTTAACTGGCTCTGAAAAGAAATTTAGGC ATGCATAGAGAAATAGCAGTGTTTTTATGGCGAGAAAAGAAATCATGACTTTTTT/AJAAAAATACC AGACTAATGATTAAATAAATAACAGTCCAGGTTCCGGAAAGTGGCCTAAAGCACGCTAGTAGCCCT CCTTAGA
WI-10020a	39	T C A TAAAT	TGTCATCTGA CTCGTATTAA	AAATTCTTTTC AGAGCCAGTTA AC	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTAATGTTAACTGGCTCTGAAAAGAAATTTA GGCATGCATAGAGAAATAGCAGTGTTTTTATGGCGAGAAAAGAAATCATGACTTTTTTAAAAATACC AGACTAATGATTAAATAAATAACAGTCCAGGTTCCGGAAAGTGGCCTAAAGCACGCTAGTAGCCCT CCTTAGA
WI-10064b	170	C T TTTACATG	CCTTTAGATAT ATTGTGATTGT	ACCITTTCTGAA GCCAGATTTC	TCTGAGTCTTTCTGAGACACTTGGCATGGTCAAGGGTAGCAGGATCAGGGAAGGCATTATAATAAT ATAATTTGCAGAGCATCTCTCTCTATGCACCAGATATTGTGGTGACACTCTGTTTAAATCCAGTATCC CTACTCCTTAGATATATTGTGATTGTTTTACATGCTGAAATCTGGCTTCAGAAAAGGTTAGGTGTT T
WI-10064a	54	C A CAGGGAAGG	GTAGCAGGAT	CAAATTATATT TATTAT	TCTGAGTCTTTCTGAGACACTTGGCATGGTCAAGGGTAGCAGGATCAGGGAAGGC/AJATTATAATA AATATAATTGCAGAGCATCTCTCTCTATGCACCAGATATTGTGGTGACACTCTGTTTAAATCCAGTA TCCCTACTCCTTTAGATATATTGTGATTGTTTTACATGCGAAATCTGGCTTCAGAAAAGGTTAGGTGTT T
WI-10289	29	T C CAACTCTT	TCTCCTGTCCC CAAACTCTT	ATTCTTGTTGT ATTGAATGGAA TTAA	CCAGGGATTCTCCTGTCCCACAAACTCTTAAT/CJTAAATCCATTCAATACAACAAGAAATTTATAGAA TATGCACCACATGCCACAAAGACACACCTTATATTAGT
WI-1319	40	A T ATTCTTT	TGGCACTTAG AACATAGTTT	GCCACACACCC CTATGGT	AAGAAAATCCTTGTGGCACTTAGAACATAGTTTATTCTTTA/JACCATAGGGGTGTGGCTTATCT TTTACCCTGGCATGGCTTAGGTCCCTGTTTATAAATTTGGTATCTTTTGGCCACAAAGAGTCTGTTCTGAC AGTCTTATGATCTCTATTATTAAACATTAAACACTGGTCAGATGTTTAAACCTTGTGAACCTGCAGC
WI-10316	104	T C CTCTT	CTGTTGATTT CTACCTCTATT	GCTTTGGGAATG TATCCAAAAGT TT	AGCAACGTTGACAACTTAGTGAGGTGTAATCAAGAGCATCTATATTATTCACAGTCAACCCCTG GACTATAGTCTGTTGATTTCTACCTCTATTCTCTTAAT/CJTAAACCTTTTGGATACATTCCAAAGCAT CATGGTCACTTCCAGTTATGAAGGATGTTTAAAGCCCCAGCC AGTGAGTTGTGCACAAATTTGGAGACATTCTGTGACCCCAACTTAAACACTTCTCCCACA/C/JAC AAAGTTAACACTTCAGTTACCAGGTGATGATTGAGCAGA
WI-2572	61	C T ---	---	---	

WI-10368	31 C	T	AGGCTCTGTT	TGAAGCAACC	CAAGATAATTAT ATTTATTCTCT AAGAGGGG	GAGGAAGTGCCTGAAGCAACCAGGCTTGTTCCTACCCCTCTTAGAGAAATAAATAATATCTT GAGATAGGGAGGAGGAGGCTGAGGACGCTGGGTTTGTCTACCCACTGGAAGCAGAATATCC TTCAAAGCTTTTCCAGTGAGTCATGTTGCTGCTAAACTATATGACCCCTGATGGATTGCCCTTTCAGGG T
WI-10391	32 A	G	ATGACTCCCA	CTGTCTCAGGT	GGGAGTTAGGA GTCAAGAAGTT GA	CCCTCCCGTCTCTGTCTCAGGTATGACTCCCAAGCTCAACTTCTTGACTCCTAACTCCCATCTCGGTG TCTGCTCCCAAGGGGACGCTGACACAGCCTTTGCTTGTGTGACAAACAGAACATTGACAGAAG TGATGCTGCGTGACCTCCAGGATA
WI-10567c	146 A	C	GCAA	GTTACCCAGA GTCTTCTAATA	TGCCGCTTCCA GTAGCT	AGCGATGAAATTTATATGTTATGCTGACTAGCGGGTGCATAAATAATATTCTTTTTCATATT TTCCAATTATTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAAGTTACCCAGAGTCTT CTAATAGCAAACGAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-10567b	82 A	C	---	GGGTGCTCAAT AAATATTATT	---	AGCGATGAAATTTATATGTTATGCTGACTAGCGGGTGCATAAATAATATTCTTTTTCATATT TTCCAATTATTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAAGTTACCCAGAGT TCTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-10567a	60 T	C	CTTT	GGGTGCTCAAT AAATATTATT	GGTGAATAATTC TAG	AGCGATGAAATTTATATGTTATGCTGACTAGCGGGTGCATAAATAATATTCTTTTTCATATT ATTTTCCAATTATTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAAGTTACCCAGAGT CTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-11153b	84 C	G	TACTTTA	CAAACTTCAA ATTGCTTTAAG	AAATCCAACA GTCAAGGCTCT C	CGTTGGGAATTTCTATCTCACCTAAATTTATGCGTGATTAATAATATACATTTTAAACAACTTCAAA TTGCTTTAAGTACTTTACGAAAGACCTTGACTGTGGATTTTGAGI TTTTCTTTTATTTCTTAATA AAAACATGCAATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTAATCTGATATCAGCATCCCTT TATGTATT
WI-11153a	33 C	A	AATTATG	GGGAATATTTC TATCTCACCTA	GCAATTTGAAG TTTGTTAAAT GTAT	CGTTGGGAATTTCTATCTCACCTAAATTTATGCGTGATTAATAATATACATTTTAAACAACTTCTC AAATTTGCTTTAAGTACTTTACGAAAGACCTTGACTGTGGATTTTGAGI TTTTCTTTTATTTCTTAATA AAAACATGCAATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTAATCTGATATCAGCATCCCTT TATGTATT
WI-2616	125 T	C	ATCC	CACAAATGTA ACAAGAAATTG	CCATGGCTGTA GTCCAGT	GTTGGAACCTCCAGTATCATTTCCCTCAAACCCAGCTTAAATCACAATCAGCTTTTCTTTCTGTA GAGCTCAAACCTCAGTCTGAATGAAATTTGCTGCACAAATGTACAAAGAAATGATCCTATTCJACTGGG ACTACAGCCATGGAGAAAAGCAATGTAGTCAGCAAAATGTTAACAG
WI-11163	58 C	T	TGAGA	CAAGTGAATT ATGACCAAAA	TGCTCTTTCA TTTGAGGTTT T	TGACTCAAAGGAAACACACAAAAAGTTTCCACCAAGTGAATATGACCAAAATGAGA[C/T]AAAT TTGTTAAAAAAACCTCAAATGAAAGAGACAAATATAGTTCAAGATTCAGGTTCAATATTGT ACCTACAAAATAGGGATAGTCATGGTGTGGCAGACTTTTCTTTCTTTTCTTTTGTG/GTCTCTTA GAATCCATTTTGTCTTTTGGCCAGCATTTCCCTCTCCCCATATTTTAAAGGAGAGAAATTCACCTTTTCT CTGTTGGATGATCACAGGTTCTGCTCTCCCAATCCAGAGGCGAGGTACTATTACCCCATGGGGTGCAT AGAGAGGATTAAACAGGGTGATGCCCTGCAATGGGAATATTGAAAAACC
WI-10656	59 T	G	---	---	---	---

WI-11169b	154	T G TTTT	TTAACCAAGA GTTTTTCATTC	CTAACTTAAAA ATCCTCATTC AAATATAA	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAAATTAAGCCTAAAGTAGTGTCTTTTAAACCAAGAGTTTTTCATCTTTTT TTTAAAAAAGAGCAGACAT/GJTJTATCATGTGTTCTGATAAATTTTTTATATTTTGAATGAGGATT TTTAAAGTTAGCAT
WI-11169a	95	A G TTGAAAA	AATAAGTGAA AGTAACTGAC	AAACTCTTGGT TAAAAAGCAC TACITT	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAAATTAAGCCT/GJAGTAGTGTCTTTTAAACCAAGAGTTTTTCATCTTT TTTTTTAAAAAAGAGCAGACATTTTATCATGTGTTCTGATAAATTTTTTATATTTTGAATGAGGAT TTTTAAGTTAGCAT
WI-10685	25	A G ---		---	CAAGTGCTTGGACCTTGGATAGGTC/GJACCCGGCTGAAGTTGGACAGTTGTTGGTTAGGTTGGAG ACCAAATTCAGTCATCCTGTAAATATAGATCTGTTCCCTTTTGGGTTTACCAGTGGGTCACTAAAG AGAGATGGAGACAGTCTCAATCTTGCTAAATAATCCAAAAATAGCCATGGGTTTGGACAAAATAC AAGGTTAGTGCTCTCTAACTTTAATGGGCATA
WI-10686	133	C T AAGG *	TGCCCTGTCC	CAATCTCTAAA TTCATGTGTAG ACACA	AATAACCTGTGGCACATAAGGCCAAATACTGAGCCCATACAGAGTGTTTTATGTTAATATTATGAAA AAAGTCAAGAGAAACAAGATGATAGTTCGCTAGAACTCTGAAATCTGATGCCCTGTCCAAGG/ C/JJGCTGCTACACATGAATTTAGAGATTGAATGAAATGGCAAAATTCAGAAAAAGGG
WI-11175	77	T A A	AAATGATTCTT TCTGCTCAAAG	CTGTTCTCACA TCTTTTTTGA AA	GGTAGGATGATCTAGAATGCCACTTTACAGCCACTGAAATATATTGCCCTCCCAATGATTTCTCTG CTCAAAGAGT/AJTJTJTJTAAAGTTATCTACTATTATATTCTGCTTTTTTCAAAAAAGAATGTGAGA ACAGTACAAAATGTGTTCCAGTATAGCAAAATTAATAATTAAGTAAGAAAAAGTAAGAAAAAGAGCCAAAT TGGGC
WI-10694	144	A G TATGAGTTTTC	TGCAAAATGCTT TATGAGTTTTC	GGCATTTTGTA AAGGAGGAAA	TAGAGAGGCTTTTCAGTTTCAGGGTTGGAGGGTGGTGAAGTTCAGTTCCTTAGAAGCAGCTGGC TATGTACAGAAAGATAAACTCTGAGAAAGAACTCAGTCTAAAGTGTTCAGTCTTTGCAAAATGCTTTA TGAGTTTTTC/GJTTCCTCCTTTACAAAAATGCCATCAATTCCTCAAGGAAAAAAGAAAGCTTTCT T
WI-2716	23	T C C	TGAATTCATCC AGAAAAACAG	TCTCTTTTCTC TCTTGTTGTCA TTC	GTGAATTCATCCAGAAAAACAGCT/CJGAATGACAACAAGAGAGAGAAAAAGAGATAAAGGTTTTTGT ATACGACAAGTGGCTCAAGCAATTTTCTCTGTCCAGTGCATGGAGCAGTG
WI-10719	115	T C C	TGACTCTCAAG GCCATTCTAG	GOACTGCCAGC AGCC	CAGGCCCAACTCTGTCTAATTAAGTGTTTTAGAACAGACACCTCAGTCAACAAAAGTTCTCTTTGTATGT GCCACCATAAACAGTTACTGGAGGATGACTCTCAAGGCCATTCAGT/CJGGCTGCTGGCAGTGCTT TCCAGCCTGCTGCCATAACTAA
WI-10721	40	A G CTGGCCA	TGGCTCTGCTA	GAAACTCCAC ATAAAATAAT CTCA	CAACCAATTCAGATTTAATTTTGGCTCTGCTACTTGCCCA/GJATGAGATTTATTTATGTGGAGTT TCTGAAGATTCCCATGGTAAATAGTATTCTCTTCCCTGCTTAGGTTTTGAAGAAGTTGAA

WI-11204b	88 T C ---			GCACACGAAATTGATTAAATTTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG AAAAGAAAAAAGTTTACCTTTT/CJATTTTAAAGTAACATAAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTTGGGAAGAGATTAGTGAATCAGAAAAATAAGTCTGAGGAAAAATTTATTCAGAAG GCAACATC
WI-11204a	80 T A AACTT	GTAAAAGGG TGAAAAGAAA	TGATCAGCTTAA AATGTACATAA TACCTTT	GCACACGAAATTGATTAAATTTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG AAAAGAAAAAAGCTTT/AJACACCTTTTATTTAAAGTAACATAAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTTGGGAAGAGATTAGTGAATCAGAAAAATAAGTCTGAGGAAAAATTTATTCAGAAG GCAACATC
WI-10732	80 C A ATTGGTTCACT	GCTGTGCTTC	AAGAACAATG CATAACAGAA CTTTAA	ACATGTAATTTCCCTTATAGTGGTCAGCCTTCCCTACCCCAAGAAATATCCCTGGTTTATTTGCTGTGCTTC ATTGGTTCACT/CJATTTAAAGTTCTGTATGCAATTTCTTTGAGTCCACATAGGTGTTAATCATTTCCA CACCACCTCTGTTTAACTGTC
WI-11206	127 A T ACTC	GGTTGTGTTTT CTGTATGTACA	GAGTGACAATC CTAATGGTTGG	TAGTCTTTTCTTTGTACGAGTGTCTATAAAGAAATTACCACCTCTGTCACATTTTGTAAAGATAGCACAG AGAGAAGCATTACAGGGCACAGCACAAACATGAGGTTGTGTTTCTGTATGTACAACTCJATTTCCAA CCATTAGGATTGTCACCTCTCATATATAGACAGAAATTCAGTGGTGGTGAATTTGAATTCACACATGGA ATAAGTCTA
WI-11215	68 C T ---		---	GAAAAAAAGTTTAAATTTGGATTGCTAGTTTGTCTTAAATTTGACCTACTTTTCAGATTTATTTTAGT [C/T]ATTTTCTCTATAATTTCTTGTAGTGGATTTCTATAAATTAAGGAAACAGATATTT ACACAGAGAAGACAGGATTGCTTGAATTAGTATAACATTTCTTTATCCAGCCCCCATTTCCACCATGT TTT
WI-11219b	89 G A AGAGAAA	GAGAGAATAT TCCAAAAAGT	GGTCCCTCTAAT TTTTCTACACT TTCT	ATGAAAAATGCATTAGAAGNATTGGAGGATAAAATTTGAGAGAATATTTCCAAAAAGTAGAGAAAAA GAGACAAAGAGATGAAAAATAGGA[G/A]GAAAAAGTGTAGAAAAATTAAGAGGCCATTTCTATACAG TCCAAATATTGAATAATAGTTATTCAAAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAAACATCTC
WI-11219a	18 G A ---		---	ATGAAAAATGCATTAGAA[G/A]AATTTGGAGGATAAAATTTGAGAGAATATTTCCAAAAAGTAGAGAA AAAGAGACAAAGAGATGAAAAATAGGAGAGAAAGTGTAGAAAAATTAAGAGGCCATTTCTATACAG TCCAAATATTGAATAATAGTTATTCAAAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAAACATCTC
WI-11222b	136 G A GGCTGG	CATACCACTGC	CCTGGTAGCCA AGTTGTGA	AGCCACAGTGGGAATCATTTACACTACCGAAATCAGCAATGCTAAAAATTTGGGCTTTGGATTTTGT TTTTGTTTTTCCATAGACCCCGTTGAACATTTGTTAAACATTTACCAGCATACCAGTGGGCTG G[G/A]TCACAACCTTGGCTACCAGGAGAACCTGACACAGACTTCGTAATTTGCTTTTCACAGGCTACTGG AAAGCC

WI-1122a	25 C T A	GCACAGTGG AATCATTTAC	TTTTAGCATTT GCTGATTTGG	AGCCACAGTGGGAATCATTTACACTA[C/T]CGAAATCAGCAATGCTAAATTTGGGGCTTTGGATTTT TGTTTTGTTTTTCCATAGACCCACCGTTGAACATTTGTTAAACATTTACCAGCATACCAGTGGG CTGGGTCAACAACCTGGCTACCAGGAGAACCTGACACAGACTTCGTAATGCTTTACAGGCTACTGGA AAGCC
WI-10775	39 C T CACTC	TTATGCCATA TTAATTCATTA	CTAGATGTAAT TGCTAAGAAA ATATGATG	TTGCAAGTTGTTTTATGCCATAATTAATTCATTACACTC[C/T]ACATCATATTTCTTAGCAAAATACA TCTAGACACCTGGCACTCAGTAAGGATATTCCTGGCAGGATAATCATTTGTTATCATTTAGACATTTGCA GGAACCCACCATATGGATGAATAATGTTGTTTAAATGAAGCAAGCAATTA TTGCATGCATTTATACGAAAGGAATTAATAATATCTCCTTATAGTTGAATTTAAGTAAAAATAAA GTTATACATATAATAACAAAAGTTGTAAGTATAGTAACAAATGAATAGAAAATTTGCAGTGGTTGC TAGTACAGGAATCAAAATTTGGACTATGAACA[A/C]GACATAGTTGCTAAGGATATTCACACAAATTA TTCATGA
WI-11226	165 A C ---	GCAGGGAGG AACATTTACA	---	CAGTGGCTGGCTACTGACAAAACGTAACTCGTGGCAGGTGGCAAGGGAGGAACATTTACAG[A/G] TCCATCTCTGATGTCACAGCAGGGCCAGGAAGGTTGATCTGGAG TGGGACACACTGCTCTAGACC[C/T]CCCCAGGTCCTCAAAGGTGGGTAGAGGGCCCTACTGCCCT GCCCTGGGACCGAGGACATCAGGGCCCTAGTCTCCTCTGGGACAGTGAAGGGCCACCCACC ACAGAAAAATGCCTAGGCTTTGTAGCAAGAGAGGAAGCATCTTCATGGGCAGGAATTC/T]CATTT CTGTGTTCTTAGGGTTGTGGCTGGCCATCAGTTCAACTCAGCCCTGTCCTGATCCAGCAACAT TCCGTAACTACCCCTCTAGAAGTCATGCAAAAGAGAAATGATGA
WI-10778	62 A G	AGAGATGGAC	CTGGTGACATC AGAGATGGAC	GGACCAACAGAAATTAATCTTGGCA[T/C]JAGGGTTTCTTAAACATTTTCTGCAGAAACATTTAGTAAAGT TTAAATAAGGATCAGGCTACCAGGAATACAGTTAGGGAACATGTGGATGAATATTTCTTTAGTAGAG GACITCTAAAAGGCTATAATTTGGATACATAGGCTCATTATGAATCTCAAAAGGAGCATGTAGT AGGGCATATCTAA
WI-10789	21 C T GCTCTAGACC	GGGACACACT GCTCTAGACC	TTGAGGGACCC TGGA	TATGCCCTTCCCAACGAGCCATCCACGCTGCTCTTAGCACAAAAATAGAAATACATCTGAAATG GGCACAATTAATCTGCAGGCTCTCC[G/C]TTTCTAAGTCACCTGCAGTTAGGCTGCAGACACTGTGTA TACCATATAAATCTGATTTCTGAGCAGGAGGGAGGAGATGAGAGAGGGCTGCTCCGTGAAATAC TAGTTCGG
WI-10810	58 C T GCAGGAAT	CATCTTCATGG AAACACAGAA ATG	CAAAACCTAAG AAACACAGAA ATG	GATTGAGTATTATCAAAATGCCCCAAGACCATTAAACAGATTTAATAGTTAAAGCCAAAACATA AAGAAATTAACGTTCAAAAGTGTGTTAA[T/C]TCTAATACCAATTTTATAGGGCCACCATTAACCT CTGAAGAAAGGTCAGCATATGCAACTAAATTTCTAAAGTCCAGT GGATGATGTTCTGTGGTCCCTTAT[C]AAAGCCTCTTGCAATCCCAATGTGTAATTTATTTCTCT TGGTATTTCTCGCTTACCATAGTCACCTGTCAAGTGTTCCACCCCT
WI-10828	23 T C ---	---	---	
WI-10832	91 G C AGGCTCTCC	CATTAATCTGC AGGCTCTCC	CCTAACTGCAG GTGACTTAGAA A	
WI-10834	96 C T GTGTTAAT	AGAAATTAAC GTTCAAAAGT	TGGCCCTATAA AATGGTATTA AG	
WI-2287	24 T C ---	---	---	

WI-2296	81 A	G	TGTTACTTTGA TTCTTTGCTCT	GCAATCACAC AGCTAACTGG	TGGAGGGTTAGAAATGCAGGTGGCATCCTAGAAAGGCTCAGGCTTTAGAATAAGTTGTTACTTTGA TTCTTTGCTCTGAC[A/G]CCAGTTAGCTGTGTGATTGTCAGAAAGTTACATTTGTTTGTGG
WI-2300	77 G	T	GGCACAGAAG CCAGTCATAC	GGTTGGGTCAA TTTTAAAGCA	TTTCATCATGCTGCTTTCCCTGGAAATTTCCCTTTATTTAGCGGGGCGAGGTGGTAGGCACAGAACG CAGTCATAC[G/T]TGCTTTAAATGACCCCAACCAATTACTAAGAATAGCAATTCA
WI-2371	55 G	T	GTCTTGTTCTT CCCAGCTTCT	CAAAGATTGAC AGCCACCAC	CAATGATCCCCCAACATTTCCAGGAAAGTCTGGCTTGGCTTCCAGCTTCT[G/T]GTGGTGGCT GTCAATCTTTGACATTCCTTGCTTGCAGCTGTATAATCCAAATCCITGGCTCCAGCTTTACATGATGT TCTCTCCGTGTGCTGTG
WI-2395	122 A	C	GAACATATTT GTAGAAAAAT TACTATCCAA	TCACCTTTCTA TTTATTCTGAA TTCA	GGGGGCACAAATTTAGCTACAGTGCATATTAAAAGATAACATAGAAATATCATATAAATTAACCTTGGTTTAC TGAATCTGAAAACTTAGGATGAGTGAACATATTTGTAGAAAAATTAATCTATCCAA[A/C]CTGAATTC AGAATAATAGAAAGGTGAATCATCTTATCATTAAGAAAGCTAAATTAATTAGTAACAATCTTTA CATTTACAAAAACCCA
WI-2437c	192 G	A	---	---	CACCAGCCACCACCTACAACTCCTGTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCTCTGCAAGAGGCAATCGACGAACATCACAGTG[A/G]GCTGTG GTGCCAAGGACGCATTATG
WI-2437b	179 G	A	---	---	CACCAGCCACCACCTACAACTCCTGTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCTCTGCAAGAGGCAATCGACGAACATCACAGTG[A/G]GCTGTG GTGCCAAGGACGCATTATG
WI-2437a	128 G	A	---	---	CACCAGCCACCACCTACAACTCCTGTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATCCCAATG[A/CTC] TAAATAGATGGACTCAACCCCTTCTCCTCTGCAAGAGGCAATCGACGAACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2440	71 G	A	GCAACCTACT GACAATTTAA TTTTAGTT	AACAACCTCTGC TATTGGTCTCA C	CAGTAGGAAACGGGTCTCTCCTTAGACCCCTCCAGAAAAATAATGCAACCTACTGACAAATTTAATTTTA GTTG[A/G]GTGAGACCAATAGCAGAGTTGTTACCTGCGAAGACT
WI-1356	123 T	C	TGTTTAGGAA ATAATGACAA	TGGTTACAACCT GTACCAAAACAT G	CTGTAACCTACACATCCTCCTGTAACCTCTAGGTTACTTGTAAATACAAAAACACAATGTAAATGCT ACATAAAATAATTGTCTACTATATTTGTTAGGAAATAATGACAAGAAAAAGCC[T/C]GTACAT GTTTGGTACAGTTGTAACCAAGCCATTTTCCCCCAATATTTTCAATCCACAGTTGGTTTATCCACAG AAACCACGAATG
WI-2886	46 C	A	CAGAGTCTGG GGGAGAAGA	TTGCCATGCTT TATCTCGTT	ACAGTTAAGAAAAAGGCTGCAGCCGTTGCAGAGTCTGGGGAGAGAA[G/C]A/AACGAGATAAAGCATG GCAAGACCACGCTGAAAGTATCCAGGGTGTGTATGTGCACATAGGAAGATCACTTACCTCAGCA TAGGAGGAGGGCTAGGCAAGGAAAGGTGTCAGAAAGAAACAGAGGAGCGTT

WI-2906b	77	T A	---	---	CCTGAACACCTGGAGCACTTCCCTCCCTTGACACCTTCATCTTGTGGAACTTTGCCTGGAATGCTCTTTCCCTCTT/AJGAGCTTTGCTGGCTTACTTTTCTTTTCCCTTAGGTTTCAGCTTCAAAGTGACCTCCTTAGAGTTGGTTTGTGACCAACAA
WI-2906a	50	A C	GTCTGCTGG	GACACCTTCAT	AGAGCAATCCA GGCAAGT
WI-1736	175	C T	---	---	ACCTTGG
WI-1851	136	G A	GTGTTAAGTA	GCATTGAATT AACTATAGAT	TAATCCCCACGTCCTAACACCATCACACTGATCATCAATCAGGTTTAAACATATTAACTCTGGGAGGACACAAACATTTAGACCATAGCATTTGAATTAACATATAGATGTGTTAAGTAAATATATAACATGGTACA[G/A]ACAACCTTCAGTTTAAACATTGCTAGTGATCCATGTGGATACCATGTACCTTCTTACATCATGTGA
WI-3000	62	G A	AGAGACCCC	CCCAAAACAC ACAGATCTAT	CTGATGTTTGGGAAGCACTGTCTTACATCTCTAAATGTAGCACACCCAAACACAGAGACCCC[G/A]TGAGCTTAGTCAATCCTATAGTGGCAGTACCTGAATCAGTGCCTGGTGATAGTAGACACT
WI-1754	177	G A	TAGTC	TTTCTCCCTT CTTAAAGAGA	ATGGATCTGCTCAATTATAGTCCCAGATAAACAGCCCTTCTCCCCCCCCACCCCGGATTATTTTACTTAAGGGTTTAGCAAATTCACCTGACAAAGAGTTAGGTTTCAACATTGACCCCTCATAAAGTGATTTTCTCTTTCTGTTTTGTTTTCTCCCTTCTTAAAGAGATAGTC[G/A]CCAGAGGGCAATTCGACTTTCTGTAGCCACAAGATT
WI-3167	37	T A	TAGATTC	AAATTC AACG ACAGATCTAT	ACAACACAGCAAATTC AACACAGATCTATTAGATTCTT/AJACCCCATCTCAAACACTATCACATCAAGAAAGCAAGGAGACATATTACTGGTGAGGAAGCCAAATTCAA
WI-3208	140	G A	AGATAAAGA	GTGGAGTGGG AGATAAAGA	CAAGCACACATTCAGGCAGTGGGCAGGTAGGAAGGTGGCAACTTGGCGACGAGAGAGAGGGAAGAAAGTCAGACCCGTTGGTAGGATAAGTGGATCCAAACCCCTTGTAGGGCAGGTGGTGAGTGGGCAAGATAAAGA[G/A]CCAAGCCCTAGTTTGAGTGACACTGTGGGGATTCAAG
WI-1775	47	C T	TTTCTCTG	CCTGCATGGTC TTTCTCTG	ACTCCACCAACAGTTTGTGAGCCAAACCCTGCATGGTCTTTCTCTGCTTTTACATCATTTGTCATAAATCTCAACTGACACATCAGTGCTCTGCCACCCCA
WI-3402	55	G A	ACAT	AGCATATTCA TTGATTTCCCT	CTGCCCTTTACATCCAAAGCCAGTTACTCGAGCATATTCAATTGATTTCTTACATG[A]CAAATGCTCTTTTAAAGTCCTCAACTTTTAAAGCGGAAGTTGAGACATGCACAAAATAGATTTCCCTTAGGA

WI-3416	33 C T	CCAAAGTTGTA GCATTCAGAA	ACGAGCACAA CTACCTCTAAG AG	TCTGGTTCTCCAAAGTTGTAGCATTTCAGAAAGTC C TCTCTTAGAGGTTGTTGCTCGCTTAAAA TATGTTTTCAAGATAGTATCTCCCTGTTGTACCTTCCTCCAAACAAAGTGTACCAACAGCAITTTAAAG GAAATGTGCAATGCTTGTCTACCCTCTGACGCACACATAATTAATCCCATTCCTTAAAGACACAGG TCCTATTCTACAAACACAGAAATTTAACAAATTTGAAATCAGCTACTCTTCTTAGGCCCATCAGAG AAT C TGAAGTCATGGGAAAAATTTGATGCCATGTGAATTTGGAGAAACAGACAGGCATATATGGAG AATTACAGTTTACCAGGGACACAATCCCACITTCAGAGCCATCTGTAAAGAC CATGCTAGGTAGATCTGATCATGAAGTTTGAACAAACTTAAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAAATTTAGCACAGTATTTAATGAGGTGGT G A TGGGAGAAAAATTTGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3453	70 C T	TTCTTAGGCC ATCAGAGAA	TCAAATTTCCC CATGACTTC	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAAACTTAAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAAATTTAGCAC A G G TATTTTAAATGAGGTGGTGGGAGAAAAATTTGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3474b	109 G A	---	---	TTTGACCCCATACATGAGAAATAAAACCATAAGAAATGTTGGAAAAATAAAACGGGAGAGACCTGGG TTTCTGGATGTCT C T TGAGGACAGGGTCAACCCAC
WI-3474a	90 A G	AGTCAGTTTCC CTAATTTTAGC AC	CAACCATCAAT TTTCTCCCA	TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCTCTGCTGCTTTCCAGAGTCTGATTTATCCATGCCCTG ATAGTTCTGTGAGCCACCTAAACTCGTTTCTGCTTAAAGTTATCCAGAGGTGGTTTCTAACCTGGATA TAAACATCT G C ATGGAAGGCTGCAC TGGATGAGGTACAAA
WI-3502	79 C T	CCTGGGTTTCT GGAATGCT	GGGTGACCTG TCTCA	TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCTCTGCTGCTTTCCAGAGTCTGATTTATCCATGCCCTG ATAGTTCTGTGAGCCACCTAAACTCGTTTCTGCTTAAAGTTATCCAGAGGTGGTTTCTAACCTGGATA TAAACATCT G C ATGGAAGGCTGCAC TGGATGAGGTACAAA
WI-3600b	146 G C	GGTTCTAACC TGGATATAAA CATCT	CCAGTGCAGCC TTCCAT	TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCTCTGCTGCTTTCCAGAGTCTGATTTATCCATGCCCTG ATAGTTCTGTGAGCCACCTAAACTCGTTTCTGCTTAAAGTTATCCAGAGGTGGTTTCTAACCTGG ATATAACATCTGATGGAAGGCTGCAC TGGATGAGGTACAAA
WI-3600a	78 T G	CCATGCCCTG ATAGTTCTG	GGAACGAGTT TAGGTGGCTC	TAAATCATGCTTATTTTTCACAAGGTAATCCACTCACAAATAGGCAATTTGATGTGATCTCTTCTGTAA GAAAAAGCTCTCATGCTCTTCTCTGAACCTTCTACTTACTGTGCTGTTATGATGCACCTG T CCTTTTGG ATAGATGGTTGATAGGAGATGGTTGTTAAAGACACAAATTTACCTTGTGTTTCAGGCAGAAATAG ACTCTCTCTGTGTAATCACTGAATGAGTTCCTCCAAAGCCTTTATGCTTAC
WI-3678	125 G T	---	---	AAAGCGATGTTGAGATACCACATTCATGAAAAAGTAAAAACACACACAAAAATATGACATAAAA T A C JAAAAACTACTATAGTTTATGAAAAATGACTTCCAAAAATTCAGAGAAAAAGTCACTTAAACAGG ATTCTCAATTCATTCAGAAATACTCCTCTGTCATCTTAACTTTGACTGCACAG
WI-3687	67 A C	---	---	TCTAAATGTGAAACCAAGAATCTTGACAGCCTAACTGCCAGTCTCAGTTATGTATCAAAATGA AAAACT C JACACCGGTTCAATGAAAAACAATGATTTGGTGAGCCATGTCCTTATTTAATGAAAA GATCTGGGCAATTAATCT
WI-3735	72 T C	CCTCAGTTATG TATCAAAATGA AAAAAC	GGCTCACCAT CATTTGTTTT	TCTAAATGTGAAACCAAGAATCTTGACAGCCTAACTGCCAGTCTCAGTTATGTATCAAAATGA AAAACT C JACACCGGTTCAATGAAAAACAATGATTTGGTGAGCCATGTCCTTATTTAATGAAAA GATCTGGGCAATTAATCT

WI-1819	51	C T	---				GAAAAAGCAGGAAGCCAGGCAGGACAAACATTTTGA AAAAGTCTTTCAGCAC[C/T]TTCGTGGATCCG AATTTTAGTGTGATTTGGCAGGCAATGCGGGTAACATGTTCCAGTGTTTAACTTGCACAGAAATTGC CAGATTAGCGATTGTTGACTTGTCCAAATTAATGAAATGTGGA AAAAAAAGGGTGGTAACGTGT AAGCCTGCTGCAATGTTTAGACACAGAGGGTGGGGTGGGAGGTGGAATAOC
WI-3746	116	G A	---				GGCTATTACATGACACTGGGCCAAGATCTTGCTCCCTTCTTCAATAGATAGACTAACTAGAAA ACTGCCCTGGCCAGGAAGATGGTTGTCTTCATCATCTCTGCTCTG[C/A]GCCCCAGGATAAAGCA GGCA
WI-3867	49	T C	CAA	ACAGTCATTT AGTCTTCCTGA	TAAGATAACC ATACTAGGTAC ATCCG		AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCTTGACAAAT/CJCGGATGTACCTAGT ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTGAACAAGACACAGT CATTAAAGTGGAGAACCCAGCATTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG CATC
WI-3898	25	A C	G	TGACCAATGTC TTTAGAAGCA	TCGTCGGTGTG CTCTCC		CAATGACCAATGTCTTTAGAAGCAG[C/A]CGGAGAGGACACCCGACGAGACACACAGGAAGGAGTGAG GTGAAGATGAAGCAGTGTGACGCAGCCACAAGGTGAGGAAGCAAGGGTGTCTGGCCACT
WI-3901	114	A G	---				GGACCATTTGCCCTCAGAAGTACATTC AAGCCCTGGACGGTGTCTCTTAACACTGTGACCTCAGGCA AGTCATGCTGCTTCCTGAACCTCGGCTTCCTCACCTGACAAGTGG[A/G]TATCATGTGCTACACTGC AGTGTTTATAATGCTGCAAT
WI-3914	99	C T	GC	TGATTCCTCTC AAGACTCACA	TCTAGAAGCAA TGAAGGATGG		CTGAGGAGATTGATGCTACTTTTACCTGAGGAAACITTTTATACCTCCCTGAGTTTGTTCCTTGCAA GACATTGCTGATCTTCTCAAGACTCACAG[C/T]ACCATCCTTCACTTCTTAGACCTATAACTAG ACTCAAGTCCCAGCAGGCCCTTAAAGGTAAGGTACAAGTGTGACCCATGGGAGGTATGTTACGCTA CAAAAGAG
WI-4019	33	G A	A	CCAAGAGCGT CCTATGAATC	AACAGCAATA ACAGGAACAA ATG		CCACTCCCAGGCCAAGAGCGTCTCTATGAATCAT[G/A]CATTTGTCTCTTATGCTGTTCCACAGAGT GGCAACTCTTGCAAAGGGAGGGGTACAAAGTGAAATTTTAGATGCTGCAGGAGACGAAGGGTC
WI-4091	84	A T	GTCAATGCATG	TTGAGGTCTTA GTCAATGCATG	TGAGTTCCTAT TAAGTGACAAT ATTGTT		TAATTCACATTGCTCTTGTGTGCAATTTATGCTCTCTTATGTTAAACACAATCACCAACATTGAGG TCTTAGTCATTTGCATG[AT/J]GTATAACAATATTGTCACCTTAATAGGAACTCAAGCATAGTTATGTGT ACATTTATTGCTAACAGCAG
WI-4160	117	A G	CAACAGAA	CCTATAATTTA GCAACAATAT	TGCAGGTAGAA TTTTCTAATAT AGCC		TCCTCTCTGTAATAGGAAGTCTGATTAGATGCCCTTTTGAGGTTAGGTGGCTTCTAAGATGGTAATT ATCTGTCCAAAGTTTTTGTTCCTATAATTTAGCAACAATATCAACAGAA[A/G]GGCTATATTAGAAA ATTCTACCTGCATCCCCCTGGATCTGAACGTTCTTCATGATACT
WI-4168	32	A G	AAACA	GGTGAGAGTC AAATTGATAC	ATTGCCAAACA GATTTTCAGA		CGTTGCTGGTGAGAGTCAAAATTGATACAACA[A/G]TCTGAAAATCTGTTTGGCAATCTATTAAAGG CAAAATATACCAGCAGTGTGGTCTAGCAATTTCACTGCTGGCATTACCTAACATAAATGAT

WI-4177	68	T C	TGAATAAGCA CGTATTAAAT TACCTA	AAGGCAGCA ATCATGATG	ATGCCTGGATATACCTTCCAAATGACTAGTATGAATAAGCACGTATTAAATTTACCTATTATATT AT/C/CATCATGATTGCTGCCCTCTTCCAAATTTACTACAAATTTGATTGTACATGAGGCACATG ATCCCATTAACCCAAATAG
WI-4199	51	A C	CTCCCCAAGTT AGTCAATATA AAAA	ATATGTTGATT AGGTATAACA ATATGTGTG	GCCATGAGCACAGAGGCTGAACCCACTCCCCAAGTTAGTCAATATAAAAAAA[AVC]CACACATATTG TTATACCTAATCAACATATAAATGTTATAGATTAAACAGTCCACAGCAAAACAA
WI-5163	24	C T	CTGCACTGGT CTGCCCTGT	AAAGGAACAC AGGAACAGAC C	TTCTGCTGTCACGGTCTGCCCTGT/C/TGGTCTGTCTCTGTTCTTCAATGTTCACTGCTGTGAT CTGTGCCCACTAAGGTATCAGGTTTATATGGGCACAGGATGAGGGCTTTGTAGACCAGAGTTTCTT GGAAATTGCAACATTGGGCAT
WI-4250b	117	A G	---	---	TAAGTGCAATTAAGTGTACAAAGTCCACAAATACCTCTCCACCAAGTGTAAAGCAGTTTTTAATAACA GGTTCAATATGAGTCTTGTGAACAGGGGTGGGAAGGATCCTGTAAAGG[A/G]TAATATTGTTTT CCATAATATTGAAGATGTG
WI-4250a	94	G T	TCAATATGAG TCTTGTAAC AGG -	CTTTTACAGGA TCCITCCCAC	TAAGTGCAATTAAGTGTACAAAGTCCACAAATACCTCTCCACCAAGTGTAAAGCAGTTTTTAATAACA GGTTCAATATGAGTCTTGTGAACAGG[G/T]GTGGGAAGGATCCTGTAAAGGATAAATATTGTTTT CCATAATATTGAAGATGTG
WI-4255	68	G C	TGCTOCCCCAT CACT	AGTTGTGTAAG G	TAAATGTCTGGGGAGATAATAGGAAGGTCCCATCCCTCTGATACCTTGGTTGCTCCCCCATCACCT [G/C]CTTACACAACTTGAAGTAGGCCCTCCAAACACTGGTCAGAGAGTAATACGTGCGAC
WI-4256	57	C T	---	---	ACAGCCTCTTCAAATGGCACAATCAAAAGCACCAAGTAAAGCAGAGGCAAAATCTGG[C/T]CTCAC CATGGAAAAGTCTCTGAAGGATAAGGGAGTGAATGACTGCTAGAGAGAAATGATTGGCCTT AGTTCACTGCCTAGATGAGTACCATGTTGTCCTTTGTTAAATGTACATGGCAGGACCCGGAATGG GATG[C/T]TACTATAGATAATCTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACAGCCAC CCAGGACACTGCCATATCT
WI-4325b	71	C T	---	---	AGTTCACTGCCCTAGATGAGTAGACCATGTTGTCCTTTGTTAAATGTACATGGCAGGAC[C/T]GGAAA TGGGATGCTACTATAGATAATCTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACAGCCAC CCAGGACACTGCCATATCT
WI-4325a	58	C T	---	---	TGGCAGAAAGTCGGGTATGGCAAGTCAGGGTGGGTTAACTTGGATGCCACTTCTGCTGTCACCTTCT CTAGACTCTTGACCCCTGCAGAGGATCCCTGGCCTCCTGAGTTTATCATCTCCACCTCCAGCCAG GGCCCTGTATCTGTTTCAGGCC[C/V]GAATCTGACGGCTCACAACCTGTGGAGGTAGGAATGACGA G
WI-4347	158	A G	---	---	CCAGTCTAGGCTGCAAGGACTTCAATTCTGGGCAAGTCTGGTGTGCTAGGGTCAGAGGCAGCG ACCTGAGGGACACACAAACAGTGGGACACCCAGGGGTACTTGTATCACCT[C/C]TCCCGCAACCCCA AGCAGCACAGCTTGCAGCTCCAGGAAAGACTCCTTACTTCCACTTGAGAAAAGGAGAGGGGAAGAGA AAAGAGGACTTTGACACACAACCTTGGA
WI-1936	117	T C	---	---	

WI-5204	54	C T ---	---			TAGATTTGATTGATGACAATAGGGAAGCCTTTGTTAAATTTGGGTTTTGAAGAA[C/T]GAAGAAAA TGGAAAGGGAAGATTGACAGAAACCAAGAGAGTGTGAGGGGCAGCAATCCAGTTTACTGGA ATATAGAGTGATGTCAGGGTTG
WI-5215	70	A G C T C A A A A A	AGATAATTTTG TAAAGATAGTT TTGGC			TTTCCCTTATTTATTTAGGAAGCAAAATGTTTCATACAGGACCTTAATAATTTAACAGACTCAAAAA TAT[A/G]GCGAAACTATCTTTACAAAATTATCTCCATAGCAAGTAGACATTTTAGCACATTTTCTCT GTAGTCAAGGTTTTAAAGGCCAAATGAAGTTGACTAAAGACAAT
WI-4448	112	T G A T A A A	AATTAAGAA ATCTTTACATG GTTCTTT			CCCTGAATGTGCTTTGCTTCTCTCCAACTCTCTAGGGAACTTTTCCTGTCAGGTGAAGTTTGA AGAGTACTTTAATTAAGTTGATCAAGAGATGGGTATATAAT[G]AAAGAACCATGTAAAGATTT CTTTAATTAGTGAATTTTCATCAGGGCTCTTCCACTGCTATCAGTAA
WI-4456	49	C T T A T A G T T C C	AGTTGAATTA TTCAGAAAAT TATAGTTCC			ACACATTTTCATTTTGCCTTAAGTTGAATTTATTCAGAAAATTTATAGTTCC[C/T]CAAGTTTCATGCATAA CAGGAACACACCAGGTTGGGCAATTGATTGAATTGT
WI-4461	49	A G C C T T C C	TCACTGTTATT TTAAAATTAT CCTTCC			CTGAAACTAATGAGGTGCTAAATCACTGTTATTTTAAAAATTATCCCTTCC[A/G]TGAAAATTGGTGAAA GGTCAAGAAATGAATTTCCACTTTTAGATTCTTGAAATTTTATTTGCGATGATAATGCAATGGGC
WI-4465b	75	G A ---	---			CTACTGGATTTTACTTTGCTCAAGCCAGACACACGAAAGT[A/G]TATAAGAAAACAGTTAGTAAT CTTTCACCTTTGTAATTTCTCTCTACCTCAGGGAATC
WI-4465a	41	A G A C A C G A A G T	GGTGAAGATT ACTAACTGTTT TCTTT			GGGGTAGGACCTCGAGATCTTTTCAGAAAGCACAATTCAAACCAATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTTCAAGGCTGCTGACATGGTCAATGCTGAATATATGTTGAAGAAATAAA
WI-1949b	160	T C T A A T C	TGAGAGGTGGG GACAAAA			GGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTGTCCCACTCTCACACCTTTCCCTGG CACA
WI-1949a	86	T G A T G C T C T G A G T	CCATGTCAGCA GCTTGG			GGGGTTAGGACCTCGAGATCTTTTCAGAAAGCACAATTCAAACCAATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT[G]CAAGGCTGCTGACATGGTCAATGCTGAATATATGTTGAAGAAAT
WI-4529	64	T C A A G A T G	TTCTAAAAATA ACACTTCTGA AAAA			AAAGGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTGTCCCACTCTCACACCTTTCCCTGG CACA
						TGAGAGAGTTTTGGATTATTCATCTCTGCAACACTCCAAGTAAGTCTATCATCTCTGAAGATG[T/C] GAGTTCTCTTTATATCTCTATGATTATTTTCAGGAAGTGTTATTTTGAATATAAACTCTCTGGGT CCATCCAGGCTAGGGTCAATGGCATCCATGGGTCGCTGGACAAGATGGGCCCTAGGATCATTTT

WI-4540	110	A	G	GCACATGTGG CATCC	GACATGGAGC CATGCA	AGCTTTCCCTTTCTTAAAAATTGGTGCCATAGTACTGGCTTCTGTGTGTCATCAGGAAGCAAGCCTAT TGCTCGGTAAACAGTACTTTGCAATAAGCACCATGTGGCATCC[A/G]TGCATGGCTGCTATGTCCAGTCA AAATGAGACAACTTCCCTAT
WI-4582	226	T	C	---	---	AGCAAGCATCTGGCAAGCCTCGGTGACCAAGAACATTAAATTCACCAAAACACCACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAAGACTCCAGTAGCATTCAAGGCCAGTTAACTTATTCTCTGTACACA AATAACTTTATGGGAGACAGCATTTGTAATCAAAATCAATAAATGACTCGGTTGGCTGTACAAAGCAT AAACAGAACGCTTGCAAAATATGGT[C/C]CTCTGCTAGAAACCATTTGAT
WI-1965	105	G	C	AG	GAATGGATGGG TCATCTCTCT	CAAAGTTAGTTAACTTGGGGGCAACACAAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGGCAATTGAGGAAGTGTAAAG[C/C]AGAGAGATGACCCCATCCATTCTCTGG GCTTCTTATATGACACCATACTATCCACACAGATGTGGAGTCATTTATTTGGTTGGTGTATGACAGT CATGG
WI-5248b	99	C	T	TTG	AGAAAAAGAG AAGAAGGGAA AAA	TGTTTAAAAACCATACAGTTTGTGCTGCTACGTTGTTAGAGCAACCCAGAAAAATTAACAGCCTAC CATTTTCACTGTTTCTATTGACCGTACTT[C/T]CTTTGCTTTTTTTTCCCTTCTCTCTTTTCTG CCCTCTTTTAACTATT
WI-5248a	38	G	C	CTACGTTGTT	TTTTAAATTTTC TGGGGTTGCT	TGTTTAAAAACCATACAGTTTGTGCTGCTACGTTGTTAGAGCAACCCAGAAAAATTAACAGCCTAC TACCAATTTTCACTGTTTCTATTGACCGTACTTGTCTTTTGTCTTTTTTCCCTTCTCTCTTTTCTG CCCTCTTTTAACTATT
WI-4596	69	T	A	AGCACTGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGTCCAACTTCTCGGTGACATTACTCTGTTGACTTGTCTGAAGCAGAAAAAGCACTGTGA C[T/A]CATTATTAGGCCCATCTCTGCTGAAGCCTGCTACAGCAATTTGTACATATGGCATTGGG ACATACTCTGAGCCCCCACTATTGACAAGATTCTCTCTTTTAAACA
WI-5252	119	A	C	---	---	GAAATAGGGCAAAATTAAGACTTCAATAATTAAGAAAGTCTTGGGAAAAGGATTTGTGATGATCATTTG AATCTGTTTAAATACAGAAATTAATACTGAATACCTGTGTGAATCATTTGCTTT[A/C]TACCATGTACA TATTATATGAATTAACAATGTAAATAGTATGACTAAGAAATATTGGGCCCT
WI-4606	61	A	G	CT	TTAGGTGCTTA AGTTGTCTACT TGG	TGCAAAAAGGAAAATGATAACCAGGACGTGTTGTTCAAGCAATGCTAGAAAAATTTATGCCTA[A/G]C CAAGTAGACAACCTTAAGCACCTAAGGCAGAAATGAAGTTTCTCTCTGTGCTAATTAAGTCTCTATTCA ATTACCAATTTATCGGGTAAATTAACACTGGAAAGTAATGCCAGGCTAATTTGTTAGATTATGATAAT TACACGCTTTGCTATGCT
WI-5257	77	C	A	GCAAGAGG	CCAGGGGCAGA TGAAAG	CAATGAGAAGTTACCAGATGCGGGGCAAAATTAAGCATATGAAAATACCAAGTGTGGCAGAGGCATG AAGCAAGAGG[C/A]CTTTTCATCTGCCCTGGTGGTTTTCAGTAACTGCAACATGCTTTTGCCTCC CGGATGAAAAGATACCCCTTCTATGACTCAGCAATTCACCTCCCTAGGTATGCACCCTAAACATGGGTG GCAAAAT
WI-4649	50	C	T	TTCCGAATG	TGTACTAGGTG TACTTACAAGA AATCATC	TCACTGTTTAGAAAATTTCTCTCTCCTCAGTGAGACCATTCTTTCCGAATG[C/T]GATGATTTCTTGTA AGTACACCTAGTACATCTATGAGCACACAATTAACAAGTACTTGTCTACCTGAATTTGTATTTTTTAA AAAATCCTCCCAATATTG

WI-4650	148	A	G	G	GCACAAAGAA AGTATAAGTT GTCCTT	CTGAAGTGTTA AACTGGATTG G	AACTGTGGTATGTAATTGTTGTTGTTTCTGGAGAGTCAGTACTCTCACTAGATCATAAAGGG GACTTGGGAACCAAAAGTATCTCAAGACATTTAATCTAGAGCACAAGAAAGTATAAGTTGTCCTC TTATAATTGCTTTT[A/G]CCAAATCCAGTTTAAACATTCAGTAACGTT
WI-4677	82	T	C	AAA	TCCAAAAGTG ATTAGGTGAA CCT	TTTCAACAGTG TCATTATTCAA CCT	AATTCAGATTTTGAACATACGTCGACATTTTGGAAAAAATTTGCCAAAAAGTGATTAGGTGAAAAAAT GAGTTGAAATAAATGTC/JAAGTTGAATAATGACACTGTTGAAAAATGATGAATCTGCTTTCAATTCA CATGAAAGGAGACTAGAACACACAGCAGGTTTATAGGGGAATACAT
WI-4698	135	C	G	---	---	---	ATGATGCTATCATGAGGAATCTGTAGAAAAATTTACCTGGCAATGATTCAAATAAAGTTTGTC TCACCTGGAAACTGCTTATCTTGATGTCAGTGACATTTCTTTCTTTGACGGAAAGAAACTTCAA C/GTTTCGAGAAGGCTTAGATTATATCGCTGAAGCCCCATCTG
WI-4722	88	G	A	AACACCACAG	TGCATTCAGTT G	AATATGGAATC TGCATTCAGTT G	CTTCCATTCTGCCAGTTAGATGACTGCCTCTCCACCAGCCTAGAAAAAGATGGGAGATTTATTTTC TGCACTATGGAACACCACAC[G/A]CAACTGAATGCAGATTCCATATTGAATACTGGGAAATCAGTGA AAG
WI-2020	145	C	A	---	---	---	GCCACAGTAAAGAGGAAAAATGGAGCCATGTAAACAGAGGAGAGCTTTCTGAAGATCAGTGTATTGTCA TAAAGGTCAAGTAAATCATTGATGGTTGAGATTTTCAGAAAAACGTGAAATTTATTGAGTAACCATGGG TCAACTATGAT[C/A]CCAAAACAGCAGTGTGCTAAAAAATATGATAGTTCTCTCTCTGTCACCC GCAATGAAAAGGAGTT
WI-2028	176	T	C	CCTGCTCATC	TGTTACGTTT GAA	GGTTGGAACT CAAATTACCTA GAA	GACTACAGCGCACAGACAGGCAATGTGTGGCTTGCACAGGTGTTGGTTTGTGTTTAAGTTAGATT TGAATCCTTTAAAGAAAGTGGCTCTTCAGTTTACTACAGACCTCATCATCTCCTGGTCTCTTG CACCCAGTCCACTTCACTGTTTACGTTCCCTGCTCATCT/CJTCTIAGGTAATTTGAGTTTCCAACC TGTTGG
WI-2033	183	T	C	A	GGGTGCTAGA ACTAATCCCTC	CAGTGGTTCCA CGTTCTCC	ATGTGTATGAGCTCCACATTCGCAGATTCAACCAACTATGGATAGAAAAATATAGTATTCACAGATGG GCAGCCCAAGGATCAGAGGGCTAATTTTAAATTTTCCAAAGTTATACAGGACCCAGTGTGGAAATTT AGCATTTCTGGGTTTGGCATCCATCAGGGTGCTAGAACTAATCCCTCA[T/C]GGAGAACGTGGAAACC ACTGATATACCAAT
WI-4745	131	T	C	---	---	---	TTATGGATACATGTTTCTGGTGAAGGACAAGAGTTGAAGCAAAAGGACAAGGAGATCAACTGGG TAGAATAACTCATCGATCCCAAGGCTCCTTCCACCAATCTCCACTCTACTTTCTACTCTGA[T/C] AGGCAGACTTATGGAAGGGA
WI-2034	150	T	C	CCAAGGAC	CCACAGTGCA CCAAGGAC	GGGTAAAGAT AGAGTGCAGGT CC	CCACGACTATGCTTTCAGAGTCCCTGGTACTGACAGAGAAGGCTTTGAGGACCATGTGGCGCCCAAGA CCTCCTTCTCGGGTTTCAGTGAAGAACGATGAACCTCTTCTATCTTACAGCAGCTGGACTTCAACA CAGTGCACCAAGGACT[C]GGACCTGCACCTCTATCTTTACCCCTTCCGACACCAAGATGCTGAGATGCC ACACTCTGAGTG

WI-2038	155	C	T	TGTCCTTTAAA GTGTGTAAGT ATTAATTAG	ATTCTCTTGG AAAGAAACAT CA	TCAGGTGACAAGAAAAAGTCACATTTCTTCAATCACTACCATTTGCTGTTATTGCTCTTGCAGTGT ATCCAAGGATGTCACATTTTGGAACTCTGTAGATCAGAAAAAAGTGTGCTTTAAAGTGTGTAAGTATTA ATTAGATTTCTATTTTGATA/C/TTTGATGTTCTTTCAAGAGGAAATTTGTGTAAGAGGATTCCCATTT TGCAATTCCTATTGGC
WI-4782	113	C	T	GATGCAGAAG ATAAAGTAGAA AATGC	GAACTCTTCTG GTATTTTCT GTTC	TCATTGACTTTTATAGATTCCTCAGTCTTATGCTTATTTCTTTAGGAAAAAAGTCTAGGCTAGGAGAA CACAATTCAGGTCTCTCCAGATCAGAGAATACTAGAAAAATGC/TTGAAACAGAAAAAATAACCA GAAGAGTTTCATTAIGGTTTTTCCAGAACGATTAC
WI-4788	65	A	G	GCATAGAATC ATCTTGCTAAG ATCC	GGATAAAAT AAAATTTTGGC ATAA	AGGAGAGTTTGGCTCTTTCCGGACTCTTGGAAATTCAGTGCATAGAAATCATCTTGTCTAAGTTCC/JA/G JTGAAAAAATAATATGCCAAAAATTTAAATTTTATCCAACTTTAAGTCGAGATTATAATTGATATTT AAAAAACTATATTGAGTCTTTCTTAAAAAGATGGCGTATCACTCTA
WI-5300	38	T	C	TCCAGAGAC CACTTCATTC	CTACTCTTCT ATTCATAATC CAAAA	CTTACTTCCAAAGTGTTCAGAGACCACTTTCATTC/T/CJTTTTGGATTATGAAATAGAAAGAGT AGGTGTTATTATTCCTCTTTTACCAAGGTGAAATTTGAGGCTCAGAGACAAGGTAGATGATGAGCCCA AGGTCAAGTGACAGAGCCA
WI-4818b	121	G	T	TGATAATGGG GCCCTGTT	CCCTCCTTTTA TATGTATGCCA GA	TATAATGTTTTGTTCCATAGTGGCCATAGACTAGGTTAIGTCCACACATGAATAAACAATCTTATATA ATAATTTATCAAGAAGGAAATATACATATGGGTGATAATGGGGCCCTGTTG/TCTCTGGCATA CATATAAAGGAAGGCTAA
WI-4818a	43	A	G	TTGCCATAGAC TAGGTTATGTC AGC	CATATGTATAT TTCTCTCTG AATAAAT	TATAATGTTTTGTTCCATAGTGGCCATAGACTAGGTTATGCTC/JA/GTACATGAATAAACAATCTTAT ATAATAATTTATCAAGAAGGAAATATACATATGGGTGATAATGGGGCCCTGTTGCTC/GGCATA CATATAAAGGAAGGCTAA
WI-5317	139	T	C	TTCAATTTCTG GTAGCAGGT	GATGCAAGA AGAAATGAGTC C	TTTTCCATTTTGTGATTCTTTTGTCTGAGCCCTTAGATCTCCTTTAAATTAATAGCAAGGTTAAT AATATAATAATATGATGTTATATTAACAATTTCAACTCAACAGGAATTCATTTCTGGTAGCAGGT ATA/T/CJGGACTCATTTCTCTTTCATCTA/TCTAGGTTATTTGCAGCCCCGAGATCTACCCAGG
WI-4888	56	G	A	GCAAGATATA AAGATTAAGA AAGATAACA	CAATTCACCTA CCTCATTTATT CA	AAATGAGTAACCCCAAGTTACTCGGCAAGATATAAAGATTAAAGAAAAAGATAACAAGA/G/AJATGAAT AAATGAGGTAGTGGAAATGCTTGATAACTGGAGTAGTGCTT
WI-5328	44	A	G	---	---	AACATTTTAAACCATGCTACATTTACAAACACTGAAAAGACAG/JA/GAAAAAAGAAATATTTTG CCTCAAAAAGCTCTTAAGAGATTATGTAATAAAGAAAAAATATGAATCAGAAAAAGGAAAGAAAT AGAAACACGTGATCTGGAAGGAG
WI-4897	93	A	G	---	---	GCCTTTTGTAGTTAAGCTTTTGTAGTGTCTTTTTTCCCCCACTAGGTACTCTCGGCCCAAT CCCCAAAGAAAAAAGCGCTGG/JA/GATAAACACATCTTC
WI-5345	29	G	A	---	---	CCCTGCTATAGGTCAGTTTAAAAATCCTT/JA/CCTGCTATGGTTGCTTGTGAGGCCACATCCACT GAGGTATATTCTGTCTGCTGCTATTTCTATATCACTCAGCTTTGAGATCCACTCCCACTCAACTTGCAG

[illegible]

TIGR- A004W22	232	C A ---	---	GGATAATCAGTACATAATGGGACCTTAAACTGCTGTGATGCAGGAGTGGGGCTGGGCAGTG CCCGAGGACAGGGAGGACAGTGGGACAGGGATGCTCAGTGGTGGAGCCACAGCCCTGGGCTCTGGA TGGGCATGGGAATGACCAGGTTCCACATCATGCACAGAGGGGCTGTAGCTTGAGTCCAGACAG GCCTGCCACATTTGGTCTGCCCGCCCTA/C/CTGGAGATGCTCTCTAAAA
TIGR- A005D24 b	138	C T ---	---	CATAGAAAGGAGTCTTTGAGTATTGACAGTTTGAATAATCTCTTTGAGATAATTGATTTCATATTC TGTGGCTTTC AACCTCCATTACCTCTTGTCATTC AACATCTTTATAGAGAAATAAAACCCAAATTT CT/C/TTTTCACCATTTAGTTGATTATCATCTGGATTTTCACTCAAGATGCAGCTCCTAAGATTATT GTTATGTTAAATTCATAAACTCCTTCACCTTTAATAATTAGGAAACAAT
TIGR- A005D24 a	123	A G ---	---	CATAGAAAGGAGTCTTTGAGTATTGACAGTTTGAATAATCTCTTTGAGATAATTGATTTCATATTC TGTGGCTTTC AACCTCCATTACCTCTTGTCATTC AACATCTTTATAGAGAAATAAAACCCAA TTTCTCTTTCACCATTTAGTTGATTATCATCTGGATTTTCACTCAAGATGCAGCTCCTAAGATTATTG TTATGTTAAATTCATAAACTCCTTCACCTTTAATAATTAGGAAACAAT
U03735	74	C G ---	---	TGAGTCTGAGCAGAGTGCAGCCAGGGCCAGTGGGAGGGGCTGGGCCAGTGCACCTTCCGGGGCC GCATCC/C/GTTAGTTCCACTGCCCTCTGTGACGTGAGGCCCATCTTCACCTTTGAAGCGAGCAG TCAGCATCTTAGTAGTGGTTCTGTTCTGTTGATGACTTTGAGATTATCTTTGTTCTCTGTTGGA GTTGTTCAAATGTTCTTTTAA
U39840b	42	T C ---	---	GGTTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAATCAACAGCAAAACCAACACA CAACCCAAACCGTCAACAGCATAATAAATCCAACTATTTTATTTTATTTTTCATGTCACAACG TTGCCCCAGTGC AAAAGACTGTACTTTATTGTTATTC AAAATTCATTGTGTATTTACTACAAA GACGGCCCCAAACCAATTTTTC
U39840	56	A C ---	---	GGTTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAATCAACAGCAAAACCAACACA CAACCCAAACCGTCAACAGCATAATAAATCCAACTATTTTATTTTATTTTTCATGTCACAACG TTGCCCCAGTGC AAAAGACTGTACTTTATTGTTATTC AAAATTCATTGTGTATTTACTACAAA GACGGCCCCAAACCAATTTTTC
WI-8997	41	G A O O O C	---	GTGGCCATCGATCTGGACCGTCCCTGCCACTTGCTCCCG[G/ATGAGCACTGCGGTACAAACATCCA AAAGTTCAACAACACCAGAACTGTGTCTCATGGT
WI-7008	180	A G ---	---	TATACCACTTCCATTTGATGATGGAATGCTGCTGTTTCATGACCAACTTTATGGCTAGATGGGTCAGAA AGCACCCAGTTTCATGATAGGCAGTTCAGTTCATATGGTACTTGATGACCCAGAGTCAACAACTTCAG TTTCCACCAAGCCAGTAACAGGCCAAGAGCTGCTCTCAAAAG[G/AGAGTAGTTATCTGCAGA AGATGGCAGGGCTTGCTCCGAAAGCCTAGAGACCGCCACTGTGATTCACCT
WI-9005	26	C T G G G A A T C T	AAA	GGTCCCACGAATTTGCTGGGGAATCTC/CTGTTTCTTCTTAAGACTTTTGGGACATGGTTTGACTCC CGAACATCAGCAGCGTCTCTGTTTCTGGGTGG

WI-7593	46	G A ---	---	---	TTTTGTTTGCTCTGGACACCCACTGCTCCAGGATGAAGGAGAGIG/AJAATGAGATCAGTTTGGGACCTTCCTCTTGAAATATAAAGAATCAACAAGTTACAGTCATGTTGGGACTTCTCTCTCTCCAAAGTGCATCTTGGGGAAAGGCTCCAGTGTTATCTGGACCAAGTTCCTTCAATTTTCAGGTGGGACICTTGATCCAGAGAG/GAGACAAAGCTCCTCAGTGAGCTGGTGATAATCCAAAGACAGAACCCAAAGTCTCCGACTCCTGGCCTCTATGCCCTCTATCCTATCATAGATAACATTCTCCACAGCCTCACTTCAATCCACCTATTCTCTGAAAATATTCCTGAGAGAGAACAGAGAGATTTAGATAAGA
WI-6962	78	A G ---	---	---	GCAGAGAGAGAACCATGCCAGGGGAGAGGCCACCCAGCCATC/GIGTGACCCAGCGAGGAGCCAACTATCCCAAATATACCTGGGTGAAATATACCAAATTCIGCATCTCCAGAGGAAATAAGAAA:AAA
WI-7059	43	C G GCCATC	AAGGCACCCA	GGTCA	GATGAATTGTTGCAACTCTTAAAAAA
WI-9063	53	A C TT	CACTTCACTGA	TTCTACTTTCTG	AGCAGCCATCACATGATCTGTTTTTCCACCATTCTCACTGAAGACACCACTTTAT/ACJTACCCCAAGGGCAGAAAGTAGAAGTTACTATTCTAATAATGTTTGACACAAATTGGAATTGTC
WI-7079	293	T G ---	---	---	AAGGGGCATTGAGACTATAAAGCAGTAGACAATCCCCACATACCATCTGTAGAGTTGGAAGTGCATTCTTTTAAAGTTTATATGCATATATTTAGGGCTGTAGACTTACTTCTTATTTTCTTTTCCATTGCTTATCTTTGAGCACAAAATGATAATCAATTATTACATTTATACATCACCTTTTGACTTTTCCCAAGCCCC
WI-9074	38	A G AAAAG	GGTAAAGTT	GACAGATTTT	TTTACAGCTCTTGCCATTTCTCTCGCCTAGGCCCTGTAGGTAACTGGGAT
WI-7104b	249	C T ---	---	---	TGGATGCCGAGGTAAAAGTTCTTTTGTCTTAAAGAA/GAAGGAAGTACAGGTCAAAAATCTGTCCGTGACCTATCAGTTATTAATTTTAAAGGATGTGCCACTGGCAATGTAACTGT
WI-7104	249	C T ---	---	---	GGAGTTGCCCTTCTAAGGAAGGAGATCTTATCTTTCTGGTTGGCTTGACCAGTCACGTTGGGAAGAGAGAGAGTGCCAGGAGACCCCTGAGGGCAGCCGGTTCTTCTTGGACTGAGAGAGGGAGGCCCCAGGCTGGAGCAGCATGAGGCCAGCAAGAGGGCTTGGTCTGAGGAAGCAGATGTTTCATGCTGTGAGGCCCTGCACCCAGGTGGGGGCCACAGCACCCAGCAGCATCTTGCT/TT
WI-7104	157	C A ---	---	---	GGAGTTTGCCCTTCTAAGGGAGGAGATCTTATCTTTCTGGTTGGCTTGACCAGTCACGTTGGGAAGAGAGAGAGTGCCAGGAGACCCCTGAGGGCAGCCGGTTCTTCTTGGACTGAGAGAGGGAGGCCCCAGGCTGGAGCAGCATGAGGC/CAGCAAGAAAGGGCTTGGTCTGAGGAAGCAGATGTTTCATGCTGTGTGAGGCCCTTGACCAAGGTGGGGGCCACAGCACCCAGCAGCATCTTTGCT
WI-8974	34	C T AAGAACTCA	CCTGAGCCCTC	TGTAGGGCTGA	CATACAATGAGAGCCCTGAGCCCTCAAGAACTCA/C/TGCCAGCTCAGCCCTTACACCAGTTTCCACC
WI-9161	61	C T CCTGGC	CCTAAGCATTG	GCTGGC	TGGAGTTCAATGCAAGGGCAAAAGGCAGTGGCCATGCAAGCTGTTAA
WI-9014c	93	T C ---	---	---	CTGTGAGGGTGACGTTAGCATTACCCCCAACCTCAATTTAGTTGCCTAAGCATTGCCTGGC/C/TTCCTGTCTAGTCTCTCTGTAGGCCAAAGAAATGAACATTCCA
WI-9014c	93	T C ---	---	---	CCCTGTCCCATGCTGACCTGTGTTTCCCTCCCAAGTCATCTTCTCTGTTCCAGAGAGGTGGGGCTGGATGTCTCCATCTCTGCTCAACTTTA/T/C/GTGCACCTGAGCTGCAACTTCT

WI-9014b	44 C T	---	---	CCCTGTTCCCATGCTGACCTGTGTTTCCCTCCCCAGTCATCTTTCTC/TGTTCCAGAGAGGTGGGGCTG GATGCTCCATCTGCTCAACITTTATGTGCACTGAGCTGCAACTTCT
WI-7023b	206 C A	---	---	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAGACCCCTGCGTGCT CAGTGCCCTTTAAGTGCATCCCGCTGTGCTGACTTGTAGTGGGATCAACATCTGTCTACGGGTCCCC TCTTTTGGCCCCAGTATTCATGCGAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCACAC A/C/AJACACACATCTTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7023a	56 A C	---	---	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAG/C/CJCCCTGGGT GCTCAGTGCCCTTTAAGTGCATCCCGCTGTGCTGACTTGTAGTGGGATCAACATCTGTCTACGGGTG CCCTCTTTTGGCCCCAGTATTCATGCGAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCAA CACACACACATCTTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7093	54 C T	---	---	CTGAAATCCCCCTCTCTGCCCCTGGCTGGATCCGGGACCCCTTGGCCCTCCCTC/TGGCTCCAGCC CTACAGACTTGTGTGACCTCAGGCCAGTGTGCCAGCTCTCTGGCCCTCAGTTTCCAGCTATG AAAACAGCTATCTCACAAAGTTGTGTGAAGCAGAGAGAAAGCTGGAGGAAGGCCGTGGGCCAAT GGGAGAGCTCTTGTTATTATTAATATTGTGGCGCTGTGTGTGTTGTTA
WI-9171	62 G A	---	---	ACATATCTGAAAAATGTTGAAAGCCCTAAGCCAGGAATAAAAGAAAGTAGAGATAATAATCA[G/A] TTCTTTACAACCGATGGTAATTAAAGCTTGTATTACAAAGACTTCATGC
WI-9174	47 T C T	---	---	GTGTGAGACCATCATGGTGCCAGCTAGGACCCCATCTCCTATTAT/T/CJAGTCCTGTCCCTATATA CCCTCTAGAAACAGAAAGCAATTTTAGGCAGCTATGGTCAAAATTGAG
WI-7753	52 A G	---	---	AAGGCCAGATGCACATCCCTGGAGGACATCCATGTTCCGAGAGAACAGAT/GJATCCCTGTATT TCAAGACCTCTGTGCACTTATTATGAACCTGCCCTGCTCCACAGAACACAGCAATTCCTCAGGCTA AGCTGCCGGTCTTAAATCCATCCTGCTAAGTTAATGTTGGGTAGAA
WI-9186	76 G A	---	---	AAAGAACTACAGAGGAGCATGTCCAAACAAACAAATGGCATCCTGTCAAAATGGAGTTCCACT TCTCCCGCA/G/AJACCTAGGTCAGACTTTCCTTTTCATCTT
WI-9193	94 G A C A	---	---	TTGGACAAACCTAGAAATTTCTCCCTTTATGTATCTCTATCGATTGTAGCAATTGACAGAGAATAA CTCAGAAATATTGCTGCTGCTTAAAGCA/G/AJATCCCCCTTACCACACACACCCCTGTCTC
WI-9015	48 C T	---	---	TTTGATTGATATCGTGAATCCTCAGCCGAGAAATGGGCTGGATTG/C/TJGCTTTGGTTAATACAT CTTTCCCTAAAGAGAGATAAACACAAATCCATTCCAGGTAGTCGGCACCACTAAGAA
WI-7254	37 A G	---	---	GGAGCCAGGAGACAGCAGGGTCTGAGAGAGAGGCCAC/A/GJGTCCCTTAATGACACCCACTCCTAGCC CTGAGGCTGTGCCCTCAGACTGGGGAAGAGTCCAAAGGAAGGAGGAGGCCACTCCTCAATGC TCAATGGCTCCCCTGAAATCAAGACAGG

WI-9231	32 G C	CAGGTC	CAGTCC	CACCTGCCAC	ACTCAGAC	CACTTGCCAC	GTGACCCGTGTGAGGTCAGGTC
WI-7836	120 T C	CAATTAACA	ATGCAACGTT	CAAGATTAGA	AATC	CACTTGCCAC	GTGACCCGTGTGAGGTCAGGTC
WI-7286	65 T C	CACTTCAGCT	TAACTGACAG	CAAGATTAGA	AATC	CACTTGCCAC	GTGACCCGTGTGAGGTCAGGTC
WI-7858	91 T G	CTAAGCATGT	ACGTGAATTT	CACTAT	CACTAT	CACTTGCCAC	GTGACCCGTGTGAGGTCAGGTC
WI-7860	50 C G	CGTACCTCCAA	ACATAATTGA	AGTCTCGCAGA	AGTCTCGCAGA	CACTTGCCAC	GTGACCCGTGTGAGGTCAGGTC
WI-9064	29 A G	TTT	TTT	TTT	TTT	CACTTGCCAC	GTGACCCGTGTGAGGTCAGGTC
WI-7307	128 G T	GAAATGTGAC	TTCACCTTGGT	TTCTGTCCATT	TTCTGTCCATT	CACTTGCCAC	GTGACCCGTGTGAGGTCAGGTC
WI-9274	25 C T	TTT	TTT	TTT	TTT	CACTTGCCAC	GTGACCCGTGTGAGGTCAGGTC
WI-7313e	266 T C	TTT	TTT	TTT	TTT	CACTTGCCAC	GTGACCCGTGTGAGGTCAGGTC
WI-7313c	256 C T	TTT	TTT	TTT	TTT	CACTTGCCAC	GTGACCCGTGTGAGGTCAGGTC

WI-9281	68 G A ---	GCTAACACTTT TTAAACCGT	CAITTTATTTG AAAGCTATTCA GACA	--- GACA	ACTGGTGGGAGACTGTGAGGATCCAGGATTGAGTATTCCTGGCCAGAGGGCCTTGCTGGCTACTGG [G/A]TGTAGTTGAGTCTGCTGCTCCCTCTCTTATGACTGTGTCCC
WI-7848	142 A G CTC	GTATATTACA ATGATCACCG	CCACACAGAAC TATTGTAAAC	AA	TTCTGAAATATAACAGCCATTGAGCTATTTAAACCTGTAATTTTTTAAATTTACAAAAATATAA AATATGAAGACATAAACCCAGTTGCCATCTGCGTGACAAATAAAACATTAAATGCTAACACGTTTTTAAA ACCGTCTC[A/G]TGTCTGAATAGCTTTCAAAATAAATGIGAAATGGT
WI-9304	70 G A ACTGA	GTATATTACA ATGATCACCG	CCACACAGAAC TATTGTAAAC	AA	TCACGTTTGGTGCTTCTCAGATTCTGAGGAAATGCTTTGTATTGATATTACAATGATCACCGACT GA[G/A]AATATTGTTTACAATAGTTCTGTGGGGCTGTTTTTTTGT
WI-7933b	314 C A ---			---	TTACAGAACTTGGCCTGTGCCTGTGCCCCCATGCTAGGGCGGAGGGGTCTTTTCCTTCTCTTTCC TACCTACCCCTTTTCTCTGGCCAGGGCCCTGATCCTACCTTCCTTGCCCCCTGGGCTGGCTGCAC AGAGGATTGCCCTTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATAGCATTTAGTATTGTCACAA AGTCTAAGGGACCATGGCTGCCTGCCCTGGGGAGGAACCATAGCTCCCT
WI-7933	96 G C ---			---	TTACAGAACTTGGCCTGTGCCTGTGCCCCCATGCTAGGGCGGAGGGGTCTTTTCCTTCTCTTTCC TACCTACCCCTTTTCTCTGGCCAGGGG[C/C]CTCGTATCCTACCTTTCTTGTCCCCCTGGGCTGGCTG CACAGAGGATTGCCCTTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATAGCATTTAGTATTGCA CAAAGTCTAAGGGACCATGGCTGCCTGCCCTGGGGAGGAACCATAGCT
WI-7374	182 T A ---			---	CCCAGATGTGCCCATCAGTTTTTCTGAGGCTTTTGACTTTTAGTAAATGCTTCCACTAAACTGAAA CCATGGTGAGAAAGTTGACTTTGTTAAATATTTTGAATGTAATGAAAGAAAGTACTGTATATTA AAAGTTGGTTTGAACCAACTTCTAGCTGCTGTGAAGAATATATTGTT[A/C]AGAAACACAAGGCTT GAT
WI-9343	78 C T CCTGTGCCA	CCAACAACAT CCTGTGCCA	AAATGAAACTT ACGTTTTGTG TG	---	GGTCTGCTCCTGCTACCTTGACCCCTTCCCTTCTCTCTCTCTCATCATCATCCCAACAACAT CCTCTGCCA[C/T]ACACAACAACAACGTAAGTTTCATTTGGGCAAA
WI-7386b	104 T A ---			---	CTATATGTGAGAGGCGTGATATCTGGATGGAGTTGGGCTGGATGATCTCCAAAGTCGTTTCAACTCT TAAAGACATCTTAATCCTGAATGTAACAATTTGTTA[T/A]GTGTTTAGAATCAGAAATTTGATTTTGA ACTTGAGTAATTCATCCTT
WI-9357	75 A G ---			---	AAGAAGGAGCTCAGTTACGGGGTTTTTAAACCTTCATGAAAACCTGAGAGTTCACTTTTGTATTAT GCTCTT[A/G]TATTACAGACTGATGCCAGACAACCTTGGGAAGA
WI-9360	79 T C TTGG	CTTTAGAAAA TCTGCTTTAAC	CCTAGGGAACA CAATTAGAGGA A	---	TGAAGGGGTGGGCATCTGTGTTTCTGATGCTTACTACAATATGTAACCACACTACTTTAGAAAACTCG CTTTAACTTGGT[C/J]ATTCCTCTAATTGTGTTCCCTAGGAATGACTGTCCCAAG
WI-7423	107 T C GTTC	TGCTGGGCTGT	GGTCCAGAAGA GGOOG	---	TGCTCCCTGTCCCATCTGCAGTGGACCCAGGACCCCTTTTGGAGGTGGGGTGAAGTCTCCTT GGCAGGGATTGTGACACTGCAATGCTGGGCTGTGTTCC[T/C]CGGGCTCTTCTGGACCTTGACCCGTG GATACCAGGCCATGTGCCATGGTATTGGGTCTCTGGAGGGTGGTGAATAAAGGCATCTGCT

WI-7424	131	T A	CAAGAGAGAG AGAGGAAAGA	TGCAAAAGAAA GAATGAAAGTT G	CCAGGAGCACTAGAGAGGGGGGAAGCAGACAGTTAGAGAAAAAAGCCACGGAGGAAAGG AAAAACATCGGCCAACCTAGAAACGTTTTTCATTCGTCATTCAGAGAGAGAGGAAAGAAAA TT/AJACAACCTTTCATTCCTTTTCACGTTTCATAAACAATTCACATA
X86400	118	A C		---	TCCTGCAAGAAGTTCTCAAGCCTTTTGAATTTTGTGCAATAAAGTACAGCTTGCATAAGAGTGAAA TTGGGCTAGCTTAAATGGATCCATAAACTTCTCTCAATTTTAAGTGAGA/CJCTCTTTTAAACACCT GTTAAATTTAATGTAGCAGCTGAGAAATCTAAATATGTACCACCTCGTTATTTGTTCAATCATCCA TCCCTTTTCCCATGAATATTCA
WI-8053	242	T A	---	---	GTGGCCACTACATGTTATAGAAACCATCATCTTGTACACAGCAGCTATGAATAAAGGCTGAG TTATCACTAAGCAGGAGAAAAAGCATTAAAAGTGTCCTCAATTAAGGGGACTTTTAAATCAACCTAA TAACTCTAATCTGCTGACTTTTAAAGATCTAAGGTCATTTAATACATGCTGAAAAGGGTCCACA ATTAATCTTTGATCTTTTACTCACTGTTAACTTATATAIT/AJTTCAGAAC
WI-6190	165	G A	---	---	TACACAATGAATTCCTTTATTCGGTATGCATCCACATTTAGTGCTCTGAACAGCAAG TGGAAGACGCGCAGCAATTTGCCAGGAGGTCAAGCCACCAATTTCCGGGATCTGCTGTGCACACCCGG GTTCCCTTCTTAATCCCTGCTGAGGATCTTG/GA/GAAGCAGCAGCACCACCAAGGATGCA CCGGATTCAAGGTTCTTTTGTCCAGTTGTCAGATTCCAACTAGACCCCA
WI-6275	148	G C	---	---	AACAGTCACCACCAACCATGACAACTCGCCAGGCAAGGCTTGCTTCCCTCCCTCTCTTGCCTCCC ATGTGCTAGTCAGCAAGGTCGGGAGGACCGGATGTTAGCTTCGCCCAAGGGAGTATTACAGAGA GAGGCTTGGGAAAG/CJGGAAAGGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCACTTAAACTG ATTTGCTTTCAGTAACGGTATGCTGAA
WI-6421	41	G T	---	---	ACCAAGAGATCAGCTGCTAAACAGCAGCTTTTGTGATTGT/GTGGGCTTCTCTGAAGAAACCTTGC TGACAGCTTCTCACTGACCTGCAGGACGGAACCGTACCTGAGAGGGGATGGGGCTCTCTCACA GAATATTTGGGGCAGAACCTGGAACCTGGCCACCGGACATCCCAATATCCCTCTCTCAGGG CTCACCCCGACATCCTCAGCCAAATGAAGGCTCTGAA
WI-6905	215	T A	---	---	GGGTGAGACGGGTTTATTGTGCACATTTACACAGCGTCACAGCTGTGGGCTGGCAGCGGCCATGCTC CTGTGGTCGGGCTGCTCTACAAAGGGCTTCACTTTTCTTCCACACACTATGTACAGTCAGTCTCCAA GGTGATGGGCTACAGTGTGTCATCAGTGTGTGTACACACATTTTACATAAATTACACAGGACTC ATACATGAAAAAT/AJAGAGCCTAAGGGCCTGTATTTTAAATGAGAAAAAA
WI-9420	202	G A	---	---	AACTGTTTACAAAATAGGCTTTGCAAACTTCACTACTGAATGTAAAGTCAATGACTGTGTTT TAAATATGTACCAAGGAAATACAAATGGATAATGATCAITTTTCTCAGGAGAGAACAGCAG AGAAATAAGGATACTGCACAAAGGTGCAAGGAAACCGGAACCCATTGTGTACACTGTCTTCACACAG [G/A]GCATTCCTTCTCACCTTAACCTGCAGCTGTGCAAGATGCCCTCAGTGTG

WI-9448	184	G A ---	---		TGGGGCTGCTTTAGACTTCATTTCTAGAGCAGAGCACCTAGTAGAGAGGAATACCTGGGAGAGAGAC TGCCTTGCCCATGGTGGTTAAACCTACATGAGGGGACTGAAATCTCTTTGGATGCCAGTCCAGATCCC TTTTAAGAAAAATGGGCTTGTTCCAAAGGCTGAGAGCTGGACACAC[G/A]CACTGGTTTCTAAA TCTCTGGCTGGATTATCCAAAGCGCATGTTCTTAACGTGCCCGTGAGCAG
WI-9470	204	G A ---	---		ATGTCAAGAGACACAGACAAGGAGTTTTCCCTTTTAAATGCTAAACAAGTGCCACTAATCCACA GATCTGAAAAGTACAGCTCTCCAGGTTGATAAATCAGATCCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCACGAATATGATCTCCCTAAAGCCCCAGATTCTTACTAGAGCCGCTGGGACACTGATGAC AA[G/A]GCAATCAACTCATCTCTCAAGCTCACCCAGGGCTCACCTTCCCAAG
WI-1245b	201	G T ---	---		GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCCTATAAGGAAGAGTAGGTAAATGGCA TCCTAGGGCAATGGTAGGTGCTGATGCAGATCTGCTGTGAGCCATGTCTGGCATCACAGGGTGGT TTATTAAATTCATTTATCATCTGGACAGCCCTTCTTATAACGTACATCCTTGCCTCTTCTGAGGC[G/ TCTAAGATCCCAAGGTGGCTCTGTATCCAGAAA
WI-1245a	85	T C ---	---		GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCCTATAAGGAAGAGTAGGTAAATGGCA TCCTAGGGCAATGGTAGGTGCTGATGCAGATCTGCTGTGAGCCATGTCTGGCATCACAGGGGT GGTTTAAATTTCAATTTATCATCTGGACAGCCCTTCTTATAACGTACATCCTTGCCTCTTCTGAGGC GCTAAGATCCCAAGGTGGCTCTGTATCCAGAAA
WI-1031	149	G A ---	---		TTCAGTGATAAGGACAGGTCTAGAACAAAGCGTTCCCAACCCCTGGACCAATGACAGTTTGGACCAAA TAACTCTTTGTTTACAGGGGACTGTCTCTACACATTGTGGATGTTAGAGCCCTCCGTGGCTTACCCA CTAGATGCCAGCA[G/A]CACAAACACCCCTCCCCAACCAATCATGACAAATGAAAATGCTCTTAGACATT GCCAAATATACCTTGTGGGACAAAATGGCCCTGATTGAGAACCACTGGTT
WI-5385	110	G A ---	---		AATGAGTCATTGTGGAGTTAGAGGAGGTACTGAAAATGGTGACTCCAATGGTGGGATTGAAAGAGG GAAGTCTCGATAATTTTAAACATATGGTTCTTGCCAGGAATCG[G/A]CAATGCTAATCTATTGCTTAA TTCITTTATCAACAGACICTTTGAATCAATTTAGAGATACCTCAGTGACCCCATGGCTAGAGTTCCCTGAC CCCTGCTACGGGAAACATTGAATGCA
WI-5403	199	T G ---	---		ACCAACCGTTGGCAAGGCTCCCCAAGACTCACACCCCAACTTTGGTGCTTACCCTATG:CGGGTG GGATTGAAGAAATAACCAATAATAATTGCTACAAATTTCCAGTAGTTACCAGGCCACCCAGCCTAT TGGAAGAAATCATAAATGTAAACCTACAATGATTGCTCTCTGGCTGGTGCCAGGCATAGAGTT/G JGGCTACAACCCATTTTATCATTTGAACCCCTCAGAACGATCCAGTTGGGGCT
WI-5801b	157	G A ---	---		TGGTATTTTCTTTCTTAAATGTTATGATTAAATAGTGCTTTGTAGAATTTGAAAAAATGTAAA TCAGAGAACAGAAAGAAAATAAGATATAGTTGAAACCTCTAACAAATTTTAGATTTTAAAGGCCTAG GGAAAGAAAGAGAGCCTGGGA[G/A]AGGGAATGAGAAAAGCACAACCCAGAAAAAAGTGTGT GGCTTAAGGGAGCCCAAGGAAGTTAAGT

WI-5801a	48	A G ---	---	TGGTATTTTCCTTTCCCTAAATGTTATGATTAATAGTGTCTTTGTA/GJGAAATTTGAAAAAATGT AAATCAGAGAACAGAAAGAAAATAAGTATAGTTGAAACCTCTAACAATTTTAGATTTTAAAGGCC TAGGAAAGAAAGAGAGCCTGGGAAGAGGGAATGAGAAAAGCACAACCCAGAAAAAAGTGTGT GGCTTAAGGGAAGCCAAAGGAAAGTTAAGT
WI-5696	61	C A ---	---	TTCTATTTAAATCCTGTGCCCATTTGCAAGACTGCATTCAGTCTGCATGAGCCTTAGTTTC/AJTA AAGCCCCCTCACACCGAGGGGACAAATGTTCAGAACTAAATGACTGCAGGTGAGCAATTCCTGTATTA TACAACTGGGACCAAGATGACTTTATAATAGTGGCAAGAGACAATCAGGCAGACTGGGAGGACC TTATAATAGATTATAAGGCTGGGTGAGTTTATTTAACTT
WI-7461	153	C T ---	---	TATTACTAGGTTTCATAGAGCCCCGTTGTAATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATTTCTAACGCTCCTCACTTCCCTTCGAACCCAGCCTCAGAGATGACACTTAGGCTGCACATTCCCTG TGGCAGGGACTGTGCTC/TJGTCCCTGTGGTCCCGGAACCCAGTGTGGTGCCTGGCACAGAG GAGGCCCTGAGTAGCATGTCTGCA
WI-9716	221	G A ---	---	AGAAGACAGGAGCACTGGGATCAAGGACTGATAAACTCTGAGGCTTTAATGGTCCCTGTCTCTAAC GCTTTTGGTACTTCTCTTTCTGAAGACCAACCCCTTTCAAACCTCTCAGAACACAGGCAAGATGCAT ATTCTGTAGTTTCAGATGTGACTTCTCTACATTCGGAACACTAGATGAGTTAGGCTCTCTTCATCT CAATTGAAAATTTAGAA/GJA/AAAACACCTAATTGGCTCATCTTGGATCA
WI-9760	49	C T ---	---	TTTTGTTAAGTCTTGTAAGCCACACAGAAGTGAATCTCTCTTTAC/C/TAAGTGTACTTTTGCA TATATTTATGGGATGATTCATCCCTACTTAAGATTTCTCTCTCAGGTTAAATATCCATTTCCCT TTGTCAGGAGTTTCTAATTTGGCCTTCTTTCTAAACCCCTAACCAATTCCTGCTTATCTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
WI-9855	31	A C ---	---	GAAAACCTCGTTGGCTCAAAGGAAACTGTAG/C/AAATCTTTTTTTTATTTTGTTTTAACTC AAAGAGTGGAGTTTGCAATTGACCTTGATGGCAGCTGCTCTTTGTTTGGTGAATCCCTCTAGT GGGCACTTTGCAAAAGCAATTTAGAGCAAAAGGTGGTGGCATGGAGTTGTGTGAGGTTGCTGAAAAAG TAGCAAAATGGAAGAAAGGTTAATGGA
WI-10312	41	A G ---	---	AAGGCCAGTGGGAAAAGCAGACAAAACACTCCAAAGAAATAC/A/GJAGATATAAAACATCATCA GTAGAGATGGGATGACCTAGGAGGTCTGCTGATGAGGGCATGTGAGCCAAAAGACATTTGGGTCT TGAGGGTTGAATAGGAGTTTGTCTGGTGAGTCTTGCCAGTCCCATAGTAGGTGTTCCATAAATAAAC AGTGACTAACTGAGGTAGATCACAGAAGAAATTTCA
WI-11152	179	C T ---	---	GATTCCTTGGCAGATGCAGAGCAGATACGGCAAGGCATCTTGGGCATTTGGAAGGAAACGAGCCCTA ATTTCATAGAAACAGACTCTACAAAGGACCAGTTAAAGGTCTCGCACCCAGGGGACTGGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGACAAAGTGGGACAAAAGGCTTGTC/C/CTGTCTCAGAAAACATTGAA AACAGCCAGTACATGCCACTGATAGA

WI-1968	167	A G ---	---	---	TGGTGAGGAGCTGTAAAGGCTGAAAGAATAGTCTCTGGCTCTTGGTTGGAAATGGATGAGTCTCTTTACAAAATTTTCCCTTGCCATGGGTGTTATGTTAGAAATCATGGAGTTGGAAGACTTAGATTCAATTTGGGGCTGTACAGTTTACTGGAAGTTGJAVGJTGAACTTGAGCAAGTGCTCTTAATGTCTCTCA
WI-4701	198	GA ---	---	---	GCCTCAATGCCCCTTCCCTGTAA GGGTTTCATTTAACAGCCTTCCACTGGGTCTCAGATTGCAGGAGATGTAAAAATAGGAAGAGATAGAAAAATGGTCCCCACTATTGACTTGATAACACCTACAAAAACAACACATTAAACTCCTCCCCACTCTACCCGCCAAAGTCTACCTTTTGTTCTTTTATTTCTGCTAATGACCATACTATTTCCCAATTAGA[G/A]CCATGTCAATTTTCAGAAAAGCAGTATA
WI-4823	164	C A ---	---	---	TTTATCTTTCCAAACCATGTGTGTTTCTTCCACATACTTACGTAATTTTAAATCATGTCAATTAATTAATGACATTACTTGTGGCTACCAGACATTGCTTCCAAATGTAAATCCCTAACACAGCAAGCATAAAGTGTGTCATCTTTGTATTCCTAAA[G/A]AAAGAAAAGTGCTTTTGTGTCATCTGCCCTCTCTGTCTTCCCTGTTTCACCTCCTGTATTTCCCTATTTCAGCATTCATGATTA
WI-48 2	72	A G ---	---	---	AAAAACAACCTTCATTTGACATTTAAGAAGATAAAGAAAAACAACGATCCACTGTGTGTTTGCTTGATT[G/G]GAGATAAAACCTGATCTTAAGAAAAATTAACCAAGAGCAGTACACTAAAAATAGCCTTTGTGTGTGGTTTCAGGAAAGAAAGCCAAATCCAACCTAAGTTGCTAAGAAAAATATGTTTCATATCACTCTAACTCCACATAGAGCATTAATATAGCA
WI-9705	111	C A ---	---	---	TGAAGGACCAGTTCGAATGCCCTACCAAGGTAAGTAATCGGAGGGGCGGAGGAAGTAGGAGTTGCTTCCGGATGTTGCATAAATTCAGGTTCTTAAGGAGTTCCGCTGCC[G/A]AAAAATTTTAACACTGATGCCGTCTACAAACGCCACATAGAAATCGGTGGTAGATTGCGGTCTCTAGTAAGTAGCTAATGTTTAGATA
TIGR-A004248	177	A G ---	---	---	TGATGTGAATATTGTTGCTGTGTTCTGGG CAATAATCTCTGCTTAGAAGTTGCTTAGGCCATGGATTCATGTAAGGTGGGCGAGGTGGACTGAAAGATCTGTTGGCAGGGCTCACAGAGACGGGGTGAGGGGAGAGATCGTGGGTTTCATGAGATCCCATCTTGGGCAATACGGTTATCCCGTGGTCTCATACGCCACAGAGJTCCTCCAAATTCAGGGGGCTCCC
U17579	34	T G ---	---	---	GTGGGATGTGTGGAGCCAATGAAGACCAGGTAGATGATGCCACCTAGAGATG GGGATTCAAATGTGTCTCATCCAATAAGCAC[T/G]CATGACCTCAGCCCCATACTCTTCTTCCC TATGTTCCAGAGACAGAAATAGACCTGGCCCCCTTCCCTCTAGGGGATCACAATATTGGAAGGATGAGGACTCCAAACAGCCAGCTCCCATGCCAAATAGAACGATGAGTGTCTGGGATCAATTTCTATGGGAGCC
WI-7747h	88	T G ---	---	---	TGGGGAGAGGGGATCCCTTCTAGTTGA GTGAGAGCGAGGCTGAGCCTACAGATGAACCTCTTCTGGCCTGCTTTCGTTAACTGTGTATGTACATA TATATATTTTAAATTTGAT[T/G]AAAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAGTT ATTTCTGTTGTTGTTGGGTATCCTGCCAGTGTTGTTGTAATAAGAGATTTGGAGGCACCTGGA GTTTACCATTGTAATAAAGTATATAATTTTTTATGTTTGTGTTCTGA

WI-7747a	44 T C ---	---	---	GTGAGCGGCTGAGCCTACAGATGAACCTCTTCTGGCCTGCT/CJTTCTGTTAACTGTGTATGTAC ATATATATATTTTAAATTTGATTAAAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAGTT ATTTCTGTTTGTGTTGGGTATCTGCCAGTGTTGTTGTAATAAGAGATTTGGAGCACTCTGA GTTACCATTTGTAATAAGTATATAATTTTATGTTTGTCTCTGA
WI-7189	197 T C ---	---	---	TCAGAAATTTCTCTTCAGCTCATTTTGCTCTCTCAATTAAGGAGTAGGTTAAGTGAAGGT CACATACCATTATTTCCCTTCAACAATAATATTTTACAGAAGCAGGAGCAAAATATGGCCTTT CTTCTAAGAGATATAATGTTCACTAAATGTGTTATTTTATATTAAAGCCTACAAACATTTT/CJAG TTTGCAATAGAACTAATACTGGTGAATAATACCTAAACCTTGGTTAT
WI-7850	57 G A ---	---	---	AGCCCCAGCTGGACTCATGGATGTGCAACCCTTTGCTCCCTGCTCTTCTGCCCTGGG/CJCTCATGTA TCTGGCAGCTCTGGTACCTCTGTGGTGCCATCTTACCTCTGACACAGACTGCCTGCCCTTGAAGCT GAGAAAGCACAGGGCAAGGAGCCAAAGGACCACAGAGCCTCAGCCAGCCAGGATCCGCTCCTCATTTT ATTGGTGATGATGAATGGGAATGAATCAGGGGGCTGCTACTAGAGCC
WI-7907	69 G C ---	---	---	CTCTCTCTCATCCCATCCCCCTAAATAGGTCAGGTGAGGAGGCTGGGAAGAGGTGGGAGGAGG G/G/JAGAAGTGAAGGAAGATAGGAAGGATATTACCTCTTCTGTATTATTTTAAAGAAACATTTGTTT GGTGGCAGCAATCTCCCTGCTCCCTATCACGTGTAAGAGGCTAAATTTATATCTATATAATA1.ATTAAAA AGCAAGTCAAACTTGGATGTATCAAGGTAAATATTGTCAAAAGTTTAAAT
WI-7919	242 T C ---	---	---	GAAGGCAGCTGGATCACCTCCCGAGTCTTGGGCAGCGCTTGTGTGAACACGAGAGCTCCTCCT CAGGGGCTGGCAGTCACTCACCTTCTATCTGTATGATGATTTGGTTAAACACTGTCAAATAATAGAGAT GTGCCAGATTTAGATTTCTTACCTTAATCTGTTTAAATTTGTAACCTTTATCCATTTGAAAGTGCA AGCCCATTCAGATAAGCTATAATCTGGTCTTTAAGGAAT/CJACAACCTT
WI-7928	101 T G ---	---	---	CTCCCTTCTATGTCTCTCAGCAGCACGTTGGGGCACACTTGTTCATCTCTGACCGTTTGTGGGCTA TTCCCTGCGAGTGCAGACATCGTCAAAATTCAT/GJACAAGAGGAAATTTTCATGCAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTGCACCTTAAAACTGAAATTCAACTCTTTATATAGGATTTCTTTT CTATCTCCATCTCCTCATTAATAAAATACGTACATTTTCAGGTAATGGTA
WI-7936	131 T A ---	---	---	TTTTGAGTCAAGACTTAAAGGGCCCAATGAATTTATATACATCTGCATCTTGGTTATTTCTGAA GGTAGCATCTTTTGGAGTTAAATGCACATATAGACACATACACCCAAACACTTACACCAAAC[T/A] ACTGAATGAAGAAGTATTTTGTAAACAGGCCATTTTGGTGGGAATCCAAAGATTGGTCTCCCATATG CAGAAATAGACAAAAAGTATATTAAACAAAGTTTCAGAGTATATTGTTGAA
WI-7944	99 T C ---	---	---	TACAGTTCCAGCCCGTTGCCCACTCATCTGCGGCTTTGCTTTGGTGGGGGCAGATTGGTTGG AATGCTTTCCATCTCCAGGAGACTTTTATG/T/CJAGCCCCAAAGTACAGCCTGGACCAACCCCTGGTGTG TGAGCTAGTAAGATTACCTGAGCTGCAGCTGAGCCTGAGCCAAATGGGACAGTTACACTTGACAGA CAAAGATGGTGGAGATTGGCATGCCATTGAAACTAAGAGCTCTCAAGTCA

WI-7805	101 A G ---	---	TTTCTAGGCTGTACAGTCTGATGCATGATTTTATATAATTTTATACACTTGTGAAATTTGGATCTT TTTACTTTGAGCATATATTTAGAAATATGTGTG/GTGTAAAGGATCTCCACAATGTCTGCAGTGTG AAGGCAGGTTTCATTGTGGAATAGTTTAAACAGTCAGGAAGCTAAACGGTCAGTATTATGTGTAGC CCTACCAAAAATAGCCAGTAGTAGTATCTGAATAATGAAAAATAAATGAAGTAT
WI-7416	137 G T ---	---	GGCCAGGAGATTAGCAACAAGGATTCATCTGTTACTTACTTGGCCCTTTTATCTTTCCCTCTTGCCC CAGTCCCTTCTCTCCAGCTTCATGTGAAGCTCTGCACAGACAAGACTCAGTGTCTTGGCAGTGTCT [G/T]CTACTCCTCAGGTGCAGCATACATAACCAAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACACTCAAAAATTTGGCAAAATGTCATCAG
WI-140	252 C T ---	---	ATTTGAAGATTGGAGGGCTTTGCAGAGGAAATAGATTTCAATTTGGATCCCCAACTATAATGACA AGTTTATAATTAGGTGTGATCAAGGCTTCTAAAGTGAATGCAAGTTGTTACCAGTAAAGTTTATA TCTTCCATTCAGCCAGCTCATTTGCCAGAAAATTCAGGTGAGTGGATGGCCAGACTATCTGGCAAG GATGAAAATTTAGTTTAAAAATGTGTCATTTGTCTGTATTGGCATTCCTT[C/
WI-198	218 C T ---	---	GAGGTCTTTCAGCAACATGGAAGCCCTACTGCTTCAACCCCGAGTTCGCCGGATCAAGTGTGGCACC CATGATGGAAACTCTTGCCATGGTTTGTAGTACCTGGACCAAGTAGTCAATCCATCCTGACTTTAAAA TTCTAAAGAGCCTTGTATGGGACAATCTCTGCTAAAGACTAACCACTTCCCTTATCTTATCTTCAGCTA CCTGCTTCCCTT[C/T]GTTTAAACAAGCATAGAAATTTCTGAACAAC
WI-205c	146 T C ---	---	TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAATAAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTTCAT GCATGAGTTTGT[C/CCAAAGGCTTGATGGGAAAATCTCAACATTTGTTACCTAAGAAAAGAGGATGT ATCTTACTTTGTTTAAAAAAGTGCATATGCCCTTATTTTGTAGTTCCC
WI-205b	146 T C ---	---	TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAATAAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTTCAT GCATGAGTTTGT[C/CCAAAGGCTTGATGGGAAAATCTCAACATTTGTTACCTAAGAAAAGAGGATGT ATCTTACTTTGTTTAAAAAAGTGCATATGCCCTTATTTTGTAGTTCCC
WI-234	165 G C ---	---	GAAGACTGAGTTTCCAGGAGTTTGCAGCCGTTTCTCTCGGGCCATATGGCTAATAAGGAGCTTGAGCA GGGATTC AACCTGTTTGC AACCCAAAGTNCCTTTCCAAAGAGGTCTCAGACTACCTCCCTCCCTCCCT CTCCCCACAACACACAAAATACAGAGATT[G/C]AATCAGGAGCCAGTTTCTAGGTGGGCTTTGAGC AATCATACACAGTAATCTCTTGGTCTTTAGTTTCTCAATGGGAAATGG
WI-276b	25 A G ---	---	AGCTTTTGAATCCAAAACCACAT[G/C]TTGACTCTCTTATCTCTCTTGTGTAACTATCTATCC CTGAGGCAAAAATACAGAACACCCCTGTGGCTGCCTGAACGGAGGAGATGGGGGGGAGACAT CGGTCAATGTATCAAAAGCATCTCTGCTGCTGAAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGCTTATCTCTCTGCTATCCCTGATGACTGGGCAAA

WI-276	25 A G ---	---	AGCTTTGAAATCCAAAACCCACATAGCTTGACTCTCTTATCCTCCTCTTGTGTAACATCTATCC CTGAGGCAGAAATACAGAACACCCCTGTGGCTGCCCTGAACGAGGAGGATGGGGGGGAGACAT CGGTCAATGTATCAAAGCATCTCTGCTGCTGAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTGTCTTATCCTCCTGCTATCCTGATGACTGGGCAAA
WI-427	59 G A ---	---	TTTCCCACATCCACAGGTAAACTAATAATGGATGTATAGAAATTTAGAACTACTTCC[G/A]GTTT TTCCCTGGGAAATATTCACAAAACATTTGTGGCTGCAATCAGGTTAAAGACATAGTGTGCCA TTTGTCATCAGACAGGTAGAGGCCCTGACTCTGGCAGGATTAGCTACCACTAGCTGTGAGACTTTATGT ATTCATTTATTAGAGCCAGGGCTTGTCTGTCAACCCAGCTTTCAGTGCAGT
WI-562c	106 T C ---	---	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAAAGCCAGAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATTTTAA[T/C]AATGGTCTTTTATTAAAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562b	106 T C ---	---	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAAAGCCAGAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATTTTAA[T/C]AATGGTCTTTTATTAAAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562	103 T C ---	---	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAAAGCCAGAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATTTTAA[T/C]AATAAATGGTCTTTTATTAAAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-597c	141 A G ---	---	GTGTAATTTGGTGGCTTTGCAACTTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG[A/G]TAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAATTATTAAAC TTGATCTAATATTCTTCAACAATAATACCTGAGAGAAATAAGTCTATTAAAT
WI-597b	141 A G ---	---	GTGTAATTTGGTGGCTTTGCAACTTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG[A/G]TAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAATTATTAAAC TTGATCTAATATTCTTCAACAATAATACCTGAGAGAAATAAGTCTATTAAAT
WI-597	136 A G ---	---	GTGTAATTTGGTGGCTTTGCAACTTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GAT[A/G]CATGATAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAATTATTAAAC TTGATCTAATATTCTTCAACAATAATACCTGAGAGAAATAAGTCTATTAAAT

WI-611	66 G C ---	---	---	TTCAAAATTAACACCATGGGTATATTATAATTITNGCTCTATCCATAGTCTTAACCCCTCTTCTCT[G/ CJACAGTGAGACACCTGCTTCTATGTCCTTGACGTATTACGTATTCGATCAGTCACCCATCTGGA ACCAAGTTTCATTTCTGCTGACCCCTCCCTCCTCACCTACTTGGGCTCTGACTTCTCTTCTGCTGGCT GAACCTCTCTGTGGCTGTCCGGCTTCCCTGCTGGCTCCAATAC
WI-681b	156 A G ---	---	---	TGAAGCCCTCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGTGGTCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTCATACAGGGGAAGCACCTTGTNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATT[G]TTATACCTATGGCACCACTTGGACACAGATTATATATGTCAGA CACCACGNATGTCCTTTAAGATATGCAGCAAGCACAAATCTGTCATGGTTT
WI-681	156 A G ---	---	---	TGAAGCCCTCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGTGGTCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTCATACAGGGGAAGCACCTTGTNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATT[G]TTATACCTATGGCACCACTTGGACACAGATTATATATGTCAGA CACCACGNATGTCCTTTAAGATATGCAGCAAGCACAAATCTGTCATGGTTT
WI-867b	119 G A ---	---	---	AATCTTAACAGCCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCC[G]AJTTGTGTTTGGC CAAATAATATCTCCCGCAGGACGTCCTCTTTCTAATCCCTGAACCTGAGAAAATGTTATCTTATGC AGTGTATGGTTTGAATGTGTCCTCCCAACAAAGCACACATTAGAAACTTA
WI-867	113 A G ---	---	---	AATCTTAACAGCCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCC[G]AJTTGTGTTTGGC CAAATAATATCTCCCGCAGGACGTCCTCTTTCTAATCCCTGAACCTGAGAAAATGTTATCTTATGC AGTGTATGGTTTGAATGTGTCCTCCCAACAAAGCACACATTAGAAACTTA
WI-867	119 G A ---	---	---	TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCACAAATGTAACCTTGTCAAAACGA ATCTCAGTTTCTGCATATGTAATGGGAATGATAAGAGCACCCACCTACCTCATG[C/G]AACTGTT GAGAGAAATAAATGAGACATTGTAAGTAAAGTTTGAATGCACCTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGCTGTATTGTACATAA
WI-871b	123 C G ---	---	---	TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCACAAATGTAACCTTGTCAAAACGA ATCTCAGTTTCTGCATATGTAATGGGAATGATAAGAGCACCCACCTACCTCATG[C/G]AACTGTT GAGAGAAATAAATGAGACATTGTAAGTAAAGTTTGAATGCACCTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGCTGTATTGTACATAA
WI-871	123 C G ---	---	---	TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCACAAATGTAACCTTGTCAAAACGA ATCTCAGTTTCTGCATATGTAATGGGAATGATAAGAGCACCCACCTACCTCATG[C/G]AACTGTT GAGAGAAATAAATGAGACATTGTAAGTAAAGTTTGAATGCACCTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGCTGTATTGTACATAA

WI-884	198 T C ---	---	---	AGGTTCTGGACTTGATGCTGGGAAACAATTGGGTGNCCTGGAGAAATTCCTATTTTGGTNTTTCACAGAT CAGTAGAGCCAAATGGGAAAGGTATCCTAGTCCATCCCTTTATTAGGAACCTTCTGATCTATTGGGA ACTTCTCTCTAATAGATCAGGAAATCCACCTCATTTAATCATGGACAACNNAAGGAATA[T/C]G ATCCCGCATGCAACATTTATTGAGTAAACATGATGAAAATGAACATAAT
WI-921b	205 G A ---	---	---	CACITCCCAAGGGCTCTGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGACAGTTATCTGG CAGTGATGCTCTCACGCTGCGCCGCCCAAGAAAGTCTTNGCCAGGAAAAGCAGATCCATCTAC TCT[G/A]GGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTCCTCCGAG
WI-921	205 G A ---	---	---	CACITCCCAAGGGCTCTGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGACAGTTATCTGG CAGTGATGCTCTCACGCTGCGCCGCCCAAGAAAGTCTTNGCCAGGAAAAGCAGATCCATCTAC TCT[G/A]GGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTCCTCCGAG
WI-945c	90 G C ---	---	---	GGCTGGGATGAGAGGTCTACTTGTTGTTACTGGAGGTTTCACTGGCTTGTGCTAGAACTAGNAAAAGNA GAAAGAGACAGNGATTGGCTAAAC[G/C]CATGGCAGTAGTGGGCCCAAGGCTGAGTAATAAGAAA AAATCATTAGATAAATGCTCATGACCAAAACAAGTTCAAACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGAAATCTTTAAAGGGAATCATGACAGATTTCTTGGCTTTA
WI-945b	90 G C ---	---	---	GGCTGGGATGAGAGGTCTACTTGTTGTTACTGGAGGTTTCACTGGCTTGTGCTAGAACTAGNAAAAGNA GAAAGAGACAGNGATTGGCTAAAC[G/C]CATGGCAGTAGTGGGCCCAAGGCTGAGTAATAAGAAA AAATCATTAGATAAATGCTCATGACCAAAACAAGTTCAAACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGAAATCTTTAAAGGGAATCATGACAGATTTCTTGGCTTTA
WI-960b	167 C T ---	---	---	TTGCTTCAAAGAGTTCTTGCTCAGGAAGTTATTCATTGAGCAACCTAAATTTGTTTGGTACAT ATCAAGCACAGGGTTCTGAGCAATGCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTCTTACC CTGAGGAATTTATCAAAGATGTTAAGTTATCTTCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-960a	155 G A ---	---	---	TTGCTTCAAAGAGTTCTTGCTCAGGAAGTTATTCATTGAGCAACCTAAATTTGTTTGGTACAT ATCAAGCACAGGGTTCTGAGCAATGCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTCTTACC CTGAGGAATTTATCAAAGAT[G/A]TTAAGTTATCTTCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181 T C ---	---	---	TCCCACTGAGTATGGCTTTCAGTAGTTTATTATGATGTCCTAGGTACATTTGTTTATTGTTCTG CGAATTGTTGATTACTTTGGGAGAAATGCTCAACTATATAATTTGCTCTGACCCCTTTCTGTGTTTC CTTCTTAAAGATACAAAATAAATGTAACATTAGACCTCTCACTA[T/C]GCTGTTTTTACTCTCCTCTG ATTTTTTTTCCATTATTTTATTGCTCTGGCTTCATTTTGTAATNTG

-110-

WI-1147b	204 GA ---	---	---	TTGGCCATTATTTGAAGATAACCCACACCTTGGTGTCCAGGGTTTCACAGGTATTAGTGGTCAGTCA CATAGGCATATAGTACCTGTATGACTTCTATTCAGCCACCGCAACTTCTCCTCCCTGGCTC CTGAGCCAAAACAGGCATTTACCAATAATCACTTTGTTAGGATGAATATCTGGCCAACTGATA C/GA/GCATGACCCACAGCCTCAGGTATATAAAACACTCTCATCAGGCAGA
WI-1158b	147 CT ---	---	---	GCATTGAGAGGGTTCGTTTAAATGACATTCACTGAGGCCCTGCTATGTCAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG/C/GGCCAGGT TAAGTGTGGGG/C/TJCTGGGGTCAGGCTGCCCTGGGTACATCCTGGCTCCAACTGCTTTGCTATG GCT
WI-1158a	124 CG ---	---	---	GCATTGAGAGGGTTCGTTTAAATGACATTCACTGAGGCCCTGCTATGTCAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG/C/GGCCAGGT GGCTAAGTGTGGGGCTCTGGGGTCAGGCTGCCCTGGGTACATCCTGGCTCCAACTGCTTTGCTATG GCT
WI-1304	124 TC ---	---	---	AAGTTTACAGAAAAAATACCAGAAAAGTGACTTCAAGANTCAGCTGAGATAGAAAACATATGCCCA TCATCTTCAANGTNOCCACAGACACTTATCCCTAGACAGCCATTTCTTTTGAATGN/T/CJGNCANT AAAAATGATTTGAAATTGGGAATAAGGCCCTCCCTCTAATGATTTGACAGTGTAGACCTTGCCTAG GGC
WI-1305d	202 CT ---	---	---	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTTCCATT/C/TJATGTTGGTAAATATAAAG ATTGTGCAAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAAGATAAGGTTTTCCTC ACATCCACTGCTTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305c	46 CT ---	---	---	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAAGATAAGGTTTTCCTCACA TCCACTGCTTTTCANTAAAT/CJTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305b	153 TC ---	---	---	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAAGATAAGGTTTTCCTCACA TCCACTGCTTTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATAATG/C TJAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305	202 CT ---	---	---	TTAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA

WI-1306b	248	A G ---	---	TTCTGCATTGGAATAGTTGACTTCTATGAGNINNGCAATAATAAATGGACAATCTTGTNGNNNTNG GGCTGGGTGACTGTGCCCTGGTCAITTTAGAAAGCCATAGAGATGAAGAGCTGCAATAAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAAAGTGGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCTT/GJGC
WI-1306	240	A G ---	---	TTCTGCATTGGAATAGTTGACTTCTATGAGNINNGCAATAATAAATGGACAATCTTGTNGNNNTNG GGCTGGGTGACTGTGCCCTGGTCAITTTAGAAAGCCATAGAGATGAAGAGCTGCAATAAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAAAGTGGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTT/GJHCTCCTAGC
WI-1307b	118	T C ---	---	GACAAGGCTGGTACTAGTTTCCAAATCCAAATCTATGTACACTTTCCTCTCACTTCTCAAGTGGACA GATTTCTGCATTATACTGCTTGGGGTTGGGGAGCAGTGGTGTAGGCAAT/CJGTGAGATTGTCTTT CCTACCCCTTAAATGTATCTTNNCTAATTATNATGCTAAACCGGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTGTGTGTGCTGTGTTTCTCCTGTAAAGNTGTTT
WI-1307	118	T C ---	---	GACAAGGCTGGTACTAGTTTCCAAATCCAAATCTATGTACACTTTCCTCTCACTTCTCAAGTGGACA GATTTCTGCATTATACTGCTTGGGGTTGGGGAGCAGTGGTGTAGGCAAT/CJGTGAGATTGTCTTT CCTACCCCTTAAATGTATCTTNNCTAATTATNATGCTAAACCGGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTGTGTGTGCTGTGTTTCTCCTGTAAAGNTGTTT
WI-1325b	169	T C ---	---	GAGAGATGGCCAAAGACAAGCAGAGGGAGAGAGAGCAACCNCTGTGGTTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATTAGGCCAACTACAATGTGCCCTTGTCTCTCT/CJACCCCTCAGAACTTCCCTTGAGGGCAGGC ATTATGATTCACACTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1325	165	C T ---	---	GAGAGATGGCCAAAGACAAGCAGAGGGAGAGAGAGCAACCNCTGTGGTTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATTAGGCCAACTACAATGTGCCCTTGTCTCTCT/CJHCTTACCCTCAGAACTTCCCTTGAGGGCAGGC ATTATGATTCACACTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1327b	162	T C ---	---	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAAGCTGTGTAGTGCAGAAAGTCCCTGTTATTGTAAA ACACCAAGTGGGTTTAAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTGAAGTTGGGTAGTACCAGGCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCCTTACTGAAGAGGCAATGGTTCCATCTCTAAAG
WI-1327	175	C G ---	---	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAAGCTGTGTAGTGCAGAAAGTCCCTGTTATTGTAAA ACACCAAGTGGGTTTAAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTGAAGTTGGGTAGTACCAGGCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCCTTACTGAAGAGGCAATGGTTCCATCTCTAAAG

WI-1341b	136 G A ---	---	TATCAGCATGATTGTGGCTGTGGACACAAAGTCAATTGTACTTTTGNIGCNNTCTTTTCNTTT ACCTGATCCACTATCTCTCAAGATCANGTTCAAAATTTGGCTTNCNTTTGTNAATTATACCCAAAGC [G]A]GGATTGTGATGGATCTGTTATTTCTGTGCTTGGAACAGCAGAGTCGTCTCTGNGAGTNTG GTTTCAGGATTGTCTCTGTTTCCCAGCCACTTGCACCTAGCAAGTGT
WI-1349e	192 G C ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]JTCAA ATAATTTGAGAAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAAAATA
WI-1349d	264 C A ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]JTCAA ATTTGAGAAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAAAATATGAT
WI-1349c	192 G C ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]JTCAA ATAATTTGAGAAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAAAATA
WI-1349b	264 C A ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]JTCAA ATTTGAGAAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAAAATATGAT
WI-1349	264 C A ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]JTCAA ATTTGAGAAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAAAATATGAT
WI-1403b	57 C T ---	---	TGGTATTTGGAATGGGTTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/T]TCCGAAT GCCACTTTATAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACGT AAAGTTTACATCAACATAATTCTTGCCTGCATCATGCAITTTGGCAATATGTCACATAGCTGTCCCTCA TAATCCCAAAAGTGCCAAAAGGGTTGATCTGATTGT
WI-1403	58 T C ---	---	TGGTATTTGGAATGGGTTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTGCTTCTCCGAA TGCCACTTTATAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACG TAAAGTTTACATCAACATAATTCTTGCCTGCATCATGCAITTTGGCAATATGTCACATAGCTGTCCCTC ATAATCCCAAAAGTGCCAAAAGGGTTGATCTGATTGT

WI-1417c	31 C T	---	---	CAGCGGGAAGAGATTACGTGGAGAGATGTC/TJTTGGCCAGGGGGGCGAGATGTGAGCCACGGG GGTGACAGCATGCTGCTGGCAATTTGAGGGGCCAGAGAAATCCAGTGGCCCTCAATGACTTG GGTCTCTCGACTTCGGAAGTTTAAGGGGCTCGGCTTCAAAAAGCTGGTCCGGTTTGAGGGGGTTGC AGCGAGGGCCCTAGGTCCTGATTTAATGTTTGTGTAGAAAAAGTCGC
WI-1417b	31 C T	---	---	CAGCGGGAAGAGATTACGTGGAGAGATGTC/TJTTGGCCAGGGGGGCGAGATGTGAGCCACGGG GGTGACAGCATGCTGCTGGCAATTTGAGGGGCCAGAGAAATCCAGTGGCCCTCAATGACTTG GGTCTCTCGACTTCGGAAGTTTAAGGGGCTCGGCTTCAAAAAGCTGGTCCGGTTTGAGGGGGTTGC AGCGAGGGCCCTAGGTCCTGATTTAATGTTTGTGTAGAAAAAGTCGC
WI-1729	172 A	---	---	CCATGAGCAACAGCATGTTCTACTCTGTGTATGTATGTTAGGGGGCATGTATATCTGTATTTCTT TTTTATTCTCTCCAAAAGAAATTTCAATATGCAAAACATTTACAGGCAATGAGCTCGTAATAAAGA TGTTGGAGAACTGAAAAGAGAGCTTACATGCAACCCCAATAGCAAAACTCTCCACACATTTCCAGCA GATGATGTGTCCTCCGTGGTNACCTTCTCTCCACCACATCAGCTGTGTTTTT
WI-1732b	122 T C	---	---	TGCCTTACTTCTTTGTTCAATCCACCATTACATTTTGTAAATTTGAACTTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAGGGGACATATTCAAGGAGTNTCCCTGGTCAACCCCTTTTCTATTCAGTCT CTGCCACATGCTAGTAACGTGAGTGATGGTGCATCAGTATATCTGAGCCTCCCAAGGTACAGC CTTTCACACTACTTATTCATCATATTGGCTAAGGTATTCATCATATTGGCTAAG
WI-1732	114 C T	---	---	TGCCTTACTTCTTTGTTCAATCCACCATTACATTTTGTAAATTTGAACTTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAGGGGACATATTCAAGGAGTNTCCCTGGTCAACCCCTTTTCTATTCAGTCT CTGCCACATGCTAGTAACGTGAGTGATGGTGCATCAGTATATCTGAGCCTCCCAAGGTACAGC CTTTCACACTACTTATTCATCATATTGGCTAAGGTATTCATCATATTGGCTAAG
WI-1750	97 A G	---	---	GCGAATTTAATGACTCCAAAGGTAGTAATTCCTTTCCCCCAAAAAGGTTTTTAAATCTGTGTGGA CATAATGTTTGAATTTGCAGTTCACCTTGGG/GJTTAAGGTGTGCTGTTTTCTGGCAAGAGTCAAG TGGGAGTGTCCGGGAAAAGGGCTAAAGTCTTTGTAGTCAAGACAAACCCGGCTTGCAGTCTGTGAG CTACATTCACCTTTATGATCTCCAGGAGGTTCTTCCA
WI-1780	31 A G	---	---	GGTACACAAGAAATGCTTCTGGAAATCTAC/GJTAGGGCCCTTAACATTTTGGCTGAGTATTAATC TGTACATGTGTATGTGAACCCACCATGAAGCTGGGCAAGAACAAATTCCTAGGAAAGTACAATTAC TGGAAACTGTAGAACAAATAATCTCATAGTTTACACATAGCTGGGAATCACTCATGTTTCCCATCA ACTGGAGAGACCTTGTGAGTACAGAGGACATTCAGAAATAATCATAAAAAT
WI-1803c	77 A G	---	---	CCACTCAGTAATAATAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTTTTCAGGCAGAA CCATTATGAT/GJAGTAGGGTAGAGCATCACATTTGGGAGGACATATCTGGAGTNAGATATCCTG GGTGCTAATTTCAAATATATCTACTAAAGCATGACTTCTAGAAAATTAATTTACTTGTGCTCTCAA GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAAAATAACTGGAATCA

WI-1803b	77 A G ---	---	CCACTCAGTAATAATAGTGTGGAGATAAGTATATGGTAGGCACATAATAATATTTTCAGGCAGAA CCATTATGATGAGTAGGTAGAGCATCACACTGGGAGGACATATTCGGAGTNAGATATCCTG GGTGCTAATTTCAAATATATCTACTAAAGCATGACTTCTAGAAAATTACTTATTACTCTTGCTCTCAA GGAATGGGAATACCTATAATACAGTCTATTGAGGAAAATACTGGGAATCA
WI-1837b	112 C T ---	---	TTTACTTGGGATTTTTCATAGCTGATCATAATTTACCAATTTGATAATTCACCTCTTTTCCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGATAGACCCGTTTATAC[CT]CTGTCCCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACACTGGGAAGTCTGGGAACGTTTGTAGCTTTCGTGTGGCT
WI-1837	112 C T ---	---	TTTACTTGGGATTTTTCATAGCTGATCATAATTTACCAATTTGATAATTCACCTCTTTTCCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGATAGACCCGTTTATAC[CT]CTGTCCCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACACTGGGAAGTCTGGGAACGTTTGTAGCTTTCGTGTGGCT
WI-1840b	79 G T ---	---	TCACCTAGGGAGGTCGCTAAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAGT[GT]GAGAACTCTGAATATTCAGCACATACAAGTGTGACAACCACTTGTTTAGTAT ATTTTATCTCCAGAGTGTTTTGAATTTACTAAAAAGTTCCTAAAGAGCCCATGAAGAATTTAAGACT ATCGCA
WI-1840	79 G T ---	---	TCACCTAGGGAGGTCGCTAAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAGT[GT]GAGAACTCTGAATATTCAGCACATACAAGTGTGACAACCACTTGTTTAGTAT ATTTTATCTCCAGAGTGTTTTGAATTTACTAAAAAGTTCCTAAAGAGCCCATGAAGAATTTAAGACT ATCGCA
WI-1879b	110 C T ---	---	GGGCTCACTTTTCATCAGAGCACATATCACGTGATAGTCTGTTTCTCTTTTCATAACTACTCCCCCG CACTGTAGGNTTCTTTTGGTNAAGGACCTGCCNTTTTAC[CT]GTC[CT]GCNAAATAAACTCCCAAAA AAGTGGTAGTCCACAGGGTTTAAATAGTCTTGTGAATGAATTTCTGIGCGACCCCTGTGCCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCCTTACCCACT
WI-1879	110 C T ---	---	GGGCTCACTTTTCATCAGAGCACATATCACGTGATAGTCTGTTTCTCTTTTCATAACTACTCCCCCG CACTGTAGGNTTCTTTTGGTNAAGGACCTGCCNTTTTAC[CT]GTC[CT]GCNAAATAAACTCCCAAAA AAGTGGTAGTCCACAGGGTTTAAATAGTCTTGTGAATGAATTTCTGTGCGACCCCTGTGCCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCCTTACCCACT
WI-1900b	119 C T ---	---	TGTTCTCTGGTCCAGGCACCGGGCTAAGTCTTGTCTGCATATGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTACAGCTGCAAGAGG[CT]GCTCTGAGAGGT AAAGTGCCTGCCCCAACCGGCACAACTAGAGAGCAGCCAAAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTGCTTAAGTCCCATGAGAAACCACTTTTCTTTGCTCC

WI-1900	119 C T	---	---	TGTTCTCTGGTCCAGGACCCGGCTAAGTCTTGCTGCTAATGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCATCTTACAGCTGCAAAAGAGG[C/T]GCTCTGAGAGGT AAAGTCCCTGCCCAACGCGCACAACTAGAGAGCAGCCAAACAGGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGCTTAAC TGCCATGAGAAACACATTTCTTTGCTCC
WI-1943c	165 C T	---	---	ATTCCAGTTTACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAATGGGTAGGGAAGACCAGCC[C/T]CTCTGAANCTGGTCCCACGTTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCAGATGACTCCAAAGCCCGGCTGGAGTAT
WI-1943b	165 C T	---	---	ATTCCAGTTTACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAATGGGTAGGGAAGACCAGCC[C/T]CTCTGAANCTGGTCCCACGTTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCAGATGACTCCAAAGCCCGGCTGGAGTAT
WI-1943	164 C T	---	---	ATTCCAGTTTACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAATGGGTAGGGAAGACCAGCC[C/T]CTCTGAANCTGGTCCCACGTTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCAGATGACTCCAAAGCCCGGCTGGAGTAT
WI-1960c	270 A T	---	---	CCAGGTGAGGCTGAAAGAGGAGGAGGCAATTGCTGTGGAGTGAGGATTCCTGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAGGTGGCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCAGAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCACCTCCCAACTTT
WI-1960b	270 A T	---	---	CCAGGTGAGGCTGAAAGAGGAGGAGGCAATTGCTGTGGAGTGAGGATTCCTGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAGGTGGCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCAGAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCACCTCCCAACTTT
WI-1977	203 T C	---	---	CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTTGGATCTGGTAAGTAGGAGTCA TTCTGGGCATTCTTCATAGAGTNTTTTGTAGTCTCGTAATAATACTGTTGCCCTAGGAAGTTGTT TTTCTACTGCGTCTGTGAAAGCCTTCCCCATCGAGTGATACAGTACTTCCAGTTATGGAGATTIT /C/TAACAATCAAACTGCTGAGGCTGTGG
WI-2012	102 T C	---	---	AAATTC TAGAAGCCAGAGTCAGCTCAGGATTTATAAAGTTGAAGTAAATGCA TTGTAGTTTCATGT TTTCTCTTAATCTGCACAAAACAGTAAAAATC/T/C/TTTAAATCAGTTACCAGAGGCAATACCT GGGTTAATGTAAAGCACTCAAAAGTTATGTAGAGTAGCTGTCTCTGAGTCACITTTTTTCTACTCTCATT GGCTTACCATGCTTCCACTGGATC

WI-2013	127	C T	---	---	CTTTAGAGGTGGTCATTCGGTCCCTCTCGGAAGTGATTCGTGTTAAGAAAAATAGATGCAACG TTGCTAAGTACACCTAACATTTAAACAGTCTCCAGCAGATAAATGCTGATAGTACACTC/TCTCA CCAGAAAAAGAGAAATACCCATCATGAGGAAGAGAAATGACTTTTGTTGAGTTATGCTCCCGGGTCC CCTTCACTGGAGGGATATCTAGCTTCTGAGCCCTGGTTACTGCAATCC
WI-2032c	166	G A	---	---	ACCAGACATCCCATCAGGAGTAGTCTTCTGGCAAGCCAGCCCTGCCCTCTGATTCCCAAAAAACC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATCACCCAACTGGTTTCTAGATGTACACG/AJGTGGGACCTCTGTCTCAACCTCCGACTTTTCAC AGATCATTTGGTTAGGCTCACCTTCCGTGAATGCTTCTGTTTTCAAAAGG
WI-2032b	219	C G	---	---	ACCAGACATCCCATCAGGAGTAGTCTTCTGGCAAGCCAGCCCTGCCCTCTGATTCCCAAAAAACC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATCACCCAACTGGTTTCTAGATGTACACGTTGGGACCTCTGTCTCAACCTCCGACTTTTCACAGA TCATTTGGTTAGGCTCA/C/GCTTCTCTGTAATGCTTCTGTTTTTCAAAAGG
WI-2032	219	C G	---	---	ACCAGACATCCCATCAGGAGTAGTCTTCTGGCAAGCCAGCCCTGCCCTCTGATTCCCAAAAAACC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATCACCCAACTGGTTTCTAGATGTACACGTTGGGACCTCTGTCTCAACCTCCGACTTTTCACAGA TCATTTGGTTAGGCTCA/C/GCTTCTCTGTAATGCTTCTGTTTTTCAAAAGG
WI-2054b	188	C T	---	---	CGTTTCTTCTACATCTTGGGNACATAAAGANGAAGAGNAGCTGCTTTTGTGGTAGTTTGTCT CAGAGCTGCCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAATACCTTACAGACTTAGGATTGGGA TTTTCATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTTC/TCTGCTGCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTACTGGATGGGCTGCTTT
WI-2054	183	T C	---	---	TGGGATTAACACCCCTGTTTCTTCTCCAGTTCAGTGTGCCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGGCCGTTCAACAGGTGTTCCGTGCTT/CJTGGA TATCATCTGATCTCCCAACCCAGGCTTATTTATGCCCTAGGTAAAGGGGTAAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573d	129	T C	---	---	TGGGATTAACACCCCTGTTTCTTCTCCAGTTCAGTGTGCCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGGCCGTTCAACAGGTGTTCCGTGCTTTCGATAT CATCTGATCTCCCAACCCAGGCTTATTT/CJTGCCCTAGGTAAAGGGGTAAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573c	165	A C	---	---	

WI-2573d	129 T C ---	---	TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAATAGCTCTTAAATGCACCTGCCGTTCAAGGTTTCCGTTGCTT[C]TGA TATCATCTGATCTCCCAACCCAGGGCTTATTTATGCCTAGGTAGGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGCTTGGACGAG
WI-2573c	165 A C ---	---	TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAATAGCTCTTAAATGCACCTGCCGTTCAAGGTTTCCGTTGCTT[C]TGA TATCATCTGATCTCCCAACCCAGGGCTTATTTATGCCTAGGTAGGGGTAAGCAACAGAGGCTGTGT TGAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGCTTGGACGAG
WI-2573b	165 A C ---	---	TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAATAGCTCTTAAATGCACCTGCCGTTCAAGGTTTCCGTTGCTT[C]TGA TATCATCTGATCTCCCAACCCAGGGCTTATTTATGCCTAGGTAGGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGCTTGGACGAG
WI-2573a	129 T C ---	---	GACTTCATGCTCATGAACAAGCATTGTCTTAAATTTACAGACATTAAAGCAACAGCTTCC[A/G]CTC CCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCACTTAAAGAGGTTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCCACTACTCTATTAAACGCTTCCCAATGATGCAGCCAGTTCGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACACAGCTGAAAAATGAAATATCGATATAC
WI-2868b	60 A G ---	---	GACTTCATGCTCATGAACAAGCATTGTCTTAAATTTACAGACATTAAAGCAACAGCTTCC[A/G]CTC CCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCACTTAAAGAGGTTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCCACTACTCTATTAAACGCTTCCCAATGATGCAGCCAGTTCGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACACAGCTGAAAAATGAAATATCGATATAC
WI-2868	60 A G ---	---	CATGCTGTGTAACTCTGTGCTGTGCTGCGGGGAAATTAGAGCAAGGAATTGATATCCTAGGC TTCAAGGAGCTTCTCATCTCATTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] AGAAATGAATAGAGCCCCCATTTAAATTATATCACAGCTTATGTCCACTTCCCTGTTCCCTGCCATCAC TGGGCTTTTACAAAGGAGGCTTT
WI-2870b	131 T C ---	---	CATGCTGTGTAACTCTGTGCTGTGCTGCGGGGAAATTAGAGCAAGGAATTGATATCCTAGGC TTCAAGGAGCTTCTCATCTCATTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] AGAAATGAATAGAGCCCCCATTTAAATTATATCACAGCTTATGTCCACTTCCCTGTTCCCTGCCATCAC TGGGCTTTTACAAAGGAGGCTTT
WI-2870	131 T C ---	---	TGGGCTTTTACAAAGGAGGCTTT

WI-2954c	49 T A ---	---	---	TTAGCACATATCTGTTGGGACTTAACCTGAGACAAGGCATAAAAAATTAAGACACCTGGGGCA CAGAGGGAGCTCTATGCATTTNAATTCCTCATACCTACCCCTCCTCTCATTTCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954b	41 A G ---	---	---	TTAGCACATATCTGTTGGGACTTAACCTGAGACAAGGCATGTAATAAATCAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTTNAATTCCTCATACCTACCCCTCCTCTCATTTCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954a	38 G T ---	---	---	TTAGCACATATCTGTTGGGACTTAACCTGAGACAAGGCATGTAATAAATCAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTTNAATTCCTCATACCTACCCCTCCTCTCATTTCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2971b	62 T C ---	---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGAATC/G CTGCCAGCACCAATAAGCTTCTTTCAAAACAATTTGTGAACCTCCTCCTTCCCTAATAAACCTAAG ATTCTTTGTTCCCTGACATTCGAAGGCCACGCTGGTCTAGATGATGTCCTCCAGATTGCAATCCT AGTTCTTTAATGTTATCTGAAGAAACCTTTTACTTAGGGATTGCT ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGAATC/G CTGCCAGCACCAATAAGCTTCTTTCAAAACAATTTGTGAACCTCCTCCTTCCCTAATAAACCTAAG ATTCTTTGTTCCCTGACATTCGAAGGCCACGCTGGTCTAGATGATGTCCTCCAGATTGCAATCCT AGTTCTTTAATGTTATCTGAAGAAACCTTTTACTTAGGGATTGCT TTCTGGGAAAGAAAGATGGGGTTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTTTAA /TAAATCTTTCTTCTGTTTAAAGGAAGTTATCTGAAGAACCTGTTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGTT TTCTGGGAAAGAAAGATGGGGTTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTTTAA AATCTTTCTTTCTGGT/GCTTAAAGGAAGTTATCTGAAGAACCTGTTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT TTCTGGGAAAGAAAGATGGGGTTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTTTAA /TAAATCTTTCTTCTGGT/GCTTAAAGGAAGTTATCTGAAGAACCTGTTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133 A T ---	---	---	TTAGCACATATCTGTTGGGACTTAACCTGAGACAAGGCATAAAAAATTAAGACACCTGGGGCA CAGAGGGAGCTCTATGCATTTNAATTCCTCATACCTACCCCTCCTCTCATTTCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG

WI-2995c	151 G C ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133 A T ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995c	151 G C ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995b	151 G C ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995a	133 A T ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-3147	85 C T ---	---	---	GTGGTGCAGTTTCATCTCTGGAGCTCCCTGTGAGATCAGACTGGAGCCAGTCTCCAGCTTGAGACCAC ATCTCACTTAGCTCCTT[C/T]CCTGCCATATCCTGTTTCTTACTCCTATCTCCTGAGACTTCTTCCT GAATGAATTACATGCACCTCAATCCCTGCCTCAGTCTCTGCTTINAGGGAACCTTGACCTAAGACAGAA ATCTTAGTACCAATACITTTGCAAGG
WI-3234b	68 T C ---	---	---	ATTCGTAAATGTTTTCAGTCTCCAGTAAATCTTTATGAGGTCCATGTCATTACCTCTACTTA[T/C]GACAAAGCAAGAACACACAGAAAAGCCTCTGTTTGAATCTGGCCTCTTATAAATACITTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAATAAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGGAGACAAATGGAATGACTTATTTTATATCTTAT
WI-3234	68 T C ---	---	---	ATTCGTAAATGTTTTCAGTCTCCAGTAAATCTTTATGAGGTCCATGTCATTACCTCTACTTA[T/C]GACAAAGCAAGAACACACAGAAAAGCCTCTGTTTGAATCTGGCCTCTTATAAATACITTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAATAAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGGAGACAAATGGAATGACTTATTTTATATCTTAT

WI-3292b	106	GA ---	---	GTCTTGTAGCTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACTCATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCTGATGGTATGGATGGATGGATGCTTACTT GCCATGAATATTTCCATTGTTCTCATTAATGATTAATTAATTAAGTAAATATATTATTTNCCATGA GACAAATGGAAAATGGAAAACATTTCATGGAAAAAACCCATTCAATC
WI-3292	106	GA ---	---	GTCTTGTAGCTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACTCATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCTGATGGTATGGATGGATGGATGCTTACTT GCCATGAATATTTCCATTGTTCTCATTAATGATTAATTAATTAAGTAAATATATTATTTNCCATGA GACAAATGGAAAATGGAAAACATTTCATGGAAAAAACCCATTCAATC
WI-3355	19	GC ---	---	CCATGAACCATGGGCTACA[G/C]ATATTCTTAACTTCAGAGTCCCTTACTGGAGAGGGATCCA CTTTTAAATATGATTTCTTGAAGTGGCTGCATCTATCTCCAGCACCTTAAACCTCATCAGAA AAAAAATCATCAAAAAGTCGAAGTTAGTTTNNATTACCTTCACCTTTTCAATGGAAAACCTTTATAA ACTGTGGATCAATTTATATTACTTTTGGATCAGTTTAGATGACTTTNAGTTG
WI-3449	194	GA ---	---	CCATGAAGAATGAGTTCCTCCCTCCCTGGGTACGTCAGTCTAAGATAGCACACCCCTTGAGAAATTNACT TAGCACGTGGCATTGTAATGGCTGGATTTCCCTCGCTCTAAGACACACACCTTTATGCTTTNAAAGCTTT CTGGAATGGGATGAATCNACATTCATGTGCACCCCTCGTGGGATCACCTTCTCC[G/A]TGGCCCC ATCTCTGNAGAAGCCACTGGGAAGTCGAAGGAGTGACTTCAATCAGG
WI-3505b	131	GA ---	---	TAACCTATGCTCATCTGGCTTACTGCTTAGTTCCTCCATTTGTCATCAGTGCACCTTAAAAAATTTT GAAAAATTGCCATTTTAAATATCTTTGGAACTTCCTAACACATTACCTATTTTNAACCAAAC[G/A] AGGTGATTCCTTATGGGAAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTTGCATAT
WI-3505	131	GA ---	---	TAACCTATGCTCATCTGGCTTACTGCTTAGTTCCTCCATTTGTCATCAGTGCACCTTAAAAAATTTT GAAAAATTGCCATTTTAAATATCTTTGGAACTTCCTAACACATTACCTATTTTNAACCAAAC[G/A] AGGTGATTCCTTATGGGAAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTTGCATAT
WI-3564b	177	CT ---	---	GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGAGTCACCTAAATGTTTGGAAAAATAAAGT GAAATCAATGTGTCTTCCAGTGTATTCACATGGCAGTGTACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGCTGTCTTC[η]AACAAAGTGTGTTGTTGTTGTCATC AGTGTACACATGCTACCTTCTTCACAAAAACAAA
WI-3564	177	CT ---	---	GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGAGTCACCTAAATGTTTGGAAAAATAAAGT GAAATCAATGTGTCTTCCAGTGTATTCACATGGCAGTGTACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGCTGTCTTC[η]AACAAAGTGTGTTGTTGTTGTCATC AGTGTACACATGCTACCTTCTTCACAAAAACAAA

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WI-3649	64 A G ---	---	AATGTCATGCTGTGACTGACCTGTCTAACACCTTTCCCTAGTATCCCTTAGTGAAGATTAC[A/G] AGACCAGTTTGCCCTTCACTTAGTAGGGCCAATGATAGACTTTTAGTGCTACCACAAAGGTACCTGC ACAGCCACATCATATGTCACAGTATGGTTGCAAGGACCTGTCTAGACTCTTTCTGCCTGCCTTGGTC TTCCTGTTTACCATAATATGATGACATGCAAACTCAGAGCCTTTTA
WI-3674b	133 G C ---	---	ACAGTACACATGGCCCCATTATGGAACAATCATCTGACTTATGTTACCTGAGAAGTCCCTCTCTAA ATTTAACTACCAGGGGAGTGCTTTTATAGTAATTAATAATGTTTATTTAGAAAATAACAAAAT[G /CJAAAGAAAATAATGATAGTCAAGTTGTAGACACTATTTAAAATTTGTAACCTGGTCAAATGATTGT AATCTTAATTAATGTTTATGTTTATGTTTNAATGCTCAATCAGGCCAAG
WI-3674	133 G C ---	---	ACAGTACACATGGCCCCATTATGGAACAATCATCTGACTTATGTTACCTGAGAAGTCCCTCTCTAA ATTTAACTACCAGGGGAGTGCTTTTATAGTAATTAATAATGTTTATTTAGAAAATAACAAAAT[G /CJAAAGAAAATAATGATAGTCAAGTTGTAGACACTATTTAAAATTTGTAACCTGGTCAAATGATTGT AATCTTAATTAATGTTTATGTTTATGTTTNAATGCTCAATCAGGCCAAG
WI-3682	137 G A ---	---	CAATATAGACCAAATGACTGCCACAAGAGAAAATTAGTGGATCTACATTTAGAAAACCCACATGTTTT ATTGGCTCTCTCTCTCTCTCTCTTTTAAATGCTCTCTCCAACACCAAATTCACCTTTATCTTTTCAA T[G/A]JAGCATTTGTCCAAATTTAAAGTCAATGAAAAATAATGTACATTTTCAACAAGTATACATTA GCCCTGCCAAAAGTCTTATATGCTAT
WI-3854b	194 G A ---	---	GGTATGTTGAGGTCAGCTAATGGTCACTGTGGTTGGAGTGAATCTAAATGGATTTTTGCCCTTGG CAAAGACCAAGGACAACCTGAGGACTTCTGCATGGTCTACCTCACCTTAGGCTTCTTGATTAATAACTC TGGTTCAGGAAGGCAAGGGCAGTTATGACCACCTTACAACTGAGGAAATCAAAGCAAC[G/A]JAGAA GTTAAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
WI-3854	194 G A ---	---	GGTATGTTGAGGTCAGCTAATGGTCACTGTGGTTGGAGTGAATCTAAATGGATTTTTGCCCTTGG CAAAGACCAAGGACAACCTGAGGACTTCTGCATGGTCTACCTCACCTTAGGCTTCTTGATTAATAACTC TGGTTCAGGAAGGCAAGGGCAGTTATGACCACCTTACAACTGAGGAAATCAAAGCAAC[G/A]JAGAA GTTAAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
WI-4039	210 G A ---	---	AGCCAGCCACATGTTGAGTCCCTGCTCATCTCCCATCTCTTATTTCTCTACTGCCTTCACCTT CCATTAAACAAGAACTCTTGTTGATTACATTTGTTTGGTTACACTACAGAAATCCAAGATGACCTC CCCATCTCAAGGTCAACTAATTAACACCTTAATCTATTTGCAATCTTTGTCAATTACCATACATATT CATGG[G/A]TTCTGGGATAAGGGGTAGACATTTTATGGGAGGCATTA
WI-4110b	130 T C ---	---	GAAAAATGATGTTTTGATTTCCCTTCCCTATCTCAGATTATGGAGTGCATTAGAAAACTGATAGT AACCTTTTATTTGATGAAACTCTGTCTATAAATTAACCTTCTCTCTCTCTTTATTTGCCCT[CJACA GTTAGGTAAATAAAGATGCCCAAGAAATTCAGTATTCAGGTACAGTAAAGATGACCAACCAATGGG GTAGGGACAAGTNCAGAAAAAGGAGGAGGTNGGGGGTTTTTCTGGGAAGA

WI-4110	130	T C ---	---	GAAAAATGATGTTTGGATTTCCTTCTATCTTCAGATTATTGGAGTGTCAATTAGAAAACTGATAGT AACCTTTTATTTGATGAAACTCTGTCTATAATTAAACCTTCCTCTCTGCTTTATTTGGCC(T/C)ACA GTTTAGGTAATAAAGATGCCAAGAAATTCAGTATTCAAGTACAGTAAAAAGTAGCAACCATGGG GTAGGGACAAGTNCAGAAAAAGGGAGGAGGTTGGGGTTTCTGGGAAGA
WI-4119b	168	G A ---	---	ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGGTGGGAAAAGTAATAAATAG AATGGAAGGATAAATAAAGGTAACACGGGGAAGAACAGGACAAGACAGACAGAGAAGGGGT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAAATTTGTTTTCTTCA TGAGACCGTCTGCATCTTTTGTTTTTAAAGGGCTCTGTTGATCATCATCTTCA
WI-4119	168	G A ---	---	ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGGTGGGAAAAGTAATAAATAG AATGGAAGGATAAATAAAGGTAACACGGGGAAGAACAGGACAAGACAGACAGAGAAGGGGT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAAATTTGTTTTCTTCA TGAGACCGTCTGCATCTTTTGTTTTTAAAGGGCTCTGTTGATCATCATCTTCA
WI-4123b	51	T G ---	---	CAAAGTCAGATTTTGATTATTCAGGATAACAAATTTGAAAATAGAAAAGTG(T/G)TTAAACTATTT CAAATAACAATAAAGAAAACATGATGAAATTCCTCGTTACATAAATGATAGAAATTTAGTGGG TTCTCCATGACATGGCTTGTCTTCTCAACAGTGGTGGTTTGGATGTTTCCATGCTTTCTC AGGCACAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4123	51	T G ---	---	CAAAGTCAGATTTTGATTATTCAGGATAACAAATTTGAAAATAGAAAAGTG(T/G)TTAAACTATTT CAAATAACAATAAAGAAAACATGATGAAATTCCTCGTTACATAAATGATAGAAATTTAGTGGG TTCTCCATGACATGGCTTGTCTTCTCAACAGTGGTGGTTTGGATGTTTCCATGCTTTCTC AGGCACAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4149b	145	G C ---	---	TTGTACATGTTTCATTCATCCCTCCCATCTTTTCTGTCTTAAAGAACCTCGCTTCTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTTTTATTTCCATCAAGCTTCTCAGCATCTCTATATACT GTGCTG(T/G)CCTTGGAAGAGCCAGAGCCGAGCATACCAACATGATCTTTTGCITGAACGTAGT AGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG
WI-4149a	137	T C ---	---	TTGTACATGTTTCATTCATCCCTCCCATCTTTTCTGTCTTAAAGAACCTCGCTTCTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTTTTATTTCCATCAAGCTTCTCAGCATCTCTATATACT T(C)GTGCTGTGCTTGTGAAGAGCCAGAGCCGAGCATACCAACATGATCTTTTGCITGAACGTAG TAGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG
WI-4182	188	G A ---	---	TAACACACTTTTCATTTGGTTTCTTACTGCAGTTAAAGGACCATCCATTATATTACAATTCCTC AGTTCTATGCTTTAGAGTNCATTTATAGACTACTGTAAATTTTCAAGGGAATTTACTCCTTGAGTA GGGGAATGAGTTAAATAATCTACCACATGCCAAATTCAGGGGACTGTGGTTAA[G/A]ATGTCCTCTCT TGCCCCCTTCCCAAGTTCTTAAATTCCTAG

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WI-4230	93 T ---	---	AGAGACGTTGAATGGGGACATCTTTCTATTCGATTTTAGTTTAAACATTTGATAAGAAATGATGAAA GTTTGACATCCAGATTTATCTTTATAGCAGCAGAGCTGGCAAAATAAACAGCACACTGACT TTTCCATGGTAAAGAAAGTTAGAGAAAACAGCCTATTTTCTTTAATGTTAAATGTAATTTCTGAAT ACATTTAATGGAGGAGAAATGAATAGTGACCTTTGAAATTTTGAATTTATGG
WI-4241	118 C T ---	---	GAAATTCCTATTGAAGTTTGGACCTTGAACCTGATCTCATTAATACTTTTNCCTGTAGTGGTTGTTATTT CATTTTGACAAACAGAACAGACGAAAAATTTCCACTTAAAAATTAATTTCTC[CT]AAGTATCTATGAT TTAGCACTGTTAGCACCAGAAACTGTGAAATTAATCTCTAGATATTTCTTCAGAAATCTAGGATGGAAG AA
WI-4271b	151 A ---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAGATCAAAATAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCAACCCCTCCCTTTTGTCTCAGG CTCTAGAAGGTCCAGTCAGGGGC
WI-4271	151 A ---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAGATCAAAATAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCAACCCCTCCCTTTTGTCTCAGG CTCTAGAAGGTCCAGTCAGGGGC
WI-4389b	156 G A ---	---	AATCGAAACATTGATTTTGTAAAGGAACCCACATTTATGATATTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAGAAAGGATATTATGTCATAACCTTTGGA AGGTAAGATGTGAACCTATACA[G/A]TNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4389	156 G A ---	---	AATCGAAACATTGATTTTGTAAAGGAACCCACATTTATGATATTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAGAAAGGATATTATGTCATAACCTTTGGA AGGTAAGATGTGAACCTATACA[G/A]TNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4488	31 A G ---	---	GATGACAAATTTGTGTATTGGCATTTTAAAG[G]GTACCATTCATTTTCTTCTGGCTTTTCGTGTGTT TGTTGTTGAGAAAGTCAGGGGTAGTCGATTGCTCCTTTTCTAGTTCTTCTCAGTAGGAAGACTGATC CTAAACAACTAATTACCCATGCCAAAGTACGTCCAAACTGATCTTTAAAGAACATAAATCAAAATTG TATTATCCTATGCTTAAATGCTCAG
WI-4491	145 G C ---	---	ACCATCAATGTATCACCTTCTAAAAATTTATTAGATGATTAACTGGCTCTGTTAAAAAATAAAACCT GTCTTGGACATTTGAAATAAAACATTACTATTGTTGATTTTCTGCTACTTACAAAGGACTGACTA AACAAGTTAAG[G/C]GTTTGTGGAGGGGAAAAATCATAAAAATGCATAAAAAATTTCTACCACCTGTCA TTTCTTGTOCCATAAAATAAAATTTTACATGCCT

WI-4584	144	A G ---	---	TTGGTTGGCATTAGCCTCATAACAACTATTACAATCATAATTGTTACTCTTATTACAAACAAG AAAATGAGGCTTAACATCACACTCTGCTTAGTCGCAGAGCCAGATTGAACCCAGGAATCCATT CACCGTAC[A/G]TGCTACCTGGTAAAAATGTTTAAATAAATCTATGGCATTAGATTTCAAAGA GTCCTAATGTGGTTTGAAATAGGTGTGCTTAAATTTGTTATCAGTATGC
WI-4639	185	C T ---	---	TTTCTGCATTTGAATGTGTATGGTCAGACTTCAGAGGAACCCAGGAATCTCATTTATTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTTCCAAATCCACCAATTTAC TGACCATATGACTTGGGAACATTATCTCACCTATCTGAGTCTGTATCC[C/TT]CATCTTTAAATGTGA AATTTAAGGACACCTATCATAGTAATATTGTGAGGATAAAATGAAATAA
WI-5327	63	A ---	---	AAATGAATCCGCTTTAGAGCAATACCAGTAAGGGCTGGTGAGGATGGTGGCTGAGAGA[A/-] JGATTACTCATAAAGCATATTAAATTTATAAATATGAAAAATTTAACTAGATAAATAAATGTGAAT TGAGTTGAAGGTGCATGAGAGTAGGAGGAGGAGGTCTACTTATAGGGTTTATATAAGTNGCT TCAATAGAAATGGCTCTTTCCGGATGACAAATGATGAACGTCTTAAGCAGACAG
WI-5390	87	C T ---	---	GCCTTGAGAAATGAAAAGGGGAGCCTGGACCATTGCGAGGGCTTCTCACTCTGATTTTGTGTAT TTATTGTTACATTATTAT[C/TT]GTCTGTCTCCCTTCTGGTATGCTTGTGTCATGAAACAATGAATTC CCCAGTGCCTGGCCGATTGCTGGCTCCTAGAGGTGTCAGAAAAAAGTTTCGGTGAATAGAAATTG ACGAATGGGTTCAGAAITGAACCTGTGAATCTATGGAAGACAAACGAAT
WI-5404b	87	G A ---	---	CCTTGCCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCCTGTCAAGAAATCAATTATTAGCAGT GCAACATTATTTTAAATTT[G/A]AAAGAAACCTGTTTCTGAAACTTTGTACTCTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTTCCATGGTCGTGAATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTATAGAGTTTATAACAA
WI-5404	87	G A ---	---	CCTTGCCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCCTGTCAAGAAATCAATTATTAGCAGT GCAACATTATTTTAAATTT[G/A]AAAGAAACCTGTTTCTGAAACTTTGTACTCTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTTCCATGGTCGTGAATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTATAGAGTTTATAACAA
WI-5545b	77	A C ---	---	TAGGAAAGGGGATGGTGATGGCCTCTGAGACATTTAAATCTATTCTTACCACCTCACACTGCCGCCA TATCTCCTC[A/C]CCAAACACCTCTGTTTCTGACAGCCAAAGTTCCATCAGTTGATGGGACTATTT GTTGCAAAACAATTTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCATTCA
WI-5545	77	A C ---	---	TAGGAAAGGGGATGGTGATGGCCTCTGAGACATTTAAATCTATTCTTACCACCTCACACTGCCGCCA TATCTCCTC[A/C]CCAAACACCTCTGTTTCTGACAGCCAAAGTTCCATCAGTTGATGGGACTATTT GTTGCAAAACAATTTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCATTCA

Accession	Position	Sequence
WI-5860b	134 A G ---	ACTCAAGTTTGGGGATAAAATCAGAAAGTTTCTATGTACAACTTAAATTTTGCTAAGATTTTATTGTTTCTTTTATATAAAATTATGGATTGTTTCTACCTCCCTAACCAACCTTCTAAGTGGGAACTACATCACTGTTTACTGGAATCATGTGAAGACATTTAAAGGGTACCCAGGTGCACATAGTTTAAAGGGAATCAATTTCCAAATCATCAACTTCTGTAT
WI-5860	134 A G ---	ACTCAAGTTTGGGGATAAAATCAGAAAGTTTCTATGTACAACTTAAATTTTGCTAAGATTTTATTGTTTCTTTTATATAAAATTATGGATTGTTTCTACCTCCCTAACCAACCTTCTAAGTGGGAACTACATCACTGTTTACTGGAATCATGTGAAGACATTTAAAGGGTACCCAGGTGCACATAGTTTAAAGGGAATCAATTTCCAAATCATCAACTTCTGTAT
WI-6106	208 C G ---	GCAACAACCTATTATACCTGATTCACCCAGGTCTACTAACATTATCAACCCCTAACCCACAATACATATATTGTCTGTTCTGAATTATTTCAATTAGAATCTGATGAGATTTAGCATGGGATTAAGTGCAGTGCAGAGATAGTAAACACTGCTCTTTTGTCTCCAGGAGTCTCAATGTGAAGTATAATCTTACAGAGTAATTTCGATAGTCCACCAAGTCTATATTGTATGTGAAGGAAAG
WI-6109d	129 T C ---	AAGATAGACAAACATATGCCAGACCACAAACAAAAACACAGACCTGTCTATATTCTGAGAGAAATGTACATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAAGGAAAAAACCTTC/TAACCCCTATATTNCTGCTTGTCATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGTGNAAAATTATCCCTGAAAATTTTATACCA
WI-6109c	147 T C ---	AAGATAGACAAACATATGCCAGACCACAAACAAAAACACAGACCTGTCTATATTCTGAGAGAAATGTACATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAAGGAAAAAACCTTAACCCCTATATTNCTGTC/CTTGTCATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGTGNAAAATTATCCCTGAAAATTTTATACCA
WI-6109b	147 T C ---	AAGATAGACAAACATATGCCAGACCACAAACAAAAACACAGACCTGTCTATATTCTGAGAGAAATGTACATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAAGGAAAAAACCTTAACCCCTATATTNCTGTC/CTTGTCATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGTGNAAAATTATCCCTGAAAATTTTATACCA
WI-6109a	129 T C ---	AAGATAGACAAACATATGCCAGACCACAAACAAAAACACAGACCTGTCTATATTCTGAGAGAAATGTACATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAAGGAAAAAACCTTC/TAACCCCTATATTNCTGTC/CTTGTCATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGTGNAAAATTATCCCTGAAAATTTTATACCA
WI-6112	96 T C ---	AATGCCTATCACCTTCCATCATGCTGCATAACTGATTGATTCATAATGCTTATTGTTTAGCACCTGCTTCCAAACACATGCTGTTTGTTCATGATTC/CGCATATCCCAAGTCCCTTAGACAAATGCCTCCCATACAGTGAACAGTATTTGACTAAACATACCTGTTAAATCAATAAAATTAATCAACTTGGCATATGCGAGGAAC

WI-6244	103 C	---	---	TAATGCACAACCTACATATCAGGGTTTCTGATTGAAAGGAAGAGAATATCCCTTCTTTAGTGATT GCTTAATATTAAATCATAATAAGTGCACCATCTCTT/CJGCTCCTTATAAATGTTGTAGAAAGAGG AAATTGAGTGTGGGAATTAGCAACAGGAGACATTTTATATACTCTACAGTGGGGAAGACTT CCTATTCTTCCCAAGGATGGATACATTCTAC
WI-6268	124 C	---	---	CTGGCCTTATAATCCAAAGTTTAGGATTAACTTACCCCAACTTAATAGACTTCCAGACAGTTGCAGTT GTCTACAAGATTTCCTCCTAGTAGGGCTTGGGTGTGGCACCGTTTGGCTCATTC/CJACTCTCCCT GGGTCTTATTGACTTTCAGGGAGCCTAGAAAGAGCTGGACAAAACCTGCTTCTTTGCAGAAAGAGTCG GGGTCCAAAGATTTCGTACGATTITTA
WI-6336b	234 C	---	---	AGGTGCCATTAAATCCATTCAAAATTTGGAAGCTACATCTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATTCCCCCTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCAGATGAAATGGACCATGTG GTACCCAGTGCATTATGCTTGGTAGAGCC/CJTJGAGGACACTGACAGT
WI-6336	234 C	---	---	AGGTGCCATTAAATCCATTCAAAATTTGGAAGCTACATCTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATTCCCCCTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCAGATGAAATGGACCATGTG GTACCCAGTGCATTATGCTTGGTAGAGCC/CJTJGAGGACACTGACAGT
WI-6381	92 C	---	---	TTGGATACAAAAATTCAGTTACACAATCAGTAGCATTCAAAATTAGTTATGAGTATTTATACAATTA CAAAAATGNTTCATGTTTAAACA/CJAJGTAATTTAAAGCTCAAAACATTTTAAACAGGCACAAAT ATTCTAANGGCATATGCATTCACCATGGGCTTTTGAATGTCTCACTCCCAACTTCACAATCAAAATC TACAGANGCGCAAAAGATCAGAGTTCAG
WI-6436	198 C	---	---	GGTTGAGGCATTGGGAAAGGCAGAAATTTGAGGCAGTAGAANAATGGACATTTTAGGAAAAGAGAAGT TCAGAGGCAAAAGTCATGACAGACAGGAAATACAAGGCTTAGGAAGACAGTAGTCTCTGTGGTTGAA ATTTGGTGTCAATAAAGAAGTTTAGACTTTGGTGGTTGAGTAGTTGATAGTAGGTAGCGTT/CJ GJATTGGGTGATTCCACAGACAAGGTGATGTTCTAAGATTGATATTATTGT
WI-6449	186 C	---	---	GAGGCTCTTTGCTTTCTCAGTCAAGGCTGATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTCTGATTGGTGGTGTGCTCAGACTGCCAGATTGTTAAATATTTTGAATAATC GTATCTGGTCTATTCAATCTGCATCTCTGATCTTAIGCTGGCTATT/CJATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCCTCTAAATTTTCIGGGIGATTATA
WI-6449	186 C	---	---	GAGGCTCTTTGCTTTCTCAGTCAAGGCTGATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTCTGATTGGTGGTGTGCTCAGACTGCCAGATTGTTAAATATTTTGAATAATC GTATCTGGTCTATTCAATCTGCATCTCTGATCTTAIGCTGGCTATT/CJATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCCTCTAAATTTTCIGGGIGATTATA

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WI-6463	72 T C ---	---	GCTGGAGAGAAAAGACCTCCAAAAGAGAAACTAAATCAGAGTCTCTTGAGCAAGAGGAATTGAAA AGAACATTCJTGAAAAAAATTAAGTAGAACTCAAGAGAGCCAAAAAGTCCCAATTTGTGTCATTA TAAGAAATATTTGAATGGAATCTTAAGAAATGATTTTATTGATCAGTTAAATGTTCTTCCTCTCCTC CAGTCCCATTTATATGACATCCGCATGCTG
WI-6474b	76 C T ---	---	AAGCAGTAAATCTTCCATCGCATGGATGCCAGTGGGTAATGTTATAGAAACTTCAGAGGANAC AGAGGCAAA[C/T]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCACAGAGAAAAGGGGTGTAAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACATAAGTATAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6474	76 C T ---	---	AAGCAGTAAATCTTCCATCGCATGGATGCCAGTGGGTAATGTTATAGAAACTTCAGAGGANAC AGAGGCAAA[C/T]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCACAGAGAAAAGGGGTGTAAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACATAAGTATAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6478b	175 T A ---	---	GAACCTCAATTAACTTTGCAACACTGAGAAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGGAATGCCACGCTTCGAGGCTGTCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCAATAGTGGAGAAATCAGAGT[A/G]CTCCTTGTCAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6478	175 T A ---	---	GAACCTCAATTAACTTTGCAACACTGAGAAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGGAATGCCACGCTTCGAGGCTGTCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCAATAGTGGAGAAATCAGAGT[A/G]CTCCTTGTCAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6559	149 G A ---	---	CACATTTTGAATGCAACTGAGAAANTGGTTTNTAGGCTACCTTTTATTAAGAGTACATCTGGCTC CAATGTTACCCCAACATGCAAAACATAAGGCAACAATTCGATCATTTTATAGNTCCCAAGCCCA TTAGCAATATCTTA[G/A]TCAAATTTTAAAGAGAGAACAGGAAATAAGGAAGGCCCTAACAGAGGAG TTAAATAATTGTGCAAAACTTATCAGTTCTTC
WI-6564b	54 G A ---	---	TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCACGTGTTCTATGC[G/A]CACTGGCTTTG TAGGCATTCACATCATATGCTGTGCTGCTGAAATCTCAATTAATTTCTCCTNCCTATTCCTTTCCAT GCTCTGCCTCATTTNCTCAGAAATGAAGGCATTTGATTATNATTTTGTGTTGGTGTGTGTAAG GTTCCTTGGCAGGAGAACATGCATATGACTTTAAAAATAAGACCAACA
WI-6564	54 G A ---	---	TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCACGTGTTCTATGC[G/A]CACTGGCTTTG TAGGCATTCACATCATATGCTGTGCTGCTGAAATCTCAATTAATTTCTCCTNCCTATTCCTTTCCAT GCTCTGCCTCATTTNCTCAGAAATGAAGGCATTTGATTATNATTTTGTGTTGGTGTGTGTAAG GTTCCTTGGCAGGAGAACATGCATATGACTTTAAAAATAAGACCAACA

-128-

WI-6608b	46 C	---	---	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCTCAGT[C/- JAGTTGAGGAGCTAAAGGAGGGGATTTCCCTCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGTATTTCTAGAGGAAAAAGAACTGAACTCCAGCACTAG GTAAACTGCAAAAAAGAAAAACACCTGTGCCAGGCACTAGCTACAAGGCCACACCCAGAAAAAGGAA AGC
WI-6608	46 C	---	---	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCTCAGT[C/- JAGTTGAGGAGCTAAAGGAGGGGATTTCCCTCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGTATTTCTAGAGGAAAAAGAACTGAACTCCAGCACTAG GTAAACTGCAAAAAAGAAAAACACCTGTGCCAGGCACTAGCTACAAGGCCACACCCAGAAAAAGGAA AGC
WI-6666	68 C	---	---	GTAGACAGTATCCAGCAAAAAAGGTTATTTATACCTCTACTTTCCAAAAAGGAAACCTCCCC A[C/A]AAATCCCATCAACACACAGTCATGCTGGAAGGCATTCTGCTTACTCTGTGGTTTCATGTAA ATGTTGGGTGACTCATTCGGCTCTCTNTCTCAAGTTCAGGCTTCTTGGGTAGACCA ^A AACTA ATACACAATGTTAGAGCACACAAGAGA
WI-6670b	120 A	G	---	AGATTAAACATAATTATCTAGGGCCATTGTAGGGTNGGAGGAGTGTTTTCTATCTGCAGCCAAA CAGAAATACGTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTTAGCCA GCATTGCCATTGAGGCCGAGTCAAGGTTTGTGGGCCAGAACTTTAGACAAATTTGGGGAATCTGA AAAAAAAGAAATACAGAATTGTAAACACAGACACAGAACTTTAGAGGGGAT
WI-6670	120 A	G	---	AGATTAAACATAATTATCTAGGGCCATTGTAGGGTNGGAGGAGTGTTTTCTATCTGCAGCCAAA CAGAAATACGTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTTAGCCA GCATTGCCATTGAGGCCGAGTCAAGGTTTGTGGGCCAGAACTTTAGACAAATTTGGGGAATCTGA AAAAAAAGAAATACAGAATTGTAAACACAGACACAGAACTTTAGAGGGGAT
WI-6704c	33 T	C	---	TTTGAAAAATAATTTCATGCACCAATGTTTTAACT[C/C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAAT ^A AGTTTTCATGACACACCGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCAATTAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704b	33 T	C	---	TTTGAAAAATAATTTCATGCACCAATGTTTTAACT[C/C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAAT ^A AGTTTTCATGACACACCGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCAATTAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704	28 T	C	---	TTTGAAAAATAATTTCATGCACCAATGTTTTAACT[C/C]AACTCACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAAT ^A AGTTTTCATGACACACCGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCAATTAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG

WI-6710	106	GA	---	---	CCATGGACAGTTTAATTAGGAAGCTTCGACTTGTAGAATAACAGAGGAAGTCCCGAGTTATCTACCT ATTCCCTTAAACACACATTTTGTCAAGCTGGAATGATTCCC[G]ATAGTAAACTCAACATCCACACCT GCATAAACATCGCTCCCAAGTGACTATTTAATCTAGTCGACACAGGATGTCACCAGTGAGCCTC ATCTCCAGTCCAATGGAGGAGTTGACTTAGACCTTCCTTGGACAGGAAGGGTC
WI-6766b	148	GC	---	---	AAACAAATGGTGCAATTCGATAATATTGGGTACACAGTATAAAACAATACAATTAGTTCATATAAC ATTGGATATGGACAAAAATACACANGATCCTTTCTTGTCTACGGAAAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACACAGTGAGGNGAACTTACCCAATCCAGTCCCTCTTC
WI-6766	148	GC	---	---	AAACAAATGGTGCAATTCGATAATATTGGGTACACAGTATAAAACAATACAATTAGTTCATATAAC ATTGGATATGGACAAAAATACACANGATCCTTTCTTGTCTACGGAAAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACACAGTGAGGNGAACTTACCCAATCCAGTCCCTCTTC
WI-6787b	97	A	GC	---	ACAGATAAAGTCTTTATCCCTGTATGTTTACATAAGAAAGTCTTTACAGACTTTTTTTTATACA ATACCTTGTGCAGCAATGTTCAAATTTACAG[G]TTTTACTGCATAAGATATCTTCATGTACAACCTGT ATGCTTTGTCTTCTTGGGAAGGACGGTTAAAGACCTATGATAAACACACATCCACATGACAAAGGA GAGTGCATAGGGCAGAGTAGANTACTCACAGGAAAAAGAGTAAATTCAGGT
WI-6793	105	C	GC	---	GAACCCACAGGTCCTGTTATTTTAAAGGAGCATTTACATTATGATAGCAAGTTTCAACACATTCA TCAACAAGGGGCTCTCAAATCAATCAGTCAACCCCTC[G]GAGTTAGAAAGTAGAGTCATGAGGAA GAGCTGCTTGGCTGTAGGAAGTAGGGTTAATGCCCTCTAATCCCGGAAAGGGCAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACCAAGTTCTCATCACAGGTAAAAGGCAAC
WI-6810b	37	T	C	---	CACAATAATAAATCACTCCCTACCTGAAACCTTTA[T/C]JAGAAAGCATTTTAAATTTACAACACA AAGCTCAACGNACCTACAATAAGTCTAGTGTGTTACGNGCCAAAGGATAAGGCTGAACAATA AATTAACCTTTAAATGCTATGNACAAGTACAATTTCTTTTGTAGTTCGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6810	37	T	C	---	CACAATAATAAATCACTCCCTACCTGAAACCTTTA[T/C]JAGAAAGCATTTTAAATTTACAACACA AAGCTCAACGNACCTACAATAAGTCTAGTGTGTTACGNGCCAAAGGATAAGGCTGAACAATA AATTAACCTTTAAATGCTATGNACAAGTACAATTTCTTTTGTAGTTCGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6817b	145	C	A	---	GCATGATTAACCCAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGTCTTTTGTATCCAGTTAAGACCATCAGCATATACACATCATCACTAATCAACAATGTAGCT GCAGGTAAC[C]ATGTGGATACCTGTGTCTCTACTNGCCTCCAAAGGCATTCAGGGGATCATCA AAGATGTTGGACACCTTGTGTTCAATCTTGGTTCAGGTGGGCTGTGCAG

WI-6817	145	C A ---			GCATGATTAACACAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTGTAATCCAGTTAAGACCATCAGCATATACAACTACTACTCACTCACTCACTCACTCACT GCAGGGTAAC[C/A]TGTGGATACCTGTGTGCTCTACTNGCCTCCAAAGGCAATTCAGGGGATCATCA AAGATGTTGGACACCTTGTGTTCAATCTTGGTTCAGGTGGGCTGTGCAG
WI-6813b	221	C ---			GATGGAAGCCATTATTTTCTCTAAATTTAAATAGAAGACTTTAATGGAAAAACATTTAGTAC CATATGTCACCCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCCTAGTAAAAAGCCC CGTCAGTAGTACACATTTCTATGGTCCCTTCAACAGTTTGCATATACAAAAATTTCTGCTATTTTG CTTAGCAAAACAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCAG
WI-6819a	175	G T ---			GATGGAAGCCATTATTTTCTCTAAATTTAAATAGAAGACTTTAATGGAAAAACATTTAGTAC CATATGTCACCCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCCTAGTAAAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCCCTTCAACAGTTT[G/T]CATATACAAAAATTTCTGCTATT TTGCTTTAGCAAAACAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATAT
WI-6826b	154	A G ---			GCAAAAGCTTTATTTGGCTCCCAACAAATATCCCTTTTAAAACTCCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTCCTTAAGAACCATATAAATAC ATGCAAAACCTTGACAT[G/G]GAGCTTAAATAATATCAAAATGCAAAATATAGATTGGGTGCACGTG TAAGCTGAATTGCAAAATATGGCAACACACACTGGGCTGGGTATACGTTG
WI-6826	154	A G ---			GCAAAAGCTTTATTTGGCTCCCAACAAATATCCCTTTTAAAACTCCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTTGAGATTTGCAGTTTATAGCATTTTTCCTTAAGAACCATATAAATAC ATGCAAAACCTTGACAT[G/G]GAGCTTAAATAATATCAAAATGCAAAATATAGATTGGGTGCACGTG TAAGCTGAATTGCAAAATATGGCAACACACACTGGGCTGGGTATACGTTG
WI-6857a	122	T C ---			AGTGCAAACTATTTTGAACAAAAAGTAACTATGAGTCACAGCAATTCAGCAAGACATCAGACACGGA AGAGTGAACAAATATTCACCTAAGTAAATACAGCAGATGAGATGCTCTCACATGTAT[C/A]TTTAAAT TATTCATGCTTTTCAATAGTCTCTTAGTCAACTTTTCAGTGTAAATTTCCACAAATATATAGCAGCTCA AACACAAATGCAGGAGCACAATGGCAAAGTTTGGCAACTGTITGGGCTAAAT
WI-6865	153	G A ---			TTATAGAATACTTATGGGCGCATACNGTAAATGAAGTGTCAACCTTAAATCTAAACAAACAGCTTG TTTGTTGCTCGTCCCTGAATCCCTGCTCACAACACAGCCAGCTACTNGGTTTCTAAAGACGTA ATTTGCAGGCAAACTTC[G/A]TAGAGCCATTCGTGCAGAAAGGGAAGGAGAGCTGTTTGT TTACCTGTAGTATGAAGATATCTTTGGCGCTGTAGAACTGAGCTCATTA
WI-6909	73	C T ---			ATTGAAAACCTGGTTAGCAACAGATAAATTTACAAATAGAGCCTGGATATAAAATGAGAGAAGATGC AGACTTA[C/T]AAGCTTATAGAGAAAGTCAAAAGGAGCAAGTTTGAATCAGATTTTATGATAC GGAAAAAAATTTCTTTTGGCAACAGGATTTATTCGAATAATAAATCTGCCAGTGCCCAATCAG AAACACCATTTCCACAATATTTGCATGCCCTAGTTGCCTATTTTATACATATC

WI-691 ^b	163 G T ---	---	CACTCAAAACCTTTTATTCATTGATTACAAACTGTACAATATTTACAAAGTTTAGGCATTATCCCA TATTGACATGAATGCTGTGGAGAGTCTAAAAATAAATATGTGGCACATAGCTTAATATACACATCAT GGCTCTTTACACITTAAGCCATTACCAATAGTJTGAGATGTAATGGAGAAATTTAATGTGGTAGAAAA GTCAGAGTGGCTGACCAGTCCGGACCTCCATGTGAATGACTCTTCCTTGGC
WI-6915	144 A ---	---	GCTTGTTTTTTTGTGTTTTTAAAGTGACACCTTGGCCCTTGTGGCAATTCCTTCACITATCTTACCC AAAAGTGCCTTTGGGCCAGCCACTGACTGATTTAAACCCAGAAATGTGGTTTTAAACAATGTGGT CGTGGTGAATTCAGGTGATTTTATTTCTATTTGGTAGTATTTTCAGATTTTCCACAAAGAACATG TATTGCTTTGTAATTTGAAAAAAAATCAACACAGGATAGTAAAGATAT
WI-6928 ^b	175 T C ---	---	CAATCAAAAAGTTCCAAAGTTTCAAGCTGGGATGAAAGCCAGGCTCTCTGACTTGCACCTGTGCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATAGAAAGTTCACTCTTAATTTTCATGTCCCATG CTTTGCTTGGTCCCTGTGAGGAAAGGGGTGAGCTAAAGGTTC/AACTGTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTCCTCTGAAATAGTAAAGTGACCTTAGAAGTTA
WI-6928	175 T C ---	---	CAATCAAAAAGTTCCAAAGTTTCAAGCTGGGATGAAAGCCAGGCTCTCTGACTTGCACCTGTGCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATAGAAAGTTCACTCTTAATTTTCATGTCCCATG CTTTGCTTGGTCCCTGTGAGGAAAGGGGTGAGCTAAAGGTTC/AACTGTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTCCTCTGAAATAGTAAAGTGACCTTAGAAGTTA
WI-6955 ^b	79 G A ---	---	TTTTATGAACATTTTCAGATTCCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAAATTCCTAGGTAAGATATCAAGTTACAAANTAC AAGTGCCGNTAATTAACTATAGGTAGTATATTAAACAAAATGNGTTTTTNGCAAATATGTGAAAT AAGGCTTTAACCAAAGC
WI-6955	79 G A ---	---	TTTTATGAACATTTTCAGATTCCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAAATTCCTAGGTAAGATATCAAGTTACAAANTAC AAGTGCCGNTAATTAACTATAGGTAGTATATTAAACAAAATGNGTTTTTNGCAAATATGTGAAAT AAGGCTTTAACCAAAGC
WI-6957	47 C G ---	---	AAACTAAAACCCCTTATTGTCTCCAAGTGTGGCAAAATAGAAAATTC/GJTTCAATTACATTAGG AAATCGGGTGGATAACGGAGTATAGTTATTCACCTTAAGAAGCATTCAGTCAAAATATACAAAA ACAAATTCAGATTGCTTGGATCTTGGTCATTTATGGCTTGAAGAAGTGGATTTGAAAACCACTTTAGG CTAAAATAAATGTATGAATAATGCATAGACTGTGATCTAGAAAAATCATGC
WI-6996 ^c	242 G T ---	---	ACTCTAGTGCCTCTGTACCAACACCTCTAATGCCCTCTGGTCCCGCACCTTCGTGATGTCGGAGCCT TAAATCTGCCTGGCGTCCCTCCCTCTGTCTCAGCACCCAGAGGAGAGAGCCGGCAGTTCCCTG CAGGAGAGAGGAGGGGCTGCTGGACCCAAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGCTGACT CTCTCCTGATGGTGGGCCCTCTGTGCTCTCTCTCTCC[G/J]GTGGGATC

-132-

WI-6996b	242	G T ---	---	---	ACTTCTAGTGCCTCTGTTACCAACACCTCTAATGCCTCTGTGGCGCGCACTCTGATGTCGGTAGGCCT TAAATCTGCCTGGCGTCCCTCCCTCTGCTTCAGCACCCAGAGGAGGAGAGCGCGCAGTTCCTG CAGGAGAGAGGGGGCTGCTGGACCCCAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCCTGACT CTCTCTGATGGTGGCCCTCTGTGCTCTCTCTCCG[G]GTCGGATC
WI-6996	228	T G ---	---	---	ACTTCTAGTGCCTCTGTTACCAACACCTCTAATGCCTCTGGTCGCCCACTCTGATGTCGGTAGGCCT TAAATCTGCCTGGCGTCCCTCCCTCTGCTTCAGCACCCAGAGGAGGAGAGCGCGCAGTTCCTG CAGGAGAGAGGGGGCTGCTGGACCCCAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCCTGACT CTCTCTGATGGTGGCCCTCTGT[G]GCTCTCTCTCCGGTCGGATC
WI-7021b	112	G A ---	---	---	TGGGAGGACAGGGAGATGCTGCAGTTCACAAAGAGAAGGTTTCTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGCTGAAAGCCACAGACAATATGGTCCCAAT[G]A]CCCGACTGCACCTTCTGTG CTTCAGCTCTTCTTGACATCAAGGCTCTCCGTTCCACATCCACACAGCCAATCCAATTAATCAAAAC ACTGTTATTACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7021	108	A G ---	---	---	TGGGAGGACAGGGAGATGCTGCAGTTCACAAAGAGAAGGTTTCTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGCTGAAAGCCACAGACAATATGGTCCG[G]A]G]AATGCCGACTGCACCTTCTGTG CTTCAGCTCTTCTTGACATCAAGGCTCTCCGTTCCACATCCACACAGCCAATCCAATTAATCAAAAC ACTGTTATTACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7056c	118	C T ---	---	---	GGCAGTAGGACCAACAGTGTGGGTTCTGCTGGGACCTTGAGAGCCTGCATCCCAAGGATGCGGGTGG CCCTGCAGCCTCCTCCACCTCACCCTCCATGACAGCGCTAAACGTTGGTGA[C]G]GGTTGGGAGCCTCT GGGCTGTTGAAGTCACCTTGTTGTTCCAAAGTTCCAAACAACAGAAAGTCATTCTCTTTTAA ATGGTCTTAAGTTCCAGCAGATGCCACATAAGGGGTTTGCCATTGATA
WI-7056b	118	C T ---	---	---	GGCAGTAGGACCAACAGTGTGGGTTCTGCTGGGACCTTGAGAGCCTGCATCCCAAGGATGCGGGTGG CCCTGCAGCCTCCTCCACCTCACCCTCCATGACAGCGCTAAACGTTGGTGA[C]G]GGTTGGGAGCCTCT GGGCTGTTGAAGTCACCTTGTTGTTCCAAAGTTCCAAACAACAGAAAGTCATTCTCTTTTAA ATGGTCTTAAGTTCCAGCAGATGCCACATAAGGGGTTTGCCATTGATA
WI-7091b	153	A C ---	---	---	AATTGCTGAAAAGGAACCTACCTATCCTTACATTTACCTACTAATGTCCTCTTAACATCTTAGAG GTCCATGGAGAAAGGCATATGGAGAACATGTTTATCTGCTCTATAAATAGTATCCAATCACTGTG CTTAATTTAAATAGCATT[A]C]TCTTATCATTATCAGCCTTTTATGATTTTCCAAAGTAAATATTA ACATATTATTCATTGGTCTCTTTTATCTGTTCTATATGAATGCTAT
WI-7091	153	A C ---	---	---	AATTGCTGAAAAGGAACCTACCTATCCTTACATTTACCTACTAATGTCCTCTTAACATCTTAGAG GTCCATGGAGAAAGGCATATGGAGAACATGTTTATCTGCTCTATAAATAGTATCCAATCACTGTG CTTAATTTAAATAGCATT[A]C]TCTTATCATTATCAGCCTTTTATGATTTTCCAAAGTAAATATTA ACATATTATTCATTGGTCTCTTTTATCTGTTCTATATGAATGCTAT

WI-7136	58 T C ---				TGTGAAGCCACATTTTCCAAACATGAGCCTCATGAAGCCAACTAAGTGTATTGAACGTGTC/JAATTC TCTCAATAACTCAGTGTAGCACITTTAAAGTCTGAAGGACAGCAACATGAAAGAGCATATCAATGTG GTGGAGAAAGGGAAGGGTGGCTTTTAAATTTATTTTCTTCATCTTTTATAACAAAGAAAGNNNN NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTAGCTTCTATATATG
WI-7146c	210 A G ---				GGGACGCCTGTTGTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTTCCATTTCGTTAGCTG AATAATGAGTTGTTCTTAGAGGAGACAGCCTGTCTCTCTTGTGGCCCCAAAGCCCCATGCCCTGCCG TGGTGGCAGCTGGGGCTGGGCTGTGGATGGAGGGTCCCCAACATGGATGTGTGGCCCCCTCTCCGCGATGCC AACGC/JG/GTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA
WI-7146b	210 A G ---				GGGACGCCTGTTGTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTTCCATTTCGTTAGCTG AATAATGAGTTGTTCTTAGAGGAGACAGCCTGTCTCTCTTGTGGCCCCAAAGCCCCATGCCCTGCCG TGGTGGCAGCTGGGGCTGTGGATGGAGGGTCCCCAACATGGATGTGTGGCCCCCTCTCCGCGATGCC AACGC/JG/GTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA
WI-7146	202 G A ---				GGGACGCCTGTTGTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTTCCATTTCGTTAGCTG AATAATGAGTTGTTCTTAGAGGAGACAGCCTGTCTCTCTTGTGGCCCCAAAGCCCCATGCCCTGCCG TGGTGGCAGCTGGGGCTGTGGATGGAGGGTCCCCAACATGGATGTGTGGCCCCCTCTCCGCGATG/A JCCAACGCAGTTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA
WI-7153	161 A T ---				ATATTACAACTTGCTTTTAGCTGATCTCCATCCTCAAAATGACTCTTTTCTTTTATATGTTAACATA TATAAATGGCAACTGATAGTCAATTTTGTATTTTATTCAGGAACATCTGAAATCTGCTCAGAGCCT ATGTGCATAGATGAAACNNNNNNN/JA/TAATAAAGTTATTTAACAGTAATCTATTACTAATTAT AGTACCTATCTTTAAAGTATAGTACATTTACATATGTAATGGTATGTTT
WI-7155	156 T G ---				TAGAAATAGATGCGGTCATATTTCTTTGGCTTCTGGTCTCCAGCCCTCATGGTTGGCATCACATAT GCCTGCATGCCATTAAACACAGCTGCCCTACCCCTATAATGATCCTGTCTCTAAATTAATATACAC CAGTGGTTCCTCCTCCTGT/JG/JTAAAGACTAATGCTCAGATGCTGTTACGGATATTTATATTCTAG TCTCACTCTCTTGTCGCCACCTTCTCTCTTCCCCATTCCCCAACTCCAG
WI-7169b	161 A G ---				AGCTCCACCAGATGCAGATTGTGTTTGTGTTTCTTGTATCAGTGTACACAGCTTATAACATGTAT GCTTTTCAGAAATACAGTTGCTAGCCAAGCCCATCAAGTGTCTGAAATCAATATTGGTTTATGCAAT ACAGCAAACTTTTATTTAAGTAGAT/JG/JGAGAGAAATGTTTAAATATTAGGAATCCTAGACCATA TTTTCAAGTCATCTTAGCAGCTAGGATCTCAAAATGGAAGTGTATATATA
WI-7175b	194 C T ---				CTCCTAGACTAGTCTTTACCTTTTATTAAATGAAGTGTGACAGGAAGCCCCAAGGAGTGTTCCTCACCA ATAACTTCAGAGAAAGTCAGTTGGAGAAAAATGAAGAAAAAGGCTGGCTGAAAACTACTATAACCATC AGTTACTGGTTTCAGTTGACAAAAATATAATGGTTTACTGCTGTCATTGTCCTATGCCTA/C/TJAGAT AATTTATTTGATTTTGAATAAAAAACAATTTGTACATTCCTGATACTGGG

WI-7175	194 C T ---	---	---	CTCCTAGACTAGTGCTTTACCTTTATTATGAAGTGTGACAGGAAGCCCAAGGCAGTGTTCCTCACCA ATAACTTCAGAGAAAGTCAGTTGGAGAAAATGAAGAAAAGGCTGGCTGAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAAATATATAATGGTTTACTGCTGTCAATGTCCATGCCTA[C/T]JAGAT AATTTATTTTGATTTTGAATAAAAACATTTGTACATTCCTGATACTGGG
WI-7178b	273 G A ---	---	---	TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCCCTGAGCCAGCTGCCTGGAG AGGGTCTCGCTGTCAGTGGCTCCTAGGGGAACAGACCAAGTGAACCCAGAAAAGCATAACACCA ATCCAGGGCTGGCTCTGCACCTAAGAGAAAATTCGACTAATGAATCTCGTTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7178	273 G A ---	---	---	TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCCCTGAGCCAGCTGCCTGGAG AGGGTCTCGCTGTCAGTGGCTCCTAGGGGAACAGACCAAGTGAACCCAGAAAAGCATAACACCA ATCCAGGGCTGGCTCTGCACCTAAGAGAAAATTCGACTAATGAATCTCGTTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7182b	116 A C ---	---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGTGTCACCAAAAGCTTGATATACAGAGAAG AAGGCTCAAGAAATTTATCACCAGTTCCTCTGCAACCCACTCTGAGCCTTAC/TCTCTCCTCTATTT TACTTGAGGCTGCCAATTACCAGCCCCACGTTTCAGCTCAAGAGATGCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGAAATGGCAGCTATTTCCCTGAAGCCTAGTACCCCAATT
WI-7182	106 C A ---	---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGTGTCACCAAAAGCTTGATATACAGAGAAG AAGGCTCAAGAAATTTATCACCAGTTCCTCTGCAACCCACTCTGAGCCTTAC/TCTCTCCTCTATTT TACTTGAGGCTGCCAATTACCAGCCCCACGTTTCAGCTCAAGAGATGCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGAAATGGCAGCTATTTCCCTGAAGCCTAGTACCCCAATT
WI-7191b	273 T A ---	---	---	ATAATTGCTTGTCTAGCCTGGCAAGATATTTTCATAAAGAGGGATAACAATGCTGATTACTAC CTTTTAAATATTTTAGATAAATGCACAGCACACACACACATCTAAGCATTTAGTGATGGTAGC TGATGTCAGCTTCATGTGGAATTTAAGCAGCTAGAAACAATGAAGCTTCITGGCATATTTTAAGGAG CTCCCAAAATGTGTTACCTATTAAATGTAACCTAGCAAGTAGAAGACCATTT
WI-7199c	112 T C ---	---	---	CCCAGTGGTGAACAGAACCTCCCAAAATTTGAGTTGCACCCCTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTCAGCTCCTTGACCTATGAGCT/CJGGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATAGCATTCCTTAATGTTTGTGGTCTCTGAATTTCTCTTTATTAT AGTCCATAGTTTTACTCCTCAGTTCCTCACCATCATCTGTCTAA
WI-7199b	112 T C ---	---	---	CCCAGTGGTGAACAGAACCTCCCAAAATTTGAGTTGCACCCCTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTCAGCTCCTTGACCTATGAGCT/CJGGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATAGCATTCCTTAATGTTTGTGGTCTCTGAATTTCTCTTTATTAT AGTCCATAGTTTTACTCCTCAGTTCCTCACCATCATCTGTCTAA

WI-7216c	237	T C ---	---		TGACACTAACACCTCTAAATTCAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGTCCTTTCTCCCC AAGGACAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCCTCCAGAAAATACGTATGT TTAAAACCCCTTCTGCTATACATAGGAAAAGACACACATCCACCTAAAATTGACTGTACTGTTTAA CTGTCAATTCTCCTGAGGCTAAACACAGTTTGTTTTT[C]CTTGTAATCAGTT
WI-7216b	237	T C ---	---		TGACACTAACACTCTAAATTCAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGTCCTTTCTCCCC AAGGACAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCCTCCAGAAAATACGTATGT TTAAAACCCCTTCTGCTATACATAGGAAAAGACACACATCCACCTAAAATTGACTGTACTGTTTAA CTGTCAATTCTCCTGAGGCTAAACACAGTTTGTTTTT[C]CTTGTAATCAGTT
WI-7220b	147	A T ---	---		AGGATGATGCTCCAAAAGGGACCTTGAACCTATTACACCTATTGCTCTTTAAGCTGGCAAAACCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCCTAGAA[A]TJAATCTTGAGCACAGTGAAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTTAGTGTGTTT
WI-7220	140	A T ---	---		AGGATGATGCTCCAAAAGGGACCTTGAACCTATTACACCTATTGCTCTTTAAGCTGGCAAAACCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGC[A]TJCTAGAAAATCTTGAGCACAGTGAAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTTAGTGTGTTT
WI-7226	232	C ---	---		GATCGAATTTTTCAGATGATCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATGTATA TACATATCAGCTCCTATTCTCTAATTTTGTAAATGTTAACTGGCAGTAAGTCTTTTGTGATCATT CCCTTTCCATATAGGAACATAATTTGAAAGTGGCCAGATGAGTTTATCATGTGTCAGTGAAAAATAA TTACCCACAATGCCACCAGTAACCTAACGATTCTTCACCTCTTGGGGTTT
WI-7228b	254	G A ---	---		ATAGCTCCAGATTACAAAGGCCAAGGTAATAGAAATGCATACCAGTAATGGCTCCAATTCATAA TATGTTCAACAGGAGATTACAAATTTTGTCTCTTCTGCTTTGTATCTATTTAGTTGATTTTAATTA CTTCTGAATAACGGGAAGGATCAGAAGATATCTTTTGTGCTAGATTGCAAAATCTCCAATCCACA CATATTGTTTTAAAATAAGAAATGTTATCCAACCTATTAAAGATACTCAATGTT
WI-7228a	163	G A ---	---		ATAGCTCCAGATTACAAAGGCCAAGGTAATAGAAATGCATACCAGTAATGGCTCCAATTCATAA TATGTTCAACAGGAGATTACAAATTTTGTCTCTTCTGCTTTGTATCTATTTAGTTGATTTTAATTA CTTCTGAATAACGGGAAGGATCAGAA[G/A]ATATCTTTTGTGCTAGATTGCAAAATCTCCAATCC ACACATATTGTTTTAAAATAAGAAATGTTATCCAACCTATTAAAGATACTCAAA
WI-7233c	213	C T ---	---		CGATCGTACTGCCAGTAGCATTGTGCTGCTGCCGGCTTGTTGTACATTCATTTCAATTGTTACA GATGTGAACCTTTATTCCTTGTCACATAATTATATTTAAATATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTTCTCTGCCACCTTTTGTGGCAATATTAAAGTGAACCTGCTAATA GTGTAAGTA[C]TGTGCACAAAACCACTGCCAGATAACCAAGAGGGGCTG

WI-7252a	520	T C	---	CCACAGGATCCAGCCAGCGGCCCTCCGCCCTCCCACTCGCAGCAGCGCGGGGACAGAG GCCTGCCCGGGCGCGCAGCCCGGCTGGCTGGAGCTGCCCCGGCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCGCAGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAATCAGTCATTAGACTCCTCCTCCA
WI-7265m	252	T A	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTCAACCATTCCTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATTATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTTCTTTAAGGAGTAAAGATTGCGCTTT
WI-7265l	231	T A	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTCAACCATTCCTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATTATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265k	121	T G	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTCAACCATTCCTGGTTCATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265j	174	T A	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTCAACCATTCCTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265i	227	T C	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTCAACCATTCCTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATTATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265h	80	T A	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTCAACCATTCCTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATTATGTAATAATAACGATCTCTT CTTAAAAATACCACAGTTTGATTTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265g	170	T G	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTCAACCATTCCTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATTATGTAATAATAACGATCTCTT CTTAAAAATACCACAGTTTGATTTTTCTTTAAGGAGTAAAGATTGCGCT

WI-7265f	231 T A ---	---	AAC TTGGTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCCACCATTCGTGTGTTCAATTGATGTT TAAGGAAACCAAGCATATAGATGATAGTATTTGTTTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTT/AJ/AAGGAGTAAAGATTGGCT
WI-7265e	227 T C ---	---	AAC TTGGTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCCACCATTCGTGTGTTCAATTGATGTT TAAGGAAACCAAGCATATAGATGATAGTATTTGTTTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTT/AJ/AAGGAGTAAAGATTGGCT
WI-7265d	174 T A ---	---	AAC TTGGTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCCACCATTCGTGTGTTCAATTGATGTT TAAGGAAACCAAGCATATAGATGATAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGGCT
WI-7265c	170 T G ---	---	AAC TTGGTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCCACCATTCGTGTGTTCAATTGATGTT TAAGGAAACCAAGCATATAGATGATAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGGCT
WI-7265b	121 T G ---	---	AAC TTGGTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCCACCATTCGTGTGTTCAATTGTA GTTTAAAGGAAACCAAGCATATAGATGATAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGGCT
WI-7265a	80 T A ---	---	AAC TTGGTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTT/AJ/TATTTGCCACCAAAAAGTAAATGCATTTTCCACCATTCGTGTGTTCAATTGTA GTTTAAAGGAAACCAAGCATATAGATGATAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGGCT
WI-7281b	183 C ---	---	GATCACCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGAGCCCAAGC ATCTCCCTGGGAAGTCTTTCTGGCCAAAGTCTGGCCAGCCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCTTGGCAAAAACGAGGTCCGAGGCCGCGAG GTGTTGTGAAGACCACTCGTCTGTGTTGGGTCTCTGCAAGAAGGCCTCTC
WI-7281	171 C A ---	---	GATCACCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGAGCCCAAGC ATCTCCCTGGGAAGTCTTTCTGGCCAAAGTCTGGCCAGCCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCTCAGACTCTC/AJ/TGGCAAAAACGAGGTCCGAGGCCG CAGGTGTTGTGAAGACCACTCGTCTGTGTTGGGTCTCTGCAAGAAGGCCT

[illegible]

WI-7301	205 A C ---	---	---	AACTATGGCAGTGGTCTGTTATAGTAGAGCGGGGTATGGTGGTGACCGAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGGAGGATATGATGGTTACAAATGAAGGAGGAAATTTTGA CGGTAGTAACATATGGTGGTGGGAACATAATGATTTTGGAAATTACAGTGGACAAACAGCAATCA AATTTCATGGACACATGAAGGGGCGAGTTTGGTGGGAAGCTCGGGCAG
WI-7314c	49 GA ---	---	---	CTCTCTTTTCTTCAGATCTGCTCCTGGTTTTAAATTTGGAGGTCA[GA]TTGTTCTACCTCACTG AGAGGAACAGAGGATATGCTTCTTTGCAGCAGTGAATAAAGTCAATTAATAAACTTCCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTGGTCTTCTGTGCACATGAACGCTTCTTTCCCAGGA CAGAAATGTAGTCTACCTTTATTTTATTAAACAAAACCTGTTTTT
WI-7314b	49 GA ---	---	---	CTCTCTTTTCTTCAGATCTGCTCCTGGTTTTAA[GA]TTGGGAGGTCA[GA]TTGTTCTACCTCACTG AGAGGAACAGAGGATATGCTTCTTTGCAGCAGTGAATAAAGTCAATTAATAAACTTCCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTGGTCTTCTGTGCACATGAACGCTTCTTTCCCAGGA CAGAAATGTAGTCTACCTTTATTTTATTAAACAAAACCTGTTTTT
WI-7314	36 A G ---	---	---	ACTCAGGGAAGGATGCCCCATTAAAGTGACAAAAGGTGGGTGGGCAACCATGGCATGAGGAAG AAACAAGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGAGCTGTTGGCATCCAGGCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNNAGGTGGCACACCCCATC[C TTGTTGCTGGGTGTGGCAGCCACATCCAGACTGGAGCAGCAGGCTGGCCA
WI-7321b	199 C T ---	---	---	AGACATTCCTGCTTCCCTGAAAGACTGAAGAAAGTGTAGTGCATGGGACCCAGCAAACTGCCCTGGC TCCAGTGAACCTGGGCACATGCTCAGGCTACTATAGGTCCAGAACTCTTATGTTAAGCCCTGGCAG GCAGGTGTTTATTAATCTGAATTTTGGGATTTTCAAAAGATAATATTTACATACACTGTATGT TATAGAACTTCATGGATCAGATCTGGGCGAGCAACCTATAAATCA[AC]CA
WI-7336b	248 A C ---	---	---	CTCTTCTCAGCACATTTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTACCATGGATAATGCA AACAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTTGGCAAAAGGTGCTTACCTTGAGC CATTATTTGTGCAGAGAAACAAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTCTCTTTACACAC[AG]TATACACACAGACATCAGAAAATTCGTGT
WI-7338c	221 A G ---	---	---	

WI-7338b	125 A C ---	---	CTCTTCTCAGCACATTGATGGCAACTAGAAATTACAGCAGTTTCAAACCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATAATTGGCAAAAGGTGCTTT[A/C]CCTTG AGCCATTATTTGTGTCAGAGAACAAAGAAACAGCAATCAATATATAAAATTCAAAGACTATCTGCAG CTAGTGTGTTCTCTTTACACACATATACACACAGACATCAGAAAAATCTGTT
WI-7338	125 A C ---	---	CTCTTCTCAGCACATTGATGGCAACTAGAAATTACAGCAGTTTCAAACCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATAATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTCAGAGAACAAAGAAACAGCAATCAATATATAAAATTCAAAGACTATCTGCAGCTA GTGTTTCTCTTTACACAC[A/G]TATACACACAGACATCAGAAAAATCTGTT
WI-7338	221 A G ---	---	CCTATGTCATGAATGCTAGGGGCCAGGGAACAAAAATTTAAAAATAATAAAATTCACCATAG CAATACAGAATAACTTTAAAAATACCATTAAATACATTTGATTTTCATTGTGAACAGGTAATTTCTTCA CAGATCTCATTTT[A/J]AAAAATCTTAATGATTATTTTATTACTTACTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7384c	146 T A ---	---	CCTATGTCATGAATGCTAGGGGCCAGGGAACAAAAATTTAAAAATAATAAAATTCACCATAG CAATACAGAATAACTTTAAAAATACCATTAAATACATTTGATTTTCATTGTGAACAGGTAATTTCTTCA CAGATCTCATTTT[A/J]AAAAATCTTAATGATTATTTTATTACTTACTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7384b	146 T A ---	---	CCTATGTCATGAATGCTAGGGGCCAGGGAACAAAAATTTAAAAATAATAAAATTCACCATAG CAATACAGAATAACTTTAAAAATACCATTAAATACATTTGATTTTCATTGTGAACAGGTAATTTCTTCA CAGATCTCATTTT[A/J]AAAAATCTTAATGATTATTTTATTACTTACTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7384	145 T A ---	---	TGAAATCCTGGTCTCTGGCCTGCTGCTGAGCTGGTTATTTTACTTTGCCCTCCCTCCCTTTT TGAGATCCATCCTTTATCAAGAAGCTGAAGCGACT[A/T]TAAAGGTTTTTGAAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGGTACCCTCTATTTGCCACAAAGCGTCTCGGGATTGTTTGA CTTGTGCTGTCCAAAGACTTTTCCCCCAAAGATGTTATGTTATG
WI-7388c	106 A T ---	---	TGAAATCCTGGTCTCTGGCCTGCTGCTGAGCTGGTTATTTTACTTTGCCCTCCCTCCCTTTT TGAGATCCATCCTTTATCAAGAAGCTGAAGCGACT[A/T]TAAAGGTTTTTGAAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGGTACCCTCTATTTGCCACAAAGCGTCTCGGGATTGTTTGA CTTGTGCTGTCCAAAGACTTTTCCCCCAAAGATGTTATGTTATG
WI-7388b	106 A T ---	---	CTTGTGCTGTCCAAAGACTTTTCCCCCAAAGATGTTATGTTATG

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WI-7388	94	T A ---	---		TGAAATCTGGGTCTCTGGCCCTGTCCTGTAGCTGGTTATTTTACTTTGCCCCCTCCCCACITTTTT TGAGATCCATCCTTTATCAAGAAAGT/AJCTGAAGCGACTATAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAAGCATTGCAACAAGGTTACCTCTATTTTGCACAAGCGTCTCGGGATTGTTTGA CTTGCTGTCTGCTCAAGAACTTTTCCCCCAAGATGIGTATAGTTATTGG
WI-7438	64	A G ---	---		TTAGATTTTAAATTGGCAACCAGCAACTCACTGCCACCATTCCACTGCAGATCTNCTATTCTCTGG[A/G] GTTGATATGACAAGGAAACCCCTATTGGAACCAAGTCTTCAGATTGTCAGATGTCAGACAGGCTCCT TGCTGTAGGTGTAGTAGCATGTACACTGTACTGTTCACTGTAACATAGTTTGCTGCTGTTGTTA TTGGAATGAATATCGCTTCCACTGACITTTTACCA
WI-7454b	152	T C ---	---		CCATGATCCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAAGCCCCAAACC CAGTACAAACTGAGAAATGAGAAACCCCTGATAGCACTGTCTGAATGGCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTTGTTTAAAGTTATTTCTAGCCACCACAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTTGCTACTTCTCAAAATGTTTTTGACA
WI-7454	152	T C ---	---		CCATGATCCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAAGCCCCAAACC CAGTACAAACTGAGAAATGAGAAACCCCTGATAGCACTGTCTGAATGGCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTTGTTTAAAGTTATTTCTAGCCACCACAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTTGCTACTTCTCAAAATGTTTTTGACA
WI-7464c	177	G C ---	---		AATTTGAAAATCTGAAAAAAGTGCATAAGCAGAGAAAATGACACTTATTCCAAATAAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAATGCACATAAATCTATTTATAATTTCCCTATGTA CAACAGAGCCACAGCACAAGAGGGTGGCATAAG[C/A]AGTTGCCAGCCAGAGAGCTTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGAGCAACGTTCAACCAAAATTAT
WI-7464b	168	C A ---	---		AATTTGAAAATCTGAAAAAAGTGCATAAGCAGAGAAAATGACACTTATTCCAAATAAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAATGCACATAAATCTATTTATAATTTCCCTATGTA CAACAGAGCCACAGCACAAGAGGGTGGCATAAG[C/A]AGTTGCCAGCCAGAGAGCTTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGAGCAACGTTCAACCAAAATTAT
WI-7464a	103	C A ---	---		AATTTGAAAATCTGAAAAAAGTGCATAAGCAGAGAAAATGACACTTATTCCAAATAAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAATGCACATAAATCTATTTATAATTTCCCTATGTA GTACAACAGAGCCACAGCACAAGAGGGTGGCATAAGCAGTTGCCAGCCAGAGAGCTTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGAGCAACGTTCAACCAAAATTAT
WI-7499b	134	T G ---	---		CAATTTCTCAATCCAACTAGTCTGTTGCTTAAACCATTCAGACAACTCCACTTCGAAGGTTTTTA AATGCAATAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCAGTTCTTTGAATGCTTCAIT /GJTATAGTCTCTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTTAGGA ACTCTGTACAAAATCCCTTTGAAAATATAAATTTTGGAAATGAGTGATGA

WI-7499a	33	A G	---	CAATTCTCAATCCAACCTAGTCTGNTGCTAA[A/G]CCATTCCAGACAAACCTCCACCTCGAAGGTT TTAAATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCACGTTCTTTGAATGCTTC ATTATAGTCTCTTCATTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTITTAGGAA CTCTGTACAAAATCCCTTTGAAAATATAAAATTTGGAAATGAGTGATGA
WI-7506b	118	A C	---	TGGGAATAGTAAGAGAAAGATGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAAGTGAAT GCATCCAGCAGCAGACCACTTNAAGAGTAGTCTGTGCTGATTGCCTAGC[A/C]GGAGAGTTGAG TGCCACAGGTAAGAAATGAGTGAAGAGGAAAATCATGATGTCATGATGCAATTAATCTATGTCA GAAGAAAATATTTAAATAATTGGACCACCTTGTTCTACCATCCCTACCCACT
WI-7506	118	A C	---	TGGGAATAGTAAGAGAAAGATGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAAGTGAAT GCATCCAGCAGCAGACCACTTNAAGAGTAGTCTGTGCTGATTGCCTAGC[A/C]GGAGAGTTGAG TGCCACAGGTAAGAAATGAGTGAAGAGGAAAATCATGATGTCATGATGCAATTAATCTATGTCA GAAGAAAATATTTAAATAATTGGACCACCTTGTTCTACCATCCCTACCCACT
WI-7534b	143	C T	---	TGTGAATTTAGCTCTGGAAGGTGTTATGCCCTTTCGGGTTCTTGATGTTTCGCAGTGTACCCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCCGTGGAACACATTCGCCGTGATAGAAATGCT AAATTGTCGTGAAATAGGTTAGAAATTTCTTTAAATATGTTTTCTTATTTCGTGAAAATTCGG AGAGTCTGCTAAATTTGGATTGGTGGTATCTTTTGGTAGTTGTAATTT
WI-7534	135	T C	---	TGTGAATTTAGCTCTGGAAGGTGTTATGCCCTTTCGGGTTCTTGATGTTTCGCAGTGTACCCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCCGTGGAACACATTCGCCGTGATAGAAATGCT /CJAAATTTGTCGTGAAATAGGTTAGAAATTTCTTTAAATATGTTTTCTTATTTCGTGAAAATTCGG AGAGTCTGCTAAATTTGGATTGGTGGTATCTTTTGGTAGTTGTAATTT
WI-7543b	162	G A	---	GGGAAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCTGTTTGACAGGGAAGCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGACTTGAAC TAGATTGCATGCTTCTCTCTTTCCTCTTGAAGAACCACTTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTTCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7543	162	G A	---	GGGAAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCTGTTTGACAGGGAAGCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGACTTGAAC TAGATTGCATGCTTCTCTCTTTCCTCTGGCTCCTTGGATGTAGTCAGTTA CTCTGCAGCCCTCAGATTATTTTCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7555c	60	T C	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCACTTCCCTCAAAATTTGTAGAGGTCCTTA AAAAAGAGTGGTATGTTGTGTGATGATCAGCACTAAGTCTGCAATTCCTGTTAAAGCCACTTGGGTC ATAAGAGGGGAAGTAAAAAATGAAGTCTGACTAGAAAATTTCTATTGCAGAGGCCAAGTACATTTAGT ATGGCAATGAGTTGTGATATAGTTTTCATTTGATGTGCAATTTGAATTTGAG

WI-7555b	60	T C ---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTC/JCTA AAAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTGCTGCAATTCCTGTTAAAGCCACTTGGGTC ATAAGAGGGAAGTAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAGTACATTTAGT ATGGCAITGAGTTGTGATATAGTTTTCATTTGATGTCATTTTGAATTCAG
WI-7555	60	T C ---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTC/JCTA AAAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTGCTGCAATTCCTGTTAAAGCCACTTGGGTC ATAAGAGGGAAGTAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAGTACATTTAGT ATGGCAITGAGTTGTGATATAGTTTTCATTTGATGTCATTTTGAATTCAG
WI-7567b	290	G T ---	---	TGAGCCATCACTAGAGAAAGCCCATTTTCAACTGCTTTGAAACTTGCCTGGGCTGAGCATGAT GGGAATAGGAGACAGGGTAGGAAAGGGCGCTACTCTCAGGGTCTAAAGATCAAGTGGGCCCTTGG ATCGTAAGCTGGCTGTTTGTATGCTATTTATGCAAGTTAGGGTCTATGATTTAGGATGCGCTAC TCTCAGGGCTAAAGATCAAGTGGGCCCTTGGATCGCTAAGCTGGCTCTGTTT
WI-7569b	63	T C ---	---	AATGATCCCTTTCCGGTCCAACAACAGGAACCTGACTGGGCGAGTGAAGGAAGGGATGGCATTC/J AGCGTTATGTTGTAACCAAGATATCTGTATGACAACCCGGGATCGTTTGAAGTAAGTAACTCCAT TGCGACATTGTGAAGGCTTAAATGAGTTTAGATGGGAATAGCGTTGTTATCGCCTTGGGTTTAAATT ATTTGATGAGTTCACCTTGATCATGGCTACCCGAGGAGAGAGGAGTTTG
WI-7574c	216	A G ---	---	GCCACAGCAGAAATGGAGCGGTGTGAGGAAGTCCCTTTTCCCTGTTTGTGTTGCCAAGGCGCAAC TCCCACCTCTGCCCCCTTTAATCCCCCTTTCTACAGTGAAGTCCACTACCCCTCACTGAAAAATCATTTTG TACCACCTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC/JGTTCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7574b	216	A G ---	---	GCCACAGCAGAAATGGAGCGGTGTGAGGAAGTCCCTTTTCCCTGTTTGTGTTGCCAAGGCGCAAC TCCCACCTCTGCCCCCTTTAATCCCCCTTTCTACAGTGAAGTCCACTACCCCTCACTGAAAAATCATTTTG TACCACCTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC/JGTTCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7574	216	A G ---	---	GCCACAGCAGAAATGGAGCGGTGTGAGGAAGTCCCTTTTCCCTGTTTGTGTTGCCAAGGCGCAAC TCCCACCTCTGCCCCCTTTAATCCCCCTTTCTACAGTGAAGTCCACTACCCCTCACTGAAAAATCATTTTG TACCACCTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC/JGTTCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7576c	168	A T ---	---	AATGATGATGATAATGATGATGACGACGACAACGATGATGCTTGTAAACAAGAAAAACATAAGAGAGC CTTGTTTCATCAGTGTAAAAATTTTGAAGAGCGGTACTAGTTGACACACTTTGGAAGTTTGTGT TCTGTTTGTAAACCTGGCATCTGACACAAAAA/JGTTTGAAGGCCCTTATTCTACATTTTCACTAC TTTGTAAAGTGAGAGACAAAGCAAGCAANNNNNNNNNNAAGAAAAATAAAC

WI-7576b	168 A T ---	---	AATGATGATGATAATGATGATGACGACGACAAACGATGCTTGTAACAAGAAAAACATAAGAGAGC CTTGGTTCATCAGTGTAAAAATTTTGAAGGCGGTACTAGTTCAGACACTTTGGAAGTTTGTGT TCTGTTTGTAAACTGGCATCTGACACAAAAAA[A/T]GTTGAAGGCCTTATTCTACATTTACCTAC TTTGTAAAGTGAGAGAGACAAAGCAANNNNNNNNAAGAAAAATAAAC
WI-7577q	77 T C ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCAACATAAGTGTTTGCCTTCTTTAA AAATATGCA[T/C]CAAAATCGTCTCTCATTCTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577p	50 G C ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCAACATAAGTGTTTGCCTTCTTTAA AAATATGCAATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577o	157 G A ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCAACATAAGTGTTTGCCTTCTTTAA AAATATGCAATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AGAAGTTCAATTTGGTTTACAC[G/A]TAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACT ATTGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577n	48 A G ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCAACATAAGTGTTTGCCTTCTTTAA TAAAAATGCAATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577m	84 G A ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCAACATAAGTGTTTGCCTTCTTTAA AAATATGCAATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577l	93 T C ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCAACATAAGTGTTTGCCTTCTTTAA AAATATGCAATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577k	154 C A ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCAACATAAGTGTTTGCCTTCTTTAA AAATATGCAATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AGAAGTTCAATTTGGTTTAC[C/A]ACGTAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACT ATTGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

WI-7577j	117 A G ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTA/GACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGIGGCCCTGTTATACATGACACTCTTCTGAAITGACTGTATTTC
WI-7577i	77 T C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCA/C/CAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGIGGCCCTGTTATACATGACACTCTTCTGAAITGACTGTATTTC
WI-7577h	50 G C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA TAAAAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGIGGCCCTGTTATACATGACACTCTTCTGAAITGACTGTATTTC
WI-7577g	157 G A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTACAC/G/ATAGGAAGAGAGAGAGCATCAAAAGTGGAGATATGTTAACT ATTGTAATGIGGCCCTGTTATACATGACACTCTTCTGAAITGACTGTATTTC
WI-7577f	48 A G ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA TAAAAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGIGGCCCTGTTATACATGACACTCTTCTGAAITGACTGTATTTC
WI-7577e	84 G A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGIGGCCCTGTTATACATGACACTCTTCTGAAITGACTGTATTTC
WI-7577d	93 T C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGIGGCCCTGTTATACATGACACTCTTCTGAAITGACTGTATTTC
WI-7577c	154 C A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTA/C/ACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACT ATTGTATAATGIGGCCCTGTTATACATGACACTCTTCTGAAITGACTGTATTTC

WI-7577b	117 A G ---	---	---	AAACATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTGCTTTCCCTTAA AAATATGCATCAAAATCGTCTCTATTACTTTCTCTGAGGGTTTAGTA/GJACAGTAGGAGTTAAT AAAGAAAGTTCAATTTTGGTTTACACGTAGGAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTTAATGTCGCTGTTATACATGACACTCTCTGAAATGACTGTAATTC
WI-7577	107 G A ---	---	---	AAACATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTGCTTTCCCTTAA AAATATGCATCAAAATCGTCTCTATTACTTTCTCTGAG/GJAGTTTAGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTTGGTTTACACGTAGGAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTTAATGTCGCTGTTATACATGACACTCTCTGAAATGACTGTAATTC
WI-7619q	106 C G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGACAAAGAC AGAGAAAGGGCCCAATGGGGTCAATCCCTCCCTAACAGAGACTTC/GJCTGTGCTGGGGTGTCTATAC ATGGCAGGAAGAAATGGGGCTCTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619p	150 T C ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGACAAAGAC AGAGAAAGGGCCCAATGGGGTCAATCCCTCCCTAACAGAGACTCTCTGTGCTGGGGTGTCTAATACATGG CAGGAAGAATGGGGCTTCJTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTCCATCTTTTCCCTC TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619o	228 A G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGACAAAGAC AGAGAAAGGGCCCAATGGGGTCAATCCCTCCCTAACAGAGACTCTCTGTGCTGGGGTGTCTAATACATGG CAGGAAGAATGGGGCTTCJTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTCCATCTTTTCCCTC CGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619n	237 G C ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGACAAAGAC AGAGAAAGGGCCCAATGGGGTCAATCCCTCCCTAACAGAGACTCTCTGTGCTGGGGTGTCTAATACATGG CAGGAAGAATGGGGCTTCJTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTCCATCTTTTCCCTC CGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619m	99 C T ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGACAAAGAC AGAGAAAGGGCCCAATGGGGTCAATCCCTCCCTAACAGAGACTCTCTGTGCTGGGGTGTCTAATACATGG TGGCAGGAAGAATGGGGCTTCJTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTCCATCTTTTCCCTC TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	189 T A ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGACAAAGAC AGAGAAAGGGCCCAATGGGGTCAATCCCTCCCTAACAGAGACTCTCTGTGCTGGGGTGTCTAATACATGG CAGGAAGAATGGGGCTTCJTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTCCATCTTTTCCCTC TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619k	90	C G	---	---	ACAAAGCGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAAGGCCCAATGGGGTATCCGCTCCCTAACGAGACTCTGTGCTGGGGTGGCTAATTAC ATGGCAGGAAGATGGGGCTTAAGGGAGTGTTGGGCTGTCTCCCTTTTTCATCTTTTCCCT CTCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619j	206	T G	---	---	ACAAAGCGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAAGGCCCAATGGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGGCTAATTACATGG CAGGAAGATGGGGCTTAAGGGAGTGTTGGGCTGTCTCCCTTTTTCATCTTTTCCCTCTCT CGCT/GTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619i	106	C G	---	---	ACAAAGCGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAAGGCCCAATGGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGGCTAATTACATGG ATGGCAGGAAGATGGGGCTTAAGGGAGTGTTGGGCTGTCTCCCTTTTTCATCTTTTCCCT CTCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619h	150	T C	---	---	ACAAAGCGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAAGGCCCAATGGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGGCTAATTACATGG CAGGAAGATGGGGCTTAAGGGAGTGTTGGGCTGTCTCCCTTTTTCATCTTTTCCCTCTCT TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619g	228	A G	---	---	ACAAAGCGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAAGGCCCAATGGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGGCTAATTACATGG CAGGAAGATGGGGCTTAAGGGAGTGTTGGGCTGTCTCCCTTTTTCATCTTTTCCCTCTCT CGCTTCTTCTTCTTACACAGAAACATTA/G/CACATACCGAGAAACCTATTTC
WI-7619f	237	G C	---	---	ACAAAGCGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAAGGCCCAATGGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGGCTAATTACATGG CAGGAAGATGGGGCTTAAGGGAGTGTTGGGCTGTCTCCCTTTTTCATCTTTTCCCTCTCT CGCTTCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619e	99	C T	---	---	ACAAAGCGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAAGGCCCAATGGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGGCTAATTACATGG TGGCAGGAAGATGGGGCTTAAGGGAGTGTTGGGCTGTCTCCCTTTTTCATCTTTTCCCTCTCT TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619d	189	T A	---	---	ACAAAGCGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAAGGCCCAATGGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGGCTAATTACATGG CAGGAAGATGGGGCTTAAGGGAGTGTTGGGCTGTCTCCCTTTTTCATCTTTTCCCTCTCT TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619c	90 C G ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGGTCACTC/C/GjCTCCCTAACGAGACTCTCTGTCTGGGGTGTCTAAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTTTTCCCT CTCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	206 T G ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGGTCACTCCCTCCCTAACGAGACTCTCTGTCTGGGGTGTCTAAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTCTCTCT CGC/T/GjTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619	189 T A ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGGTCACTCCCTCCCTAACGAGACTCTCTGTCTGGGGTGTCTAAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCATCTTTTCCCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7626d	105 A G ---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTGTTTCTGTAACAAATTGGGATCTGTCTTGGC/GjTTAAACCATCATGAGCCAAATGTG CCATACTAATGATGAGCATTTAGCACAAATTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCATTTTCCCTTGGACTGTTC
WI-7626c	155 CT ---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTGTTTCTGTAACAAATTGGGATCTGTCTTGGCATTAAACCATCATGAGCCAAATGTGCCA TACTAATGATGAGCATTTAGC/JTACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCATTTTCCCTTGGACTGTTC
WI-7626b	28 T A ---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TACTATGTGTTTCTGTAACAAATTGGGATCTGTCTTGGCATTAAACCATCATGAGCCAAATGTGCCA CCATACTAATGATGAGCATTTAGCACAAATTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCATTTTCCCTTGGACTGTTC
WI-7626	144 T C ---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTGTTTCTGTAACAAATTGGGATCTGTCTTGGCATTAAACCATCATGAGCCAAATGTGCCA TACTAATGAT/GCJGAGCATTTAGCACAAATTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCATTTTCCCTTGGACTGTTC
WI-7689c	134 A G ---	---	TCCATAACCGCTGATTCTCAGGGTCTCTGCTGCCGCCACCCAGATGGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCCTCTAGGACGCCACCCAGCAAAAGGTGTTCTCTAAAJA /GjTAAGGGCAGAGTCACTGGGGCAGCTGATACAAATTTGCAGACTGTGTAAAGAGAGCTTAAT GATAATATTGTGGTGCCACAAATAAAATGGATTTATTAGAAATTCATATGAC

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WI-7689b	134	A G ---	---	TCCCATAACCGCTGATTCAGGGTCTCTGCTGCCGCCCCACCCAGATGGGGAAGCACAGGTGGGC TTCCAGTGGTCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTCCTAA/A /GTTAAGGGCAGAGTCACACTGGGCAGCTGATACAAATTCAGACTGTGTAAAGAGAGAGCTTAAT GATAATTTGGTGGTCCCAAAATAAATGGATTATTAGAAATTCATATGAC
WI-7689	121	G A ---	---	TCCCATAACCGCTGATTCAGGGTCTCTGCTGCCGCCCCACCCAGATGGGGAAGCACAGGTGGGC TTCCAGTGGTCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTCCTAA AATAAGGGCAGAGTCACACTGGGCAGCTGATACAAATTCAGACTGTGTAAAGAGAGAGCTTAAT GATAATTTGGTGGTCCCAAAATAAATGGATTATTAGAAATTCATATGAC
WI-7690	45	G A ---	---	TGGAGAACATTCAATCTTGGCGTCACTATTCAATCAATGAAGATTAG/AJCACTGAGATCCAGAGAGG CTGGATGACTTGTCTCAAGTTCACCAAGCATGGTAGTGGCAAGAGAGGTCAGAGTCTGGCCCTTGAT GCCAGCTCAGTGCACAAAGCTCAGTAGGAGGATGTTCCAGTGGATGAGGCCACCAGGAAGCAC AGTCCAAAGGCTGGTCCACACATTATCAGCAGCAACAACCTGTCAGTTCATCC
WI-7703b	164	T C ---	---	ACAGAAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTCACATTGGAACAAGTCAGTCATTGATATGATTCAAA TGCTATAAACCAAACTGATGTAAGTAAATTCJGGTCTCTCAGTTGTTTAAACCTCTAAATTCCT TTCATTTAGGGGTAGCATTTGTGTGAAGAGGTTTAAAGCTTCCATTGT
WI-7703	156	T C ---	---	ACAGAAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTCACATTGGAACAAGTCAGTCATTGATATGATTCAAA TGCTATAAACCAAACTGATGTCJJAAGTAAATGGTCTCTCAGTTGTTTAAACCTCTAAATTCCT TTCATTTAGGGGTAGCATTTGTGTGAAGAGGTTTAAAGCTTCCATTGT
WI-7743e	106	C A ---	---	TAAATGAGTGTGTTTGTACCGTTGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTACAGAGACTCAGGGCCCAAGCACTAAAGCAGTGGACJ/AJCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACCTCACTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCAGCTCTCAGCC
WI-7743d	275	C T ---	---	TAAATGAGTGTGTTTGTACCGTTGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTACAGAGACTCAGGGCCCAAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTACCTCACTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCAGCTCTCAGCCAAGG
WI-7743e	106	C A ---	---	TAAATGAGTGTGTTTGTACCGTTGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTACAGAGACTCAGGGCCCAAGCACTAAAGCAGTGGACJ/AJCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACCTCACTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCAGCTCTCAGCC

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WI-7743d	275 C T ---			TTAAATGAGTGTGTTGTACACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCCTCTGGAGCCAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAACTCTGCTACCTCACTGGGTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743e	106 C A ---			TTAAATGAGTGTGTTGTACACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCCTCTGGAGCCAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAACTCTGCTACCTCACTGGGTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GAGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGGCC
WI-7743d	275 C T ---			TTAAATGAGTGTGTTGTACACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCCTCTGGAGCCAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAACTCTGCTACCTCACTGGGTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743c	106 C A ---			TTAAATGAGTGTGTTGTACACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCCTCTGGAGCCAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAACTCTGCTACCTCACTGGGTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GAGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGGCC
WI-7743b	275 C T ---			TTAAATGAGTGTGTTGTACACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCCTCTGGAGCCAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAACTCTGCTACCTCACTGGGTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743	106 C A ---			TTAAATGAGTGTGTTGTACACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCCTCTGGAGCCAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAACTCTGCTACCTCACTGGGTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GAGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGGCC
WI-7743	275 C T ---			TTAAATGAGTGTGTTGTACACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCCTCTGGAGCCAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAACTCTGCTACCTCACTGGGTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7758	144 A G ---			TGACATTTATTCAAAGTTAAAGCAAACACTTACAGAAATTATGAAGAGGTATCTGTTTAAACATTTCC TCAGTCAAGTTCAGAGTCTTCAGAGACTTCGTAATTAAGGAACAGAGTGAGAGACATCATCAAGTG GAGAGAAATCAGTATAGTTAAACTGCATTATAAATTTTATAACAGAAATTAAGTAGATTTTAAAAA GATAAAATGTGTAATTTTGTATTATTTCCCATTTGGACTGTAACTGACTGCC

WI-7765b	126	G C ---	---	---	ACAGGGCCCTTGGCAGGTGCAGCCOCCACTGCCCTTTGACCTGCCCTCCCTTCATGCATGGAAATTCCTT TCATCTGGAACCATCAGAAACACOCCTCACACTGGGACTTGCAAAAGGGTCAGTATGG(G/C)TTAGG GAAAACATTCATCCTTGAGTCAAAAAATCTCAATCTCCCTATCTTTGCCACCCTCATGCTGTGTG ACTCAACCAAAATCACTGAACCTTGTCTGAGCCTGTAAAAATAAAGGTGCGGA
WI-7773b	237	C G ---	---	---	TTAATTTACTGATTCAGAGAACCAATCATTTGATCAGATTATTTTAAAGTTTATCCGTAGTTTT GATAAAAGATTTTCCCTATCCCTGGTCTGTCAGAGAACCTTAATAAGTCTACTTTGCCATTAAAGCA GACTAGGTTTCATGCTTTTACCCCTTNNNNNNNNNTGTAAAGTCTAGTTACCTACTTTTCTTT GATTTTCGACGTTTACTAGCCATCTCAAGCAAC(G)TTTCGACGTTTGA
WI-7774b	170	T C ---	---	---	TGCAACCTCTTTTCGTGATGGCGCCCTGCTGGTCAGCACTCCAGTAGCGAGAGACGCCACCAGAAT CAGATCCCAGCTTCGGCATTTGATCAGACCAACAGTGTCTTCCGGGAGGAAACACTTTTITAA TTACCCCTTTTCGAGGCACCACCTTTAATCTGTCTTTCATACCTTGTCTTATTAATGAGCGACTTAA ATGATTGAAAATAATGCTGCTCTTAGTAGCAAGTAAATGTCTTGTCT
WI-7785c	165	G ---	---	---	GCAGAGACCTTCCAAGGACATATGCAGGATTCGTATAGTGAACATATGGAAGATTAGAAATA TTTATTGCTGTAATACTGTAATGCATTGGAATAAACTGCTCCCCCATTTGCTCTATGAAACTGC ACATTGGTCATTGTAATANNNNNNNNNGCCAAAGGCTAATCCAATTATTATCACATTTACCA TAATTTATTTGTCCATTGATGATTTATTTTGTAAATGATCTTGGTCTGC
WI-7785b	165	G ---	---	---	GCAGAGACCTTCCAAGGACATATGCAGGATTCGTATAGTGAACATATGGAAGATTAGAAATA TTTATTGCTGTAATACTGTAATGCATTGGAATAAACTGCTCCCCCATTTGCTCTATGAAACTGC ACATTGGTCATTGTAATANNNNNNNNNGCCAAAGGCTAATCCAATTATTATCACATTTACCA TAATTTATTTGTCCATTGATGATTTATTTTGTAAATGATCTTGGTCTGC
WI-7785	156	- T ---	---	---	GCAGAGACCTTCCAAGGACATATGCAGGATTCGTATAGTGAACATATGGAAGATTAGAAATA TTTATTGCTGTAATACTGTAATGCATTGGAATAAACTGCTCCCCCATTTGCTCTATGAAACTGC ACATTGGTCATTGTAATANN /TJNNNNNNNGCCAAAGGCTAATCCAATTATTATCACATTTATCCATAATTTATTTGTCCATTGA TGTATTTATTTGTAAATGATCTTGGTG
WI-7789c	84	G A ---	---	---	TCTCCCCCTCATCCAACCTCCGAAAGTCTGAATCCTCCAGGAGGGCCACCATCTTACAGAGACTCTCCC TGACGGTGGAAATTTAA(G)ATTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCCTGGTGACTCGGGGGCTGTCTCAGACGACTAGCCCCAGGACCCATCT
WI-7789b	84	G A ---	---	---	TCTCCCCCTCATCCAACCTCCGAAAGTCTGAATCCTCCAGGAGGGCCACCATCTTACAGAGACTCTCCC TGACGGTGGAAATTTAA(G)ATTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCCTGGTGACTCGGGGGCTGTCTCAGACGACTAGCCCCAGGACCCATCT

WI-7789	73	G A ---			TCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCAAAGGAGGCCACCATCTTACAGAGACTCTCCC TGACG[G/A]TGGAAATTTAAGTTAGGGTCCCTAAAGACATTTGACACACAGTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCCAGGCCGCTGCCCTAGGATAT GCCCTCCTGGTGACTCGGGGCTGTCTCAGACGACTAGCCAGGACCATCT
WI-7790b	190	C T ---			AATTGTCAGTCACCTCTTCAAAACCTTACAGTCTTCTTAAGGTACTCTTCATGAGATTCATCCATT TACTAATACTGTATTTTGGTGACTAGGCTTGCCTATGTGCTATGTAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTCTTGAACCTC[G/T]TCTATACTTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7790	190	C T ---			AATTGTCAGTCACCTCTTCAAAACCTTACAGTCTTCTTAAGGTACTCTTCATGAGATTCATCCATT TACTAATACTGTATTTTGGTGACTAGGCTTGCCTATGTGCTATGTAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTCTTGAACCTC[G/T]TCTATACTTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7795b	81	C A ---			CAGATGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCTCTGGCTCATATTTCTTTCTTCAT CTTGATGATGAT[C/A]GTCAATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCCCACATATAAATGTACTTTTCTCCAGAAAATCTCCTTGAGGAAAATGTCCAAAA TAAGATGAATCACCTTAATACCGTATCTTCTAAATTTGAAATATAATTCG
WI-7795	81	C A ---			CAGATGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCTCTGGCTCATATTTCTTTCTTCAT CTTGATGATGAT[C/A]GTCAATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCCCACATATAAATGTACTTTTCTCCAGAAAATCTCCTTGAGGAAAATGTCCAAAA TAAGATGAATCACCTTAATACCGTATCTTCTAAATTTGAAATATAATTCG
WI-7814c	41	G A ---			TTCTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCG[G/A]TTTCAATTTAGTCATGTGACCCTC TGCTTTGTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATAATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTTGTATATTTTAAAGAAATTAACAGAA
WI-7814b	41	G A ---			TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCG[G/A]TTTCAATTTAGTCATGTGACCCTC TGCTTTGTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATAATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTTGTATATTTTAAAGAAATTAACAGAA
WI-7814	28	G A ---			TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCGTTTCAATTTAGTCATGTGACCCTC TGCTTTGTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATAATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTTGTATATTTTAAAGAAATTAACAGAA

WI-7830d	150	C T	---			GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGTTTAGTAAGAGAAGTCTGCTGCTGATGA TGGATAGGGGGCAAAATCTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAACG ATCCATAACTTTAGT[C/T]TAATGTACACATTCGATTTTGATATAAATTAATTTGTTGTTCCCTTG AGGTGATCGTTGTTGTTGCTGCACTTTTACTTTTTTGGGTGGGA
WI-7830c	54	G A	---			GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGTTTAGTAAGAGAAGTCTGCTGCTGATGA TGATGGATAGGGGGCAAAATCTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGATTTTGATATAAATTAATTTGTTGTTCCCTTG AGGTGATCGTTGTTGTTGCTGCACTTTTACTTTTTTGGGTGGGA
WI-7830b	134	G A	---			GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGTTTAGTAAGAGAAGTCTGCTGCTGATGA TGGATAGGGGGCAAAATCTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAACI G/AJATCCATAACTTTAGTCTTAATGTACACATTCGATTTTGATATAAATTAATTTGTTGTTCCCTTG AGGTGATCGTTGTTGTTGCTGCACTTTTACTTTTTTGGGTGGGA
WI-7830	44	A G	---			GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGTTTAGTAAGAGAAGTCTGCTGCTGATGA TGATGGATAGGGGGCAAAATCTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGATTTTGATATAAATTAATTTGTTGTTCCCTTG AGGTGATCGTTGTTGTTGCTGCACTTTTACTTTTTTGGGTGGGA
WI-7865e	25	C T	---			CCACTTCCTATCTGATTTTCCCAG[C/T]AAATGAGGCAGGCAATCTAGTCTTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTCAGGGTGTCTTCCCACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865d	191	C T	---			CCACTTCCTATCTGATTTTCCCAGCAATGAGGCAGGCAATCTAGTCTTCCACAAACATCTAGCC ATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAAGATTCAGGGTGTCTTCCCACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865c	25	C T	---			CCACTTCCTATCTGATTTTCCCAG[C/T]AAATGAGGCAGGCAATCTAGTCTTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTCAGGGTGTCTTCCCACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865b	191	C T	---			CCACTTCCTATCTGATTTTCCCAGCAATGAGGCAGGCAATCTAGTCTTCCACAAACATCTAGCC ATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAAGATTCAGGGTGTCTTCCCACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTCACCCAGTAAACCCAAA

WI-7865	25 C T ---	---	---	CCACCTCTATCTGATTTTCCAGC/CTJAAATGAGGAGGCAATTCCTAGTCTTCCACAAAACATCTA GCCATCTAAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTACCCAGTAGAACCCAAA
WI-7865	191 C T ---	---	---	CCACTCTATCTGATTTTCCAGCAATGAGGAGGCAATTCCTAGTCTTCCACAAAACATCTAGCC ATCTAAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGGGT ATGCTACTCATAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTCTCAGTAC/CTJGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTACCCAGTAGAACCCAAA
WI-7867c	92 A C ---	---	---	TTCAACACCTGTCTTCCACCTCCACCATCTGTGCAATCACTTCACCTTCAGCCTCACTAGTCCCC CTAACAAATACCTGTCAAGAGG/ACJGAGTGCAGCTCAGGTGGATTTAATGTGGGTTAATATGGC CTGTTGAGTTAATGTTAATGTTGATTTTCTTTAAGTAACCATTTCTGTCTTGTCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTAAAGG
WI-7867b	92 A C ---	---	---	TTCAACACCTGTCTTCCACCTCCACCATCTGTGCAATCACTTCACCTTCAGCCTCACTAGTCCCC CTAACAAATACCTGTCAAGAGG/ACJGAGTGCAGCTCAGGTGGATTTAATGTGGGTTAATATGGC CTGTTGAGTTAATGTTAATGTTGATTTTCTTTAAGTAACCATTTCTGTCTTGTCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTAAAGG
WI-7868c	173 C T ---	---	---	TTGATCGATCTTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGGCTTT CACCCAACTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTTAATATTTCCCTGTCTTACCCCTATTCAAGCA/CTJTAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCCTAGAT
WI-7868b	173 C T ---	---	---	TTGATCGATCTTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGGCTTT CACCCAACTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTTAATATTTCCCTGTCTTACCCCTATTCAAGCA/CTJTAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCCTAGAT
WI-7868	66 T C ---	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTCTGCAGTGATTAGAAGGG GTGGGGTGGCGGGAATCC/CTJATTTATCAGACTCTGTAATGAATATAAATGTTTACTCAGAGGA GCTGCAAAATGCTGCAAAATGAAATCCCAATGAGCACCTAGATAATTTAAACATCATTTACTGCCAT CTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG
WI-7870b	85 T C ---	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTCTGCAGTGATTAGAAGGG GTGGGGTGGCGGGAATCC/CTJATTTATCAGACTCTGTAATGAATATAAATGTTTACTCAGAGGA GCTGCAAAATGCTGCAAAATGAAATCCCAATGAGCACCTAGATAATTTAAACATCATTTACTGCCAT CTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG

WI-7870	76 C T	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAATACTCTGCAGTGATTAGAAGGG GTGGGTGGC/TJGGGAATCCTATTTATCAGACTCTGTAATGAATATAAATGTTTTACTCAGAGGAG CTGCAATTTGCCTGCAAAATGAATCCAATGAGCACTAGAATATTTAAACATCATTTACTGCCATC TTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG
WI-7889c	54 C	---	---	TTAGGTCTCATGCCCCACTCCCCAGGAGCAGCTGGGCACTGACAGCCTGGGGGGCGCTCTCCCCCTG CAGCCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACCTACAGGACTGGCCGGCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCTGGAGAAAGGACATGGGAATGAATGAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAAGGCTGTCTTCTCCCAGAGCACAAAG
WI-7889b	54 C	---	---	TTAGGTCTCATGCCCCACTCCCCAGGAGCAGCTGGGCACTGACAGCCTGGGGGGCGCTCTCCCCCTG CAGCCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACCTACAGGACTGGCCGGCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCTGGAGAAAGGACATGGGAATGAATGAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAAGGCTGTCTTCTCCCAGAGCACAAAG
WI-7894c	142 A G	---	---	AGCCACCCCCAAATATACTGTTATCCAGAGCTGTATGCTCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGCTCTATGTTTTGTAATTTATTTGCGTATAC ATTATC(A/G)TATGTAAATTTGCATTTTATTGAAATTAATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGAGTATCCATA
WI-7894b	142 A G	---	---	AGCCACCCCCAAATATACTGTTATCCAGAGCTGTATGCTCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGCTCTATGTTTTGTAATTTATTTGCGTATAC ATTATC(A/G)TATGTAAATTTGCATTTTATTGAAATTAATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGAGTATCCATA
WI-7900e	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/CJCCCTGCCATTGAACAGTGATTAGTTTGATCAAGCCATGGTGA/C/TJACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900d	128 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/CJCCCTGCCATTGAACAGTGATTAGTTTGATCAAGCCATGGTGA/C/TJACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/CJCCCTGCCATTGAACAGTGATTAGTTTGATCAAGCCATGGTGA/C/A AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC

WI-7900d	128 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTTGGCCAGGCCACACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGA(C/T)ACA AAAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTTCTCTCAGATTTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAGAAGAAATC
WI-7900e	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGA(C/T)ACA AAAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTTCTCTCAGATTTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAGAAGAAATC
WI-7900d	128 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG(C/T)CCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGACACA AAAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTTCTCTCAGATTTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAGAAGAAATC
WI-7900c	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG(C/T)CCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGACACA AAAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTTCTCTCAGATTTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAGAAGAAATC
WI-7900b	128 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGA(C/T)ACA AAAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTTCTCTCAGATTTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAGAAGAAATC
WI-7900	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG(C/T)CCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGACACA AAAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTTCTCTCAGATTTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAGAAGAAATC
WI-7901c	33 C T	---	---	AGACTTAGGTACAAATTGCTCCCTTTTATATA(C/T)AGACACACACAGGACACATATATTAAACAG ATTGTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAAGAC CCTTTTTAAAAACAACTCCAGGCCCTTGGTTGGGGTCGCTGGGTTATTGGGCGACGCCCGTGGTGGT CACTCAGTCGCTCTGCATGCTCTCTGTCTATACAGACAGGTAACTAGTTCT
WI-7901b	33 C T	---	---	AGACTTAGGTACAAATTGCTCCCTTTTATATA(C/T)AGACACACACAGGACACATATATTAAACAG ATTGTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAAGAC CCTTTTTAAAAACAACTCCAGGCCCTTGGTTGGGGTCGCTGGGTTATTGGGCGACGCCCGTGGTGGT CACTCAGTCGCTCTGCATGCTCTCTGTCTATACAGACAGGTAACTAGTTCT

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WI-7901	33 C T	---	---	AGACTTAGGTACAATTGCTCCCTTTTATATA[CTAGACACACACAGGACACATATATTAACAG ATTGTTTCATCATTTGTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTTAAACAACTCCAGGCCCTGGTTGGGGTCGCTGGGTTATGGGGCAGCGCCGTTGGTCTG CACTCAGTCGCTCGCTGCTCTGTCATACAGACAGGTAACCTAGTTCT
WI-7901	271 T G	---	---	AGACTTAGGTACAATTGCTCCCTTTTATATAACAGACACACAGGACACATATTAACAGATT GTTTCATCATTTGTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGACCCT TTTTAAACAACTCCAGGCCCTGGTTGGGGTCGCTGGGTTATGGGCAGCGCCGTTGGTCTGTCAC TCAGTCGCTCTGTCATGCTCTGTCATACAGACAGGTAACCTAGTTCTGTT
WI-7926c	150 C A	---	---	CATTCCGCATCTGTCACCCAGGACAGAAAGCATGGACAAGGATGAGCTTTACAAAGATGACACT TTGGAGATCAGAAAATTCATATTTAAGCAAGTGATACAAACACAGTGATTTGGGAATGCCCTTCATT TACAATGCAATACTTA[CTAATTTAATACTCTTTGAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926b	28 A T	---	---	CATTCCGCATCTGTCACCCAGGACAGAAAGCATGGACAAGGATGAGCTTTACAAAGATGACACT TTGGAGATCAGAAAATTCATATTTAAGCAAGTGATACAAACACAGTGATTTGGGAATGCCCTTCATT TACAATGCAATACTTA[CTAATTTAATACTCTTTGAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926	150 C A	---	---	AAGAGCCAGCAGGTCAAAAAGGCCAACACACACCATAAGCAGCCAGCCACCAAGGCCAGGTCCTGT GCTATCACAGGGTCACCTCTTTTACAGTTAGAAACACCCAGCCGAGGCCACAGAAATCCCATCCCTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTTGCTCAATCAATCCATAGATTTCGAAGCCACA GA[GT]TCTCTCCCTGGAGCAGCAGACTATGGGCAGCCAGTGTGCCACCTG
WI-7947b	203 G T	---	---	AAGAGCCAGCAGGTCAAAAAGGCCAACACACACCATAAGCAGCCAGCCACCAAGGCCAGGTCCTGT GCTATCACAGGGTCACCTCTTTTACAGTTAGAAACACCCAGCCGAGGCCACAGAAATCCCATCCCTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTTGCTCAATCAATCCATAGATTTCGAAGCCACA GA[GT]TCTCTCCCTGGAGCAGCAGACTATGGGCAGCCAGTGTGCCACCTG
WI-7947	203 G T	---	---	CATGTGTCATGAAGAGCTAATTTAAAAGCAAGTAAGACTAATTAATTTAAAATAAAAATGCC ACAAATTTCAATTTCTCCTTCTAAGTATTACAATGGAGTTTATCTCTGCCCTAAAAGTGGAGAAAT TGAGTGAATGA[CT]CAATTTTGTAAATTTAGGATCAAGATCCAAATTTTCCCAACTCTTGTTCCTCC CCATAAAGTTAGGCATGAGGAGGAGCAGCTATTAAGGCAGAGACGGGAA
WI-7963b	145 T C	---	---	

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WI-8021b	57	C T	---	---	ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTAATCTCATCTGGAAA[C/][G]GATCCC ACGCTTTAGAACCTTACCACAAGGAGTTTTCTTGAGTAGATTCTCAAGCTTGGTAGGCATTGGA ACTGGTCTTTTCACTTTGAGATTCTTTCTTTGCGCTCTTATCAAGTCAGCACACACCTTTTCCAAAG GATTTACGTTGCGGCTTGTTAGGGGTGATTGGAATTCGGTGAATTGCCA
WI-8021	57	C T	---	---	ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTAATCTCATCTGGAAA[C/][G]GATCCC ACGCTTTAGAACCTTACCACAAGGAGTTTTCTTGAGTAGATTCTCAAGCTTGGTAGGCATTGGA ACTGGTCTTTTCACTTTGAGATTCTTTCTTTGCGCTCTTATCAAGTCAGCACACACCTTTTCCAAAG GATTTACGTTGCGGCTTGTTAGGGGTGATTGGAATTCGGTGAATTGCCA
WI-8024c	206	A G	---	---	CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCATGTGTCAGTCA GCTTGATTTCAGGAGGACAGGGCAGAGGATCCCGAGTGGCACTTCCCATGGGAAGACAGAAGAGAGT GGGCCACAGAGATGGAAGGACCCAGTGTATCATCAACAAACCACTTTCAGCCGCTCTAGCCTCTAA TTCCC[A/G]CTCTAGAACAGCTGGCCCTGGTCTGTCAGTACACAAAGGAAGAGC
WI-8024b	206	A G	---	---	CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCATGTGTCAGTCA GCTTGATTTCAGGAGGACAGGGCAGAGGATCCCGAGTGGCACTTCCCATGGGAAGACAGAAGAGAGT GGGCCACAGAGATGGAAGGACCCAGTGTATCATCAACAAACCACTTTCAGCCGCTCTAGCCTCTAA TTCCC[A/G]CTCTAGAACAGCTGGCCCTGGTCTGTCAGTACACAAAGGAAGAGC
WI-8077	167	A G	---	---	GAATGAGCCTTCTAGCGCCGAGGGACCTGCTGCTGTTGTTGGCTGCACATGCTATGGAATGC TTTTGGCCAAAGCGGGGCACTGAGGACTAAGCTCTGANNNNNNNNATCTGCCCAAACCTCTTTCT AAGAGTCTGGGTGTCATGCCCTACAACC[A/G]TAAATCTCATCAGATGGATTATTTAACGTT GTGATTGAGACTTACTTTCCAATCTGACTCTGGCATAACAAGGAAAAA
WI-8118f	114	G C	---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAAATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGATGAGCTTGTG/GC/JTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCIGATTCCCGCTCCCTATTCCTTCCT AAAAATCAGACTCATTTGTACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40	A G	---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAAATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGATGAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCIGATTCCCGCTCCCTATTCCTTCCT AAAAATCAGACTCATTTGTACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118	T G	---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAAATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGATGAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCIGATTCCCGCTCCCTATTCCTTCCT AAAAATCAGACTCATTTGTACCAGTAGTCTTGAGGACTCAAGCTGAATGA

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WI-8118c	44 C T ---			TCTAGGTTTAAATCAAAGCAATTTGCANITTTGGATTTTGGAAATGA/C/TJCACTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGGAACCTGGCAAAATACAGAATGTAGCTTGTGTTTGTCTTAGCCTTGAAGA TGACCAAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCATTTGTGACCAGTAGCTCTGAGGACTCAAGCTGAATGA
WI-8118b	88 T C ---			TCTAGGTTTAAATCAAAGCAATTTGCANITTTGGATTTTGGAAATGA/C/TJCACTCCCTTGCTAAGGAAGC GTACTTCATGCTGTGGAACCTGGCAAAATACAGAATGTAGCTTGTGTTTGTCTTAGCCTTGAAGA TGACCAAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCATTTGTGACCAGTAGCTCTGAGGACTCAAGCTGAATGA
WI-8171d	299 C T ---			TTTTCTCTCTCCGGGGGACCAAGGTACCTTCTGGGGCATACAAATGGCAGGCGCTCGGGAAG AGGGGTAGGAGGACCGAGCAGCATCTCTGTAGAGGAAGACAGAAAGGAGACCCCTCTTGGCACACA TTTATGGAGGTTGTCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTACTTAAGAGAAGGC ACCAAGTGGGCAAGAGGACCAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8171c	46 A G ---			TTTTCTCTCTCCGGGGGACCAAGGTACCTTCTGGGGCATACAAATGGCAGGCGCTCGGGAAG AAGAGGGTAGGAGGACCGAGCAGCATCTCTGTAGAGGAAGACAGAAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGTTGTCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTACTTAAGAGAA GGCACCAAGTGGGCAAGAGGACCAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171a	46 A G ---			TTTTCTCTCTCCGGGGGACCAAGGTACCTTCTGGGGCATACAAATGGCAGGCGCTCGGGAAG AAGAGGGTAGGAGGACCGAGCAGCATCTCTGTAGAGGAAGACAGAAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGTTGTCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTACTTAAGAGAA GGCACCAAGTGGGCAAGAGGACCAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171b	298 T C ---			TTTTCTCTCTCCGGGGGACCAAGGTACCTTCTGGGGCATACAAATGGCAGGCGCTCGGGAAG AGGGGTAGGAGGACCGAGCAGCATCTCTGTAGAGGAAGACAGAAAGGAGACCCCTCTTGGCACACA TTTATGGAGGTTGTCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTACTTAAGAGAAGGC ACCAAGTGGGCAAGAGGACCAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8314b	85 G C ---			GAGGGGAATGACATCTGGAGATCTAGGTATGTGGCCCATTCGAATTTGAGCACATTTCTTGGGTCTGT TTCTCTATCTCTAAGGG[G/C]AGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAGAGCACTGTCCAATAGAACTTTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAAACCCT
WI-8314	78 C/G ---			GAGGGGAATGACATCTGGAGATCTAGGTATGTGGCCCATTCGAATTTGAGCACATTTCTTGGGTCTGT TTCTCTATCT[G/C]TAAAGGGAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAGAGCACTGTCCAATAGAACTTTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAAACCCT

WI-8321	178 GA ---	---	TTTTAAATATGCCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTCAAGAGCTGCTGTTACTAGTCTCTGAGAAG TCCCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTCAGAAATG/AJAGTATCTTAGTATTCTTTCTA TTTTGCTATGGTTCTAGTTTATCAACCTACTTTATTAGCTGAACTGTTGGC
WI-8321	178 GA ---	---	TTTTAAATATGCCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTCAAGAGCTGCTGTTACTAGTCTCTGAGAAG TCCCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTCAGAAATG/AJAGTATCTTAGTATTCTTTCTA TTTTGCTATGGTTCTAGTTTATCAACCTACTTTATTAGCTGAACTGTTGGC
WI-8321	178 GA ---	---	TATGTACTCACTTTCAGTTACCCCGTGCCTCCAGAAATCGCATGTTGCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTCCCTCCCTGTGCAGCCTTAGA/CJACTAAGTAG CAGTACTGTTGGTGTGTTGTTCTCCCGAGCAATGCCACTGCAGCTACTAGTAACAACACTAG AGGTGGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8321	123 AC ---	---	TATGTACTCACTTTCAGTTACCCCGTGCCTCCAGAAATCGCATGTTGCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTCCCTCCCTGTGCAGCCTTAGA/CJACTAAGTAG CAGTACTGTTGGTGTGTTGTTCTCCCGAGCAATGCCACTGCAGCTACTAGTAACAACACTAG AGGTGGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8321	114 AC ---	---	TGCGGGCTTAACAGGAAGCATGACTGGGAGGCTCAGGAAGCTTATAATCATGGCAGAAAGCGAAGG GGAAGCAAGGACCTTCTACATGGCAGCAGGAGAAAGAGAAAGGAGGAGTCTACACACTTTT AAACAACAGATCTCATGAGANTCCATCGGGAGACAGCACTAGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACCCTNTCACCAGGCCCTCTCCCAACACGTTGGG
WI-8378b	311 TC ---	---	TGCGGGCTTAACAGGAAGCATGACTGGGAGGCTCAGGAAGCTTATAATCATGGCAGAAAGCGAAGG GGAAGCAAGGACCTTCTACATGGCAGCAGGAGAAAGAGAAAGGAGGAGTCTACACACTTTT AAACAACAGATCTCATGAGANTCCATCGGGAGACAGCACTAGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACCCTNTCACCAGGCCCTCTCCCAACACGTTGGG
WI-8378	308 TC ---	---	TTTAGCACATATTAGCATTAAAGCCTCAACCGATACAGCAATATGTTACATTCTTGTGAAACACAG TTGTTGTAGACTGTTAANNNNNNNAAATGTAACCTCGACTTGTGCCTAATAGGATTTGACCNTTAA GAGGNTCTTTTGTGTGGANGGGTGGCTTGTGTTGAACCTCCATTCTGTG/GCCTTGTAGCTGGTG AGGCTGGGAGTGGANGGNNCCGGGGCCCTTGGCNATNGNATTCAGTGAG
WI-8426	184 TG ---	---	TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTC/AJCA TCTTCTATCTTAGTCCAAAGTTTGTAGTTTCAATCCCAATTAACCAATCCATTGTTATTTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGCTTAAATGCAATTCAT
WI-8450h	61 CA ---	---	

WI-8450g	55 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCACACTCCCAT CTTCTATCTTAGTTCCTCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTGTTATTTTAAAGA AAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450f	108 T A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCCATCTT CTCTATCTTAGTTCCTCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTGTTATTCCTTAAAGA AAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450e	125 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCCATCTT CTCTATCTTAGTTCCTCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTGTTATTCCTTAAAGA AAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450d	125 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCCATCTT CTCTATCTTAGTTCCTCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTGTTATTCCTTAAAGA AAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450c	108 T A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCCATCTT CTCTATCTTAGTTCCTCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTGTTATTCCTTAAAGA AAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450b	61 C A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCCATCTT CTCTATCTTAGTTCCTCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTGTTATTCCTTAAAGA AAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450a	55 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCACACTCCCAT CTTCTATCTTAGTTCCTCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTGTTATTCCTTAAAGA AAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8458b	60 A/G ---			CAAGGAAAGCTGTCAGTCTTCATAAACTTCAAAAGAGTTACAAAATACGTATTTTAAAGICTA CAATTCAAGATTAGCATCCAAACCTACAAACATGATGATACATTCGTACACACCATACAACTTCAC ACCTGGCTACAGCAATGTTGACCTTACATCACCATTGTTTACTTGTGAAAACCTTATTGTGCACAGT GACATCCATTCCGCCAGACTTAATGTTATAAAGCAGCTGAGCAGAGTCTTCA

WI-8461c	105	A T ---			CTTCTCCTCCAAATCTACATGAATACTTGAAGACAATAATACTACAACCTTACAAATGCCAATTA GACAAAAGAGANTAAATGATATAATAATAATCAATTTT[A/T]NNNNNNNNCCCTTGCTTATTCACAT TCAGGGAAGTCTAGCACCAGGACAGTNTTAAACAACATTACAAANTTTNTTGAAGAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAANTCAAGGATTTCGAAAAGGGGG
WI-8461b	38	T C ---			CTTCTCCTCCAAATCTACATGAATACTTGAAGACAATAATACTACAACCTTACAAATGCCA TTAGACAAAGAGANTAAATGATATAATAATAATCAATTTTNNNNNNNNCCCTTGCTTATTCACAT TCAGGGAAGTCTAGCACCAGGACAGTNTTAAACAACATTACAAANTTTNTTGAAGAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAANTCAAGGATTTCGAAAAGGGGG
WI-8461	38	T C ---			CTTCTCCTCCAAATCTACATGAATACTTGAAGACAATAATACTACAACCTTACAAATGCCAATTA GACAAAAGAGANTAAATGATATAATAATAATCAATTTT[A/T]NNNNNNNNCCCTTGCTTATTCACAT TCAGGGAAGTCTAGCACCAGGACAGTNTTAAACAACATTACAAANTTTNTTGAAGAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAANTCAAGGATTTCGAAAAGGGGG
WI-8461	105	A T ---			AATAACATGTTATGAAACAAGCTGGTTACAAGTAGTAGGATGACCTTAATTTTGATAAAAAAAT TAAAAGCAT[G/A]AACATGCATATAAAAAATTAGATTATGTACAAAATACCAACAGTATTACTTC TGCTCAGTAATTAATAATCTCTCCCTTGTTTGTCTTTTAAAAACATTATTCTGAAAAA ATCAGAAAACATGATCGTGGAGAGATTATTA
WI-9438	77	A G ---			ACAGAAATTGACCTTTATTTGTTGTACTA/AGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAAATCCAGTCTGTAGCTCAGTACCTGT[C/T]GTGCACACTGTACCATCTCAGTCCCACCT GCCTGTAACTTAGAAAACAGCCCTACCCCGAGGGTCTGCGAGTTAATACCTTGAGAAATAGTCTA CAGTTTTCATAGTTGTCTGAGCTAGAAAACCTTGACCTGTAAACAAAG
WI-9439b	101	C T ---			ACAGAAATTGACCTTTATTTGTTGTACTAAGCCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAAAT[C/T]CCAGTCTGTAGCTCAGTACCTGTCTGTGCACACTGTACCATCTCAGTCCCACCT GCCTGTAACTTAGAAAACAGCCCTACCCCGAGGGTCTGCGAGTTAATACCTTGAGAAATAGTCTA CAGTTTTCATAGTTGTCTGAGCTAGAAAACCTTGACCTGTAAACAAAG
WI-9439a	76	C T ---			GAAGGCTTGATTAAAGGGAGGNTTTATTTGATGTNAACCTACCATTCCATAGACTATAAAGANCATTA TAAAAAAAT[C/C]CCTCTAAAGNGACACATGCCCCAAATGACCANGNCAAGCAACCTTTTAAAT TACTCATCTTTTCATATGTGTGTTGTGTCCTACTACTACTGCTGCTCTCTGCTCTTTGCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT
WI-9446b	75	T C ---			

WI-9446	75	T C ---			GAAGGCTTGATTAAAGGAGGNNTTATTGATGTNAACCTTACCATTCCATAGACTATAAAGANCATTAT TAAAAAAATTCCTCTAAAGNGACACATGCCCAATGACCAANGNCATAAGCAAACTTTTAAAT TACTCATCTTTCATATGTGTGTTGNCCTACTNTTATCACTGTGCTTCTGTCTTTTGCTACCTA TGNGAACTGCACACTATCTGTGGCAATATGT
WI-9497b	185	A ---			ATTAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATACTTTTTTT GAGATAATTATTTAGATCCAGGCTTTCTCTAGATGAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTTAATTAATCAAGTATGTTAATGTCACCT GGAATCTACATGGAAAGCCCAACAAATAACTAAACTTGACTAATGAAG
WI-9497	185	A ---			ATTAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATACTTTTTTT GAGATAATTATTTAGATCCAGGCTTTCTCTAGATGAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTTAATTAATCAAGTATGTTAATGTCACCT GGAATCTACATGGAAAGCCCAACAAATAACTAAACTTGACTAATGAAG
WI-9523b	193	C A ---			GTGAAAAAGTTTCTATTCCATCATACAAATAGATTGTGCTAAGGATCAATTTTGGAGAATGTG CAGCATTCAGAAAGTTGTATCTCATCATGTCAGTCACTCAGCAGCATTTTATCTAAAGTACGTGCACA GACTCAGACAATTACAAACTATTTAGCCATGATCTATGGTGATTTCCACACATTGTACATGTA[C/A]AGTG AAAGCTCTTCAGCTTGGAAACAACCTTGCAAGGCAGACTGCATGCACATATAT
WI-9523a	47	G A ---			GTGAAAAAGTTTCTATTCCATCATACAAATAGATTGTGCTAAGGATCAATTTTGGAGAAT GTGCAGCATTCAGAAAGTTGTATCTCATCATGTCAGTCACTCAGCAGCATTTTATCTAAAGTACGTGCA CAGACTCAGACAATTACAAACTATTTAGCCATGATCTATGGTGATTTCCACACATTGTACAGTGA AAGCTCTTCAGCTTGGAAACAACCTTGCAAGGCAGACTGCATGCACATATAT
WI-9554	202	T C ---			AAAAACACAAGTTTCATACATCACAAAAACCTTCCATTATAACACAGAAGTGATTATTACCAGAC AAGCATCAGTGATGTATAGTCCCTTTCAGTGTGTTATGTACAAATGCTGTAGATAATGCAGCCCATG CAATACCCCAAGAACACACTAGAGTCTACACCCCAAGTACAAATATGATAAAGCAGCCCTCTGCAAGTG GTTTCGCTGGATACCACTAAGAAAGTCTAGTGCAGCCATGTTGGTTATGATTTT
WI-9555	97	G A ---			CCAAAAGCCAAACCATTCATATGTATGGATTTCATAAAACATTTATTGATCCTTTTGGAGTAAGTAT AAATACCTTTACATGGCTAACCTTCTAACG[A/CTTGAAAAATCAATTTCAAGGGACTCTTTAATCA GTTAAATATCTGCTTTAGAAAGGCACAAATGATCATCTTCAGATTAAATACAGGTAAGTATTGAG GGNTAAATGGTACAAAAAGGCTGTAACTCTTTTNCCTCATTGATCACA
WI-9625b	172	A T ---			TTGAACATTTAATGAATGACAAAGACATAACATCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCCTTGGGAAAAACCTTTGGAAAAAACAACACGCACA TAAGTATCATAACTGAGGTTGTGGACAAGTTACTTCTA[ATGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCATTTAAAAAACAACACTGACAAATCTTTTC

WI-9625	172 A T ---			TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTGTATCTNCTCCTTGGGAAAACTTTGGAAAAAAACACGCACA TAAGTATCATAAAGTGGGTTGGGACAAGTTACTTCTA/TGTGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTTCATTTAAAAAACACACTGACAAATCTTTTC
WI-9647	144 C T ---			TTTTTCAGATTCAAAGAGCTACATTTTGGTTAGTGTATGCTACTATACCTTTTTCATCTTTCA ACATCTTTTGTACATTTTAGGTGATGCTCTGTAAACAGTGTATGCTAGACCTAAAAATCCAAAGCT TACAACT/C/TGTCTTTACCTGATACATTTATCCATTTACTTTTCAATTTGGATTTTAAAAATGTTA ACTTAATAGTCTCTTTTCAGATGTCCTGCTTTTAGTTAAATGTGTTT
WI-9676n	114 A G ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCA/W/GATGTGGCTTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676m	184 G T ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676l	84 A C ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676k	202 C T ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA C/TTCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676j	92 C T ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676i	173 T C ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT

WI-9676h	134	C A	---		GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGTACCAAGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCGCCCG C/AJATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTG AGGCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676g	202	C T	---		GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGTACCAAGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCGCCCG ATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGAGG C/TJAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676f	184	G T	---		GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGTACCAAGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCGCCCG ATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676e	173	T C	---		GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGTACCAAGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCGCCCG ATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676d	134	C A	---		GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGTACCAAGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCGCCCG C/AJATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTG AGGCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676c	114	A G	---		GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGTACCAAGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCGCCCG CCCATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676b	92	C T	---		GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGTACCAAGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCGCCCG CCCATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676a	84	A C	---		GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGTACCAAGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCGCCCG CCCATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT

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WI-9738b	40 C A ---	---	TGGACCAACACAGACAGATGATTCCTGGGCGCTGTGTC/C/A/JATTACAAC'TCATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTTGTTCAAAACACAGTAATAAGTACTCCACATTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTACACCTTGCCTGGAGCGGGTGGTTTTCACATATGTGAGTATCTA TCTTTTATTCTGTCCTTATGTTGGGGCACATGCTGTATTGCTGTC
WI-9738	40 C A ---	---	TGGACCAACACAGACAGATGATTCCTGGTGCCTGTGTC/C/A/JATTACAAC'TCATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTTGTTCAAAACACAGTAATAAGTACTCCACATTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTACACCTTGCCTGGAGCGGGTGGTTTTCACATATGTGAGTATCTA TCTTTTATTCTGTCCTTATGTTGGGGCACATGCTGTATTGCTGTC
WI-9756	47 A ---	---	ACTGAAATGTAATGGCCAAGCACCCAGGACCTTAAATCAATAAGAAGTTAATCTGTGGGAAAA GAGTAACATACAAAAGCATCTAAACAAGAGCAGGATGTGATGTAATGTGCCCCATTACACTTTAGTC AGTAAAGATAAGAAAAGCCCTGGTGAGTATCCACTTCCACAACACACAGAAATATACACTTTTGGAAAG ATTCCACTTAACCACCTTGATCTTCACITTTTATGATTTAAACCTCCGCTGG
WI-9758	135 A G ---	---	GATGGTCCCTTAAGGATTTGCATTGGTTAATGGGCAGACTGGTGCAAAAGAGGCTGAATTGAATAAT TAGGAAACTGGGAGAAATCAATTCAAAGAAGAAATCTTGTTCGCAAGGTCATTTTATACTATTTA A/JA/JTAAATAACTCTGGTAGGTTCTATAGCAAAATGCTAAGTAAAGTAACCGCTGGTTTCTAAAT ATTACG
WI-9778	127 G A ---	---	ATTAAATCCAGGCAGCGGGGAAATGGAATCTTTCATATGCTCTGTACCCAACTATAAATTTTG GTTCTCATGCACCATTTTCAITTTGCCTTCTACTCCAGTACCATGATTTTACCAATTTG/AJCTCTC ATAATTGACTTTGCTACTGGAAGAACTCTTAGAATGTTGGAATTTCTCTATTACACACTTTGCCTCA AAGAATGTGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116 C A ---	---	TCCTCCCTTTGCTCCTCATGCCCACTCCCTCAGCCTGCACAGAGCGTTTCTCCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCTGCAGGAC/TTGCTGACAAATGCAGTTTCTC/A/JGGATCCCAACCCAGGA CTCAAAAAAACTAGGAATGGGAGAAAGAGGACCTGGAA'CGGTGTGCTAGCAAGCCCCCAGGTGG TTTGTAAGTGGACTAAAGTTTGAGGACCAGACATGGAAGGTTGGCTTTGGC
WI-9841	101 A G ---	---	TGAAAAATAGCTTTTATCAATCTCTGATATGCTACATATGTCATGGAGAAATGCAGAAATGGCATGA TATGAAATTCATTTTGAATGAATAAAATATAC/JA/JGTTGATATGATATATATCTATTAAACACTT AGGATTATACACACAATAAAACGCTGTGAAGGATAAACTAAGGTTCTATCAGTGGGAAATGAGA TTGAAAGAGGGGATGTGTTACTTGATATGCTGTTG
WI-9880c	222 G A ---	---	GAACATAACACCTTTCTGCATGGAATTTTCTTGATATTGGCAGTTAACAATAAAATGTTATTAGATC ACTGGTCTTCTGTGGGTTGAGTTTTTATGATATCTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGGACTATATAAGATCCCTTTTAAATATATATTTTATAAAGCACATGAA AATGGAATGAAATAATGA/JATTGACATAGGAATTACCTACATATTTTG

WI-9880b	157	C A ---	---	GAAC TAACACCTTCTTG CATGGATTTTCTTGATTATGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTGCTTCTGTGGGTTGAGTTTTTATGATATCTCTGTTAGACCCATAAGGGAGGCTGTGA GTTGTTTTCTACATCCTTGGAC(A)ATATAAGATCCTCTTTTAAATATATATTTTATATAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108	C T ---	---	GAAC TAACACCTTCTTG CATGGATTTTCTTGATTATGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTGCTTCTGTGGGTTGAGTTTTTATGATATCTCTGTTAGACCCATAAGGGAGGCTG TGAGTTGTTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATATATATTTTATATAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-10183	127	C T ---	---	ACACTGCAGGCACTCCAAATCCTNACAGACATATGCACCTCGGAATCAACTCAGGCATGCACAGCAT CCCTGTGCTGGAGTTTATTTTAAAAAACAAACGCCCCAGTTATCACAGTTTCINTTTTTGTC/TCACC ATTTCCATAACAAAAAGAGCTACACAAAAATNGGGGGGAGANACTCTCTTTGGAGACTGACACATT TGCAGAGGGGTCATGAATAATGATTCCAAA
FB25G10b	109	A G ---	---	TCCCTCAATGACAGATGAACATAATTTCTCTGGGTAAGAAATACCTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAAATGGA(A)GJTGATTTTAGATCCTCCCCAG TGACAAGTAACTGAACTGACCATATTTATACATAAAATGGAATGTAAGAACCCTATTTTGGATATCC CGGAC
FB25G10	109	A G ---	---	TCCCTCAATGACAGATGAACATAATTTCTCTGGGTAAGAAATACCTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAAATGGA(A)GJTGATTTTAGATCCTCCCCAG TGACAAGTAACTGAACTGACCATATTTATACATAAAATGGAATGTAAGAACCCTATTTTGGATATCC CGGAC
IB3071	102	C A ---	---	ACAA CGCTGAACCTTCCATAACAGTCAATGGTACAGTCAACATCACATGTACAGAACACACAATTTA GATGAAC TGAATTAAGNTAAATAAAATAAAAT(A)CAATTTTCAGNAAACAAAAATCAAAAC ATTAAGN TCCCTGNATATCTTAAACCCCTAATGAGATTTCACCTGGNCTCAAGTCATTTTGTAGTGA GGCATTCACATATGACCCTATTAACCCAGTCTAGGGATTCTG
NIB551	161	C T ---	---	CGTCC TTTCC TTTTGAGATTGCAATTAAGTAGATAATATGAGAGAGAACTGACAA TTGGGTTGTCCC TACTGAGCTTGGGGCCAGGTGTGACTTAGGAACCCCAATCCACCAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGGTCTGTTGACACACATACATGCGGCCATTGGTTGATTTCAGCTTT GCAAGCAGCGGTAGTGAGAAACCAAAAAGCTTGTCC
S72904	51	G T ---	---	AGCATAGAAAGTGATTATATTTTAAATGGTTTCAAGTGAAGTTCCTTTG/JAATTTGTCAGTTTC ATTCCTGGAAAAATCTTTTGAGTTAAATAAGGATCCTAGGACAGCACCTCGAACTACAGGCCCTAAA GAGAAATTCCTCAACCAACAGTGCTGTAACCTCCCTCTTCTGTCAATTTGGTTGTCTTTAAATA TTGCAAAAGTCTGATGCTAAACAGTATTGGAGTGTTCAGTGTCTGTA

UTR	115	CT			TATCTTTTATCCTGGGGCCACAGTTCTTGATTATTCCTCTTGTTAAAGACTGAATTTGTAAACC CATTAGATAAATGGCAGTACTTTAGGACACACACAAAACACAGAGCTTACACCTTTTGATATGTA AGCTTGACCTAAAGTCAAAGGGACCTGTGTAGCATTTTCAGATTGAGC
ESTC1	33				CCCTGTAGCAGTCTCAGCCTCCTCTACCCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37				GCTACTACCACGGCTGCTCGTTTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21				GCCATCAAAATTTCTTCACANTCAATACTGTTGAACAACAAGATAACACATCTTCTTGCTCATCCC ACTTGAA
ESTC107	20				TGCTGGCTCACTTCTTCACANGCTGTATTACCTTTCAGAGCTGAGTGAGGCTGTGCT
ESTC109	35				AAACCAGGAAGGCCCTGCCCGCAGAGGCACATGNACAGGGCAGTGCACAGTGACC
ESTC110	23				AACTCTCACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37				AAGGACACAGTGTGCTGACAAGGTGACACTGAACANAAACAGTTTTCTTTAATTGTAAAGCGGG CATCG
ESTC117	24				AATTGGCTCTTCTCCACATGATACNTAAGTTCAAGGTCCTCAAAAGTTCTATCACAATTTACAAAAAGC CTCCA
ESTC119	24				TGTCAAGCAGATCTTGAGGGTTATNGTTAAGCCCTGATAACAGCCTCTTT
ESTC122	34				GACAAATAACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21				GAAGCCAGTATGTTGTGGCAANATTCGAGAAAAACACTGAAAAA
ESTC128	42				GCAGAGGCATCAGATAAGGCCCTCAGAAAAGCCCGCCATCATNTCCATGGGACCAGGCTGGCTCAA TGTGGAACCTGG
ESTC129	20				AGTCACCATGCCAGCCTAGNATGAGTTTAGTAAGATTTGGTTATGCTGGGGAG
ESTC13	46				GTGTATCTGGGCTTCATGGGATGCATAAAATTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA TCAGAAAA
ESTC130	49				GCCTGCTCACAAGGTAGACAAAAACATAAATCTTCAGGAAAAATGAAACANGAGAGCTGAAACAAT CTACACCTGAATG

ESTC132	30	---	---	---	GGTAAAGTCTAAATTACTGCCTTAGCAACNCTAIGTTGICAGGTTTTCTGCTGCA
ESTC137	21	---	---	---	CCAGTTTGGCTTCTGTCTCTCANAGTCTCTCTCCATGTGGCAACA
ESTC139	45	---	---	---	AGGAGCACAGCCTAAGGACATGAAGGTCAGAGTTTCTCAGAGAGNGGGCTGGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	---	---	---	CCCATTTGGTTCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTTCCCTTGCATGGTTTAGAAAGC TTGCCCTGGTG
ESTC142	72	---	---	---	CCTAGGCTCATAACAATACAGTCTCAATACAAAAGACGTAATACTATTTTATTCATTTTAAATC AAAGANACCATTCCTTCTTAAACAACA
ESTC143	29	---	---	---	GTTTACGAAAAGTACTGAAATGCTATTANTAGCTGAATTTTGATTTCTCTTTTG
ESTC144	26	---	---	---	AAATCCATATTTTCTTGACATGAGGTNGCTTTTITAGCAGCATTTTCGG
ESTC146	20	---	---	---	CATGTCAGGATAAGGAGCANACACCAGGATTTATACACGGTGGCAGCG
ESTC148	42	---	---	---	TCITTTGGTTGCTACACAGACACTTAAGTACTGTATCGCTGTNATGACGGCGCTGTGGAGGCCCTG GGGGTGGCTGGCGCTGTCTCTGAG
ESTC149	28	---	---	---	TCAGTTCAITTTTGCITTAAGAGTTANATACCATGAGACACACAGTTCTGG
ESTC15	28	---	---	---	GGATTGTAATATTGCCAGCTTTGTAAAGNCATTAAAGCAGAAGTTTCTTCAGTGATCTT
ESTC150	20	---	---	---	CCAGGAAAACAAAGCACACANACTTATAGAATACITTTGGTTTAAAAATTATTCATAATCAATATT AAACCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49	---	---	---	GAAGCTAAGGCCCATTTTTTTTCTTTTAAATACAAATCTACTGGTGTNAAAACCTCAGAGCTTAGGA AACACAGCC
ESTC155	37	---	---	---	TTTTTAATTGACAACTCAATCTCTACATACATACAGTNTGCACGAATTATAAGTGGATCAACAATT ATATTATTGATACAACTCATGAGCATTTTACA
ESTC156	32	---	---	---	GCAGCATTTGTGACAGGAGCGCAAAACAANCCCTGGCTGCCCTGGGATGGAGCGGGGGCGCTCA CCACCCTGCAT
ESTC158	35	---	---	---	ACCAAGCCCTGGGATTTACTGTCTTGATGACTACANGGCTTTGCACAGTCTGAGATGCTTCAGTGTGC AA
ESTC159	31	---	---	---	AGCTGGCAAGAGACTTCTTGAGGCACATCAGNTACGTTGGTCAATTTAGGCGACGGTCTGGTTCTGCA GCTTTGAAAGG

ESTC16	23	---	---	---	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCACAGTGATCATCAACCACAAAGGACAGGTT TTCTAGCATTGCTGGTGAGTGGGGGCTGAGCTGGGNGCAGTGCGGAGTGTCACCTGGGCCGTTTG GGACTGGGTTGA
ESTC160	38	---	---	---	
ESTC162	36	---	---	---	CTCTTCGTCGGTTTGCAAGTTGCTGTTGTTTCCAGNTACACCAGTCAGAGCTCCACAG
ESTC164	31	---	---	---	TCATTCTCCATAGAATATTGGTTTTGTAAACANCGAATACAATCCAATATATAACATTAAAAACAATCC GATACATACCA
ESTC169	22	---	---	---	GTCTCTGGTGTGCAGGGAATCANITTTGCTGGATTAGAGGAAAGTGCCCGCTGTCTTCCATGACTT
ESTC176	23	---	---	---	CACCTCTCCCTTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA
ESTC177	42	---	---	---	TGGGTGGCTCTTTAAATACCTTCCATTATATTTTCAAAATTTTNCITTTATTCIAATTAATAACCTTTTAT TCTCTTTATCCCATAAAAGGCAACCA
ESTC18	29	---	---	---	TCAGACACTGCCGACATCAGCATTGTCTONTGTACAGCTCCCTCCCTGCAGGGGCCCTGGGAGAC AACTGGACAAGA
ESTC181	21	---	---	---	TAGGGATTCCAAGTTGCCTGNNITTAATATAATACATATTACAAAAATTTACACAGCTCATGCATAC CA
ESTC186	43	---	---	---	GCTTGACTAGCGAGGCTACATCACAAATTTATAAAGTGCCAGATNAGTGCTAATTTGTCATTTCAGCTTG ATTTTCACTCA
ESTC187	24	---	---	---	ACCATGATTGCCTCACACAAGCATNATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGGCTGG TCTATTAAACAGGGTTATGTCACACCNTGTCAACCTCAAAACAGATGATACATCATCTTGTCTTCCAT CTTGC
ESTC189	27	---	---	---	AAAGTACAATCCAGTATATGCAGAAAGNTACTCAGCATCACACTCGTGATCA
ESTC196	42	---	---	---	TCCTCAAATACCACTTTCCCTTAACCTTATCAGTCTAGTAAGCNITTCAAAGGAGGAAAATGGGTTAC CTTTCAGGGG
ESTC197	26	---	---	---	ATCTCCAGTGTCTGCTGCCTCCTCCNGCAAAGTCTCCACAAAGCACA
ESTC20	33	---	---	---	AAGATTAGGACAGACCGGTATAGTAAGCTCTGNGGAATCCAAAGATCTAGAGGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC200	44	---	---	---	TTTGGTGAAAAATCCCAATATATGAGTTTAAAAAATAATCATTTANCATCATTAAACAGTACTTTAAAT CAATTACTCTTTTGCCTGCAACAG

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ESTC201	35	---	---	---	TCCTACITGGGAGTTTAGCAAAACATTTTAAANCCACATCCAACAGATTGGTT CTGCTGAGGGAGGACAGCGNCGCGGCTGGTGGCCGCCAGAAAGGCTGGCGTGGATGTT CGAGATGAGCC
ESTC202	22	---	---	---	ACACTTAACAGGTTAAATATCCAAATNAATTTACTGCACTTTTGAGAAATTTATTTGTGCTAC AAGACACGTTGCA
ESTC203	27	---	---	---	TATAGCCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGATAANAGCAATAACTATTGTTTAAAGC CTAAGAGTGAAAA
ESTC208	43	---	---	---	GATGAAGTGGCTTCCTTTGGCGAAGGATNAAGAAGTGAAGTGACGGTGACCTGTG GGTAACTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGCGGCTTCAGAGCAGAGGGCTTGGT TCAAGTC
ESTC210	29	---	---	---	CTCCAGAGTCCCTCTCTCANACCAGGGGCGAGGGAGTTAGGGAAT TGGCAAGAAATTTATTTACACTAACAAATTAATTTAATCAGAGGTATNTTAGATTGGTCAGAAAA CAAAAGACCA
ESTC212	27	---	---	---	TTTTGTCAGTAAATGAGCAATACACTGANTGGAATCTGCATGATTAATAACATTAACAAGTTCAT AAACACACCCCA
ESTC214	21	---	---	---	GTACACATCTCTGGGGTGAGCACACAGCAAAANGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG GCAAAAGGAAGC
ESTC216	49	---	---	---	TCATTGAAGAAATATGGGTTTTATCTTATTCTAATTGNGAGAATGCTTAATGTCACAGGCTACA TAAGGGCC
ESTC217	28	---	---	---	CITCTGAAGCCCAAGAGAGGGGCGAANGTAGTCTCTGATTAAAAAACAGAAAGGGGAGGAGGA CGAAGGTAGATTTCCCTCACATATTACAAAATACACANAACACACACACACACACA
ESTC219	32	---	---	---	TGCACGTGTACTCCCCAGACNGAGAGCTTACATACCATATAGAAAGAGCATAAGTGTCTCAGAAGGA ATGTGTAGGATCG
ESTC220	20	---	---	---	TTCTACTTTATTTTCATATTTCCACCACNATAACGACTCCTTTAATTTAACTAAAAAACCATACAGGGT TCCTGAAGGG
ESTC221	27	---	---	---	GCCTTCTCCACGAATTTGAAAGACATATTGGCTGACCTGATACNTAAGGAGCAGGCCAGAAATTAAGA CAAAAGGGTAGTCATATTTCCCANCAACAGCATGATAAAATAATTCAAC
ESTC222	27	---	---	---	
ESTC223	27	---	---	---	
ESTC224	37	---	---	---	
ESTC225	20	---	---	---	
ESTC226	27	---	---	---	
ESTC227	43	---	---	---	
ESTC228	24	---	---	---	

ESTC28	23	---	---	---	GAAGAGCTGGGCACGCATCTGACNTTCTTCCCTCTATTCTCTATAAAATAAAAGGAAGCAGAAATCT CC
ESTC3	20	---	---	---	CAGACATGACCTACCGTCCNGGCCCTCAATTCATATTTATCTTGAGCCGCTTGGTCAGGTTTGAT TCGCACACTOC
ESTC31	32	---	---	---	ACAGCCCCACAGAACCTATTGTAAACAATATTNTCAGTCGGTGATCATTTGTAATATACAAACAAAG CAATTTCTCTCAGA
ESTC33	25	---	---	---	AGCACTTCAGCTCCTTGACGTTGNGGACCAGGGAACCTCCGGAA
ESTC39	26	---	---	---	AAGGAAGGGAACCCACCTGGGCTTNGGTTCACAGAACCTCAGAGCCCTGGGCATTA
ESTC4	23	---	---	---	CCACTGAATCACACAACATGGACNAATCTCAAATCATTTATGCTGATGGAAGAAACCATTT
ESTC40	22	---	---	---	GGCATGCTAGACAGAGGCATTANTTTGAAGATCTTTTAAAAATATTTTGACTTGTTCCCTCTCAC
ESTC45	37	---	---	---	TTTGGAGGTTTGTGCTGGAGTTTGTCTTTTGTAAACNCTCTCATCATCAGAGGCTATATATAA CTGTCCGTGGTGAGCCCTGCCGCTGTCCCATGGGCCAGGGAGCCACTGGTGCAGNCCGGGCAGATG TTTACCTGT
ESTC50	56	---	---	---	GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGGAGGTGGCAGGAAGNAGTGGAGGGAAGGACACCA AGT
ESTC56	45	---	---	---	AGTGGGCCCTCCAGTCCCTCTCTGGGCACAGATCCACCAGTCTGCTC
ESTC57	20	---	---	---	CAACACAAAAAGTGTGAGAAAAAACTTCTCAAAATNGTTCAGACTTCAGGAAAAATGATTTCC ACATGGTAAGGCC
ESTC59	38	---	---	---	TCTGCAGCACTTCACCTACCAATGAGCNTTAGCTACTTTTCAGAAATTGAAGGAGAAAAATGCATTATG TGGACTGAACCG
ESTC6	27	---	---	---	AGTGATTTGGCTAGGGGTGTTCTCATCTGTGAATTCACAGCGCAATGACAGCANCCTCTCTCCC ACCCACTCAAG
ESTC61	57	---	---	---	ACAGACAGCATCACACCANAGGGCCACCGGAGGTGGGGAGACGACACTTTTCCCTGGGAAA GGCAGCTCTAATC
ESTC63	20	---	---	---	GAGAGGCTAGTCAGGAGGGAANACCCTCAAGTTTAAATCCCACACTTACTTACTGCTCATCCGT CACTTTCGCTAA
ESTC69	20	---	---	---	AGTTTCCCTAGAGCTGTGGGCCAGATAGCTGTCTGAGTTGCANGCAGATGGAGATTTGGACACT G
ESTC7	45	---	---	---	

ESTC72	37	---	---	---	GGGCTTCCAAAATGGGTATGGGGCCAGGAGGCTGGCCTTGGCGTGACGCCCTAAAAAGTGTGACC
ESTC74	49	---	---	---	AACAAATTCACAGCTACAGGAAATCTAGAACAAAATCAAATATTCATCAGCTTGGGTTGAAAAGTTG
ESTC77	40	---	---	---	GAAGA ATGACTTTCCTGTCCTCATCGGAAACCAGAGTTTCCCAGGNGAGCCCTTCCTATCTCGGGTTA
ESTC81	20	---	---	---	GGCTCAGCACAGGGATAAGANCCCCACCTCCGCATGTCCOCAGAGGGCAGCACTCCAG
ESTC82	25	---	---	---	TTTCAGATGATGGGGTCTGAGATGINTCCTCAGGCTGCATCAGCTGTCTTCAGTCTCCAGAACAGAAA
ESTC83	53	---	---	---	GAGCCTGACCCA CAAAATCAAATACACAGATCCAGATATGTGAACCATATACATATCTATACANCCATTATTTAGAC
ESTC85	28	---	---	---	TTTCACAAACCT TTTAGCTGCTATACCAAGTTTCCATAAANCTGTCTGCTGTTGGGAGGCTACAGCCTGACCACATTTC
ESTC89	22	---	---	---	TTTGC ATTGCAAGGAAGTGAACGTGNTCAAACAGAAAATGGTGACAATGA
ESTC90	33	---	---	---	CTGGTCTCTCGTCTGGCATTCTGCTCCTCCTCNGGCCAGTGCTCCACCCCAAGTGTCTTCCCGATGAT
ESTC93	29	---	---	---	CTCCCCCTCCTCAGTTCACAGTGGAGACTANGGAGATTGAGGGCAGGATCC
ESTC95	32	---	---	---	GCACGTTCTTTGTTCTCCTCTCCAGAAAGTTGNAGACGCTATTTAGTTTGATTATCTGTCG
DWU-100	127	C	T	---	AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCCTAAATTC GTGGATCTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCTTCTGACTGTCTCCAC/C/GCCAG ATTCTTATCAATGATCTTTCACCTAAGAAACAGCAAAAGATTCTGGCAAGCACACGATCTAGAGATAC ATCTTATTGCGATTTTTCACAAAATCAAAGAAGAAAGGCTTAGCTG
DWU-177	77	A	G	---	TTCCATCCTAGATATCTACTCAAATAATTGAGACAAGTGTCAAACAGAAAGACGCTTGCTGAA TGTTTATGGC/A/G/GCCCTATTACAGTAGCCAAACGATGAAACAAACCCCAAGCTATATATACCA GATGAAAGGATAAACAAAATGTGGTCCATCCATACAAATGGAGTATTACACAGCCATAAAAAAGGAAT GAAGCAGTATCCCTACTACACTGTGGAT
DWU-286	213	A	C	---	CAATACCTGGACTATCAACCTTGTGCTTAATCCCTGCAGCATCAAGGTTATCCATCTAAGTGAC ATTTTGAATTCAGCGGTGCCACCAATCATGCCAGCTTCTGTCAATGATGAGATATACATTT ATGCTGACCTTCCCTCAAGACTGATTTTCATGTCTGGGACTTACAATATCTCAAGGAACAGCAATG TCAACAGGAC/TGGGAAACCAGCCCTATCTGAGTCTCGGCTCCCTCC

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DWU-252	94	A G	---	---	AGTATACAAACATTTAAGCTGTGGTCAAGGCTACAGATGTGCTGACAAGGCACTTCATGTAAAGTGT CAGAAAGGAGCTACAAACCTACCCCTCA/GJTGAGCATGGTACTTGGCCCTTTGGAGGAACAATCGGC TGCATTGAAGATCCAGCTGCCTATTGATTTAAGCTTCCGTGTTGAATGACAAAGTATGTGGTTTTGTA AT
DWU-330	85	C T	---	---	GAACATTCCTCTGCAGCACITTCACCTACCAATGAGCATTAGCTACTTTTCAGAAATTGAAGGAGAAAA TGCATTATGTGGACTGA/CJGACTTTTCTAAAGCTCTGAACAAAAGCTTTTCTTCCCTTTTGCAA CAAGACAAAGCAAAAGCCACATTTTGCATTAGACAGATGACGGCTGCTCGAAGAACAATGTCAGAAA CTCGATGAATGTGTGATTGAGAAATTTTACTGACAGAAATGCAATCTCCCT
DWU-370	231	A G	---	---	GAATGTTAATTGGGCAGGTGAAAAGGTACAGATGTGCTGAGCAGACCITTTGGTTTTAAAGAG AAGCATATTTCCCAACAGGCAACTGTAGAGGCCAGCTGAAGAGTAAAGGAAAAGGTCTGAGG ACTGAGCCTGTGGCTGGTGGAAAAGGTGAATGTTGAGGGCCCTTCACCTCCATCACAAGAAAAGTC ATTAGACGGTACCAATTGAGTGTCTGTTCTT/GJGCACTATTTCCCTCTGTC
DWU-1537b	89	A G	---	---	CTCTTAACITTCAGTTCCTCATCTATAAGATAAGGATTGAGTTGATCACAATAGTCAAGTAATC CAGGACCAGAAACCCAGGAGC/GJTGAGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCCCTGAACACAAAGAAATCCAGTAAGCAGCACACACTGGCTGA
DWU-1537a	52	C T	---	---	CTCTTAACITTCAGTTCCTCATCTATAAGATAAGGATTGAGTTGATCA/CJTAGCTCAGGTA ATCCAGGACCAGAAACCCAGGAGCATGGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCCCTGAACACAAAGAAATCCAGTAAGCAGCACACACTGGCTGA
ESTD-ADAb	196	C G	---	---	ACCATCTTACTATGGCAGGTAACTCCATACAGAAGAGCCCTCTCTCCCTGGGATTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGGAATCCAGGGTCACTGTCTCTCCCTGCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGGCCCTCGGCACTGAGCTG/CJGAGA CCCGCAGACCAACTCCTGAGCTTCTGGGCCCTCTGAGCTCTGTCCTC
ESTD-ADAA	184	G A	---	---	ACCATCTTACTATGGCAGGTAACTCCATACAGAAGAGCCCTCTCTCCCTGGGATTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGGAATCCAGGGTCACTGTCTCTCCCTGCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGGCCCTCGGCACTGAGCTGCAGA CCCGCAGACCAACTCCTGAGCTTCTGGGCCCTCTGAGCTCTGTCCTC
ESTD-ANT1	160	T C	---	---	TCTCCTGTACTTCTACTCCATTAGTTCAGGTCAAGTCAAGAACTGGGGCAATTACCAAGTAATTCA TGGACTGCCCAACTCGGAACAAAGGGCGAGTGGAGCAGGAGTATTATGCTACGGGGTTACCTT TTTTTATGGAGGACCGAACTGAGGCT/CJGAGCTCAGATCATCCTGT
EST10398 2b	168	A G	---	---	TGCCTGGGGTGGCAAGGCTGCAAAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGATGATGTTTACATTTGGGGCTTGACTTTCCAAACACGGAGAAG CATGTCTTCTCGGGCCCAAGAAGGTATCTACC/GJATAGTGTCTATTAGGCATTG

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EST10398 2a	147 C T ---			TGCCTGGGTGGCAAGGCTGCAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGATGATGTTACATTTGGGGCTTGACTTTCCAACACGCGAGAAG CATTTGTTTCTTTC/TJGGGCCAAGAAGGTATCTACCAATAGTGCTATTAGGCATTG
ESTD-C7	14 G C ---			ATATCGTGGCCTTA/GC/TTACCTAGAGCTGGACAATCCTGCTGGA
ESTD- D4S95	90 T C ---			CTTTCATGCACGATAGGCTTTCTCTACTAATCACAGAAATTTGAGAAGAGCAAAACAACCTTTCAAGG ATAATGGGGCAATCACTTCTTTT/CJCTTCTTTAGAGTCTACCGG
ESTD- GPPK2L	38 G A ---			AGTCTTCATCTGGGTGCCAGGTAGATCCCTTTTACC/GA/JCCGAGAACTGCTCGATATC
ESTD- HRASb	82 A G ---			CTGGGCTGCCCGCAGCAGCTGCTGGCACCTGGAGCGGCGGCGCAGGCTCACCTCTATAGTGGGTG TATTCGTCCACAAA/A/GTGCATCTGGATCAGCT
ESTD- HRASa	37 C T ---			CTGGGCTGCCCGCAGCAGCTGCTGGCACCTGGAGCGG/C/JGGCGCCAGGCTCACCTCTATAGTGGGG TCGTATTCGTCCACAAAATGCATCTGGATCAGCT
ESTD- NRAMP	81 A G ---			GGAGCGAGGAGGTGGGGAGGGGCTGCTGCTCCAGGTCCCACAGACCAGAGAAGCGGCCTCAGTG TATCCCCACCCCCA/A/GJTGCGGCGCTGGGAGATGAAGAGGTTGATGCAGGT
ESTD-OTC	18 A G ---			GTGACCTTCTCACTTTAA/GJAAACCTTACCAGGAGAAATTAATATATGCTATGGCTATCAGC AGATCTGAATTTAGGATAAAACAGAAAGGAGGATGTAACA
EST36751 7	36 C T ---			CCAGTGTTCAATTTAGCTTTGCAGGTTTAACT/C/JGATTACTTTTCTATTCAAATCTCTGTGA AAATTGAATATGAACCTAGTTTCTGATCTATGTTTCAAGTTAAACAG
ES140562	109 A G ---			CACGTGGAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAAATCTGTCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAGTTTTCACCTGGATGCATTAAATAACAAAT/A/GJTTTACCTTTTGAAAAATAA ATGAAGGATTTGACCTGCTTGGCTCTGGAAGAGATCCGTACCGTCCCTGACGTTTGAACAATACA GATGCTTCCCTTGAGCAGTTTTCAGCCTCCTCTACCCCTA
EST18288 3	121 C T ---			GCCTCTATACCCCTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGTGAGAA GATTGACAGGTTTCATGCAGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGA/C/JGGGAGCCAGT GTGGACAGCACCCCTGGCTTTCACACCTACGTCCACTTCCAGGTAAGGCAACCTCTCTGTGTGGCTC TGGCCCTAGGACTTAGTATCC
ESTD-AK- 168	31 C T ---			GGGAGTGACAGTAGACACCAAGGGGGGCT/C/JTACAGCTGTGTTCTCATGGAGGACAGGCTTCT GCTCATCTGG
ESTD-ALB	180 A G ---			AATCCAGCACCTTTAGGAGGCTGAGGCAAGGATATCACAGAGGTCAGGAGTTTGAGACCAGTCTGA CCAACTGTTGAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGATGGTGGTGCATGCCTGT AATCCAGGAGGCTGAGGAGGAGAAATCGCTTGAACCTGGAGGCG/A/GJAGGTTGTGGTGAGCCGA GATGGCACCATTGCACCTCCAGCCTGGCAACAAGAGTAAACCTCTGCTTC

EST70523 3	182 G T ---	---	TTCCGGCAGCCCCCATCTTGGCACCCCTGGTCCCCCTCAGGGGCCACCCCGGGACTCACCGCTCT CGCTCTCGGTAACATCCGGCGGGCGCGCTCTTGGACACATAGCTGGACCGTTTCCGTATAGGAGG ACCGTGTAGGCTTCTGTCCCGGCTTGGCAGGGGCCAGCCCTG/TJ/CAGAGAGGGGTCCCTGT GGTTGAGCTGAACACAGCTGTGGAGTGTCTCCACAGTG
ESTD- APO.2	101 C T ---	---	CCAGGTGTGGCACGTGCTGTATCCAGCTACTCGGAGACTGAGGCATGAGAATCTTTTGAAC CGGGAGGGGAGGTTGAGTGAGTGACATGCTG/TJ/GCCACTGCACCTCAGCCTAGGTGACAGAGC AAGACTCC
EST58707 7	112 C T ---	---	CAGTGTATCGAAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGGTTACAGGAGGCTTT AAGTTACGATCTTTGGCTCACATGAAGGCCAAATTCGAGAGAC/TJCTAGAAGATACACGAGAC CGAATGTATCAATGGACATTCAGCAGGAACCTCAACGATACCTGTCTGGTAGGCCAGGTTTATA GCACACTGTCACTACATTTCTGATTGGTGGACCTTGTCTGAAGAACCCTT
EST74167 6	137 C ---	---	AGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACCTGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGGGGCACGGCTGTCCAAGGAGCTGCAGGGCGCGCAGGCCCGCTGGGCGGAC/TJ/GAGGA CGTGC GGCGGCTGTGTGAGTACCGGGCGGAGGTGCAGGCCATGCTCGGCCAGAGCACCGGAGAGC TGGGGTGGCGCTGCTCCACTGCGCAAGCTGCTGAAGCGGCTCTC
EST43211 8	132 C ---	---	CGCTGTGTGAGTACCGGGCGAGGTGCAGGCCATGCTCGGCCAGAGCACCGGAGGCTGGGGTGGG CCTCGCTCCCACTCGCAAGCTGGTAAGCGGCTCTCCGGATGCCGATGACCTGCAGAAAGCGCC TGGCAGTGTACAGGGCGGGCGGAGGGCGCGGAGCGGCTCAGGGCCATCCGCGAGCGGCTGTG GGGCCCTGGTGGACAGGGCGCGGTGGGGCGCGGCTG
ESTD- ARSB	126 A ---	---	GGAGAAATGGAGCTGTGGAGGAGGCTCGGAGGGGTGGGCTTGTGGCAAGCCCTTGCTGA AGCAGAGGGCGTGAAGAACCGGGAGCTCATCCACATCTGTACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGTGGAAACCATCAGTGAA GGAAGCCCATCCCCAGAAATTGAGCTGCTGCATAATATTGACCCCAAC
EST36770 4	144 C ---	---	TGTAGCCAAAGTCACCTGCATCATCATTTGGCTGCTGGCAGGCTTGGCCAGTTTGCCAGCTATAATCC ATCGAAATGTATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTCCATTATGAGTCCCAAAAT TCAACCTCCCGATAGGCTGGGCTGACCAAAATATACCTGGGTTTCCCTTCTTCTGATCAT TCTTACAAGTTACTCTTATTGGAGGGCCCTAAAGAAGGCTTATG
EST26021 1	137 A ---	---	TAATGTAAGCTCATCCACCAAGAAAGCTGCACCATGTTTGGGTTGAGTGACATGTTGAAACCTGT CCATAAAGTAATTTGTGAAGAAAGAGCAAGAGAACATTCCTCTGCAGCACTTCACTACCAATGA GCATTAGCTACTTTTCAGAAATTGAAGGAGAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTTCTTCTTTTGAACAAGACAAAGCAAAAGCC
ESTD- BA511	29 A/G ---	---	GGGCAACATAGTGAACCCCATCTCTACA/G/AAAAATACAAAAATTAGCCAGGTGTGGTAGCAAG TGCCTGTAGTCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTG CAGTGAGCCAAAGTGTGCCACTGCA

ESTD-BCI2	116 A G ---			AGCTGGATTATAACTCCTCTTCTCTGGGCGCCGTGGGTGGAGCTGGGGCGAGAGGTGCCGTT GGCCCCCGTTGCTTTTCCTCTGGGAAGGATGGCGACGCTGGGAGAAGC/GGGGTACGACAACCGGG AGATAGTGATGAAGTACATCCATTATAAGCTGTGCGAGAGGGCTACGAGTGGATGCGGGGAGATGT GGCGCGCGCGCCCGCGGGCGCGCGCGCACCGGGCATCTTCTCTCTOCCA
ESTD-BCR	69 C T ---			CAGTGGCTGAGTGGACGATGACATTGAAACCCATAGAGCCCGGAGACTCATCTGCGCAAGA GA/C/TCAAAGAGGTGAGTCTGTGTTGCCGGAAAGGAGGAGGTGACAAGTAACCTAAGTGCCTTC AAATCAACCATCCGGTGGACACTGTGGCTGCCATCTGCCTGGCACA
ESTD-BCRA1aa	119 C T ---			AAGAAGAGAACTAGAAACAGTTAAAGTGCTTAATAATGCTGAAGACCCCAGAGATCTCATGTTAA GTGGAGAAAGGGTTTTGCAAACTGAAAGATCTGTAGAGTAGCAGTATTTCA/C/TJGGTACCTGG TACTGATTATGGCACTCAGGAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACA GAACCAATAAAT
ESTD-BCRA1bb	139 A G --- -			ACTAAATGTAAGAAAAATCTGCTAGAGGAAAACTTTGAGGAACATTTCAATGTCACTGAAAAGAA ATGGGAAATGAGAACATTTCAAGTACAGTGAGCACAATTAGCCGTAATAACATTTAGAGAAAAATGTT TTTAAAG/A/GJAGCCAGCTCAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCA GTATTAAATGAAA
ESTD-BCRA1cc	126 A G ---			ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGGAAGATAC TAGTTTTGCTGAAATGACATTAAAGAAAGTTCTGCTGTTTTAGCAAAAGCGTCCAGA/A/GJAGGA GAGCTAGCAGGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAGGTTTACCGAAGAGGGGCCA AGAAATTAGAGTCTCTCAGAAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
EST512120	122 A C ---			ATCCTGAGCTCGCCAATAGCTTCTGTTCTACTTCTCTCTCCACAAGCCCCAATTTCACTTTCTCA GAGGAATCCCAAGCTTAGGAGCCCTGGAGCCCTTTGTGCTCCCACTCAATACA/A/CJAAAGGCCCT CTCTACATCT
ESTD-C1R	40 A G ---			ACACAGGTGCTGGCACTGGGGTGGGATCCTCCTCCCT/JGJATTI GCTCCGGGAAGCACATTCTAT CAA
ESTD-C1R	40 A G ---			ACACAGGTGCTGGCACTGGGGTGGGATCCTCCTCCCT/JGJATTI GCTCCGGGAAGCACATTCTAT CAA
ESTD-C6	31 A C ---			CCCAGTCAGTTTGGGGACAGCCATGCAC TG/A/CJGCCTCTGTAGCCTTTCAACCATGCATTCCATC TAAGCTCTGCAAAAT
EST201182	119 C ---			GTTCCGAATCCTCCTCTGAAAGTGGCCGGTTTAACTGCTCATGACGCTGCGGCTGTGGTCCAGCT GAGTGAGGGGCTTGAAGCTGGAGTGGGTTTAGGACGCGGCTCTGCGTGCACTCCTAAGCTCT GAGAGCAAACTCCCTTGAAGCTGGAGTGGGTTTAGGGACGCGGGTCTCTGCGTGCACTCCTAAGCT CTGAGA
EST530186	67 A G ---			ACAAATCCAGGTCACACATTTCCAGAAGAGGAGGGGTGGTCAAGTGAAGCTGGGTAGGTCCAGTAATCCA JA/GJGGATTCAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC

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ESTD- CB22	119 C T ---			GGCAAGTTTTATTGATAGAGAGGAAATCAATAATGGAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGCAGTGCCACCATAGGG[C/T]GGATACAAAAG ACAGGCAAGGAAGGGGTAGAACCATCAAAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGACCT AGTAACATAATTGTGCTTCATTATGGTCCCTTCCCGGCCCTTCTCTCACACAC
ESTD- CB23	136 C ---			TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTC TTCATTATGGCTTCCCGCCCTTCTCTCACACATACAGAGCCCTACCAGGACCAAGACAGCT CTCAGAGCAACCTAGCCCCATTACCTCTCCCTTCCAGAGGACCTGAAAACGTTGCCACCCGA GGTCGTGTGTTGAGCCATCAGAAGCAGATCICCCACACCCAAA
ESTD- CB24	145 A ---			ACCAGGACCAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTCTCCCTTCCAGAGGACCTGAA AAAGTGTTCCCAACCCAGGTGCTGTGTTGAGCCATCAGAAACAGAGATCTCCACACCCAAAAG GCCACACTGGTATGCCCTGGCCACAGGCTTCTACCCCGACACGCGGAGCTGGTGGTGAATGG GAAAGAGGTGCACAGTGGGTACAGACAGACCCGCGCCCTCAAGGAG
ESTD- CB25	146 A G ---			GTTTTCTTCAGACTGGCTTCACTCCGGTAAGTGAGTCTCTCTTTCTCTCTATCTTCGCCGTC TCTGCTCTCGAACCAAGGATGGAGATCCAGGACACAGGGCGTGAGGAGGCCAGAGCCACCTG TGCAGAGTGGCTACATGCTCTGTTCTTGCAACAGAGTCTTACCAGCAAGGGTCTGCTGCCC ACCATCTCTATGAGATCTGTAGGGAAGGCCACCTTGTAIGCCGTG
ESTD- CB27	125 C T ---			TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAATAGGTAACCAATAAAAAAT TGTTGTTGGCCCTGGTTGCAITTCAGGAGTGCTGTGGAGTTTCTGCTATCACTGAC[C/T]TATCTTC TGATTTAGGGAAGCAGCATTCCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCAAATGCT GCTTCTCTCTATCTCTGATGGAAGTCTCAACACCATTTCCATACC
ESTD- D4S338	59 A T ---			TTTTCTGTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGA/TATGTA TTTCTTAACAATAAACTTGAAGTCCAAATTAATCTCTGATCCATGGACTGCAGAAATAATGTTA TTTTAGCTGTCAGAAAAACAATACTATCTTGCAATGTTTCATCAGAGCCCTGGGTGACCAGGTGA TTGCCAATAAGCAGTAATTTTGAGAGGAACTTGTITCAATGCACTAG
ESTD- CYP2D6	61 A G ---			CAGGCCAGCGTGGTGCAGGTGGTCAACCATCCCGGCAGAGAACAGGTCAGCCACCCTATGCJAGJCA GGTCTCATCATGAAAGTCTCTCAGGGTCCCTTGGCTGAGCAGGGCCGAGAGCATACTCGG
ESTD- D11S1873	40 A C ---			AAAAAACACATTTAACACCTTTTCAATCATATACACCATATACJATTTCCATTTTCACATAAGTCA GTTTGAGCTGAGTTTCCAAATTAATGCAATCTAAATGTCATAACTGATTAATGCAAGTTCAACAG ACAACTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATTATGCCCA TATCTCATGTC
ESTD- D17S33b	169 C T ---			CATCCCCAAGCCCATCTCTTAGCCACTGGCATTTTGGCGCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCTTTGTAGTCCATGGGAAAGGCTCTCTGGGGCGGTG GGGTTGTGGCTATGTGGTGGTCTTGTGTAGJCTJGGGGGCTTTGGTTTCAGTTGCATATTGCGTT ATTGCAGATTGCTTGTCTTCCACCTTGAGCGAGCCTC

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ESTD- D17S33a	75 C T ---	---	CATCCCAAGCCCATCTCTTAGCCACTGGCAATTTTGGCCCTCTGACAGATACACTCAGGGCCGT CATGCTG/C/TACACATCAGGGGGGCCCTACCCCTTTGTAGTCCATGGAAAGGCTCCTCTGGGGCG GTGGGTTGTGGCTATGTGGTCTTTGTGTAGACGGGGCTTTGGTTTCAGTTGCACATATC/C/GTT ATTGCAGATTGCTTTGCTTTCCACCTGAGCGAGCCTC
ESTD- D18S8	133 A G ---	---	TTTGAGACCACCTGGCCAAACATGGCGAAATCACATCTCTACCAAAATTACAAAATTAGCTGGGTGT GGTGTACATGCCCTATCGTAATCCAGCTACATCGGAGGCTGAGGCAGGAGAAATGCTTGAACCC/A /GJGGAGGCAGAGCTTGACGTGAGCCAAAGATCACACCCTGCACCTACAGCCTGGGTGACACAGTGGA GACTCIGTCTCAA
ESTD- D3S11	44 G ---	---	AACTGATTAGAACCTGAAAATACATATTTATCTGAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTTCATCATTAAAAAATCCAAATAAGTACACTGTATAAAGAAATTAACAGAAATCATTTGT TTATCAAACTATTTATCACTTATTTATTTGTTAAGCCATACTAAATCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	37 A G ---	---	AGGTTCCACATTATGCTGATGTTTGTGATGTTTCQJ/GJGGAGCCTTGATGTCATTTCTGATCTCCT CAGGTATCCACCTTGAGACGTACTTTTCAAAAACCTCTACAGCCGTTGTTGTTAATTCAAGGT TGAACATAAAGTA
ESTD- D3S2b	247 C T ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGTAGCAGAACATTTCTGTC TGAGTCTTATTCAAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCTC AGAAGTGAACATACTGCTCTCTAGAACCCAGAGTCATCTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGTCTTTTATTGGAAGGATGCT/TTGGT
ESTD- D3S2a	248 G ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGTAGCAGAACATTTCTGTC TGAGTCTTATTCAAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCTC AGAAGTGAACATACTGCTCTCTAGAACCCAGAGTCATCTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGTCTTTTATTGGAAGGATGCT/TTGGT
ESTD- D7S399	83 A G ---	---	TGAATCTTAAATTGCTATCTCTACAAAATGTATAATCTGTAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCJ/GJGTCTCTACATCATCTTTTCAAAACATTTTCATCCATGGACTCCATAC TAGAATATTTGAAGAAACAAACATGACAAACATTTTTC
ESTD-DMb	146 A C ---	---	GTGGGGACACCGAGGGCTCCAGGCTGGGGCTTGACGTTGGCTCAAGCAGCTGCTCGGGCTCCACT TCCATGGGTGGGGCTGGGACCTCAGTCTCCCTGGGAGAGGAGGAGGTGGGAGGGAGACA GAATGCTGATTJ/VCJCTGGTGGAGAACCAAGTCTTGGCCCTGTGGGTAGGGGACGCTGCTTCCAAG ACCTCCTGATTTGAGGAAGGGGAGCAGCAGAGCGAAGAGAACAGAT
ESTD-DMa	66 C G ---	---	GTGGGGACACCGAGGGCTCCAGGCTGGGGCTTGACGTTGGCTCAAGCAGCTGCTCGGGCTCCAC/C GJTTCCATGGGTGGGGCTGGGACCTCAGTCTCCCTGGGAGAGGAGGAGGTGGGAGGGAGAGA CAGAAATGCTGATTATCTGGTGGAGAACCAAGTCTTGGCCCTGTGGGTAGGGGACGCTGCTTCCAAGA CCTCTCTGATTTGAGGAAGGGGAGCAGCAGAGCGAAGAGAACAGAT

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ESTD- DRD1	154 C T ---	---	TCCCCAGCCCTATCGGTGCATATTGGACTATGACACTGACGTCCTCTCTGGAGAAAGATCCAAACCCATCAC ACAAACGGTCAGACACCCCAACCTGAACCTCGCAGATGAATCTGCCACACATGCTCATCCCAAAAGCT AGAGGAGATTGCTCTGGGIC/TTCGCTATTAGAAACTAAGGTAC
ESTD- DRD2	144 C ---	---	TCTGCCCTTTGGTGAGGAGGCTGCCCGCGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGGACCCGGTACAGCCCATCCACCCAGCCACCCAGCTGACTCTCCCCGACCCG TCCCACACAGGTCTCCACAGCACTCCCGACAGCCCGCCCAACCCAGAGAAATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGAACCATGCCCAATG
ESTD- DRD3	109 C T ---	---	AAGACGATGCCAGGATAGCGCGCAGTAGGAGAGGCGCATAGTAGGCATGTGGCGGGCCTGGCTGG CACCTGTGGAGTCTCTGCCCCACAGGTGTAGTTCAAGTGGC/TACTCAGCTGGCTCAGAGATGCC ATAGCCACAGGGAGGTGGTGATGCCAAGGGGCTCTCTGTAGGAGA
ESTD- ERB2	93 C T ---	---	TCTTTCAGGATCCGCATCTGCCCTGGTTGGGCATCGCTCGCTAGGTGTACGGCTCCACCAGCTGG GGTGAGGGGTGGTGGTCAGTGC/TJGGGGGGCGGTGCAGACCCACCGGGCTGGGAGGACTTCA CCCCGCTACCTCCGTTCTCTGCAGCAGICTCCGCATCGTACT
ESTD- ETS2	43 A G ---	---	ACTCACAGTGCCTTTAAGTGAATAATGGTCGAGAAAGAGGCAC/CAG/GGAAGCCGCTCTCGCGCCTG GCAGTCGGTGGGACGGGATGGTCTGGCTGTTGAGATTCTCAAGAGGAGCGAGCATGCTGTGGACACA CACAGACTATTTTAGATTCTTTTGCCTTTTGCACCCAGGAACAGCAATGCAAAAACCTCTTTGAG AGGGTAGGAGGGTGGGAAGGAACAACCATGTCTTTTCAAGATTAGTTG
ESTD-F9	111 A G ---	---	AGATCCTGATGATTTTTTCCCTATTTTTCTAAATGTTTTACAGTTTGAAGTTTATAGATTTATGCCCA TGCTCCATTTGAGTTAATATTTGTGTAAGTATGATGTTTAA/JG/GTCAAACTTCATTTTTTTTTTCC ATAGGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAAC
EST68787 5	144 A ---	---	CTTCTATGGGATTGACTTTATTTCTCCATTGCTTACCTTTTACAGGTGTTAATATAGTGAAAAAG GAAGCTTGACGCTCATGACAAATTTGAAGCTGACAAATTACAAAGAAAGGAATAATTCACAGTCAA AGAATCAAGCACTTTTCGAACATTGAAGTTGTTTTGAACCTTGGTGTACCTTTAATTACAACTAG CAGACGGAACCTGAACCTCAGGGTAAGAAAT
ESTD- GCDH	200 C G ---	---	CGCAGACCGGTGAGTGTGGGGTGGGAGTGTGGAGGGAAGGAGGGAACCTGGGGGTTTAGGGACT TTCCGGGGTGACTTTCCCGTTCTGTGCTTGACAGAGAAAGCGGGAGAACACAGAGCCAACTGGCTAA GTGTAAAGGACCTCTGGTGCACCGTGTGTTCTGCTGCCCTGTTTACAGCTGTCTGTCTGCCGCACTC/ GIGACTCTGTCCCGAAATCCGAGAGCT
ESTD-GCK	88 A G ---	---	GTTTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCCTGGTCACCATGAC AACCACAGGCCCTCTCAGGA/JG/CACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGC TGGAGCAGGAATGCCGAGCGGCGCTGAGCCCCAGGAAAGCAGGCTAGGATGTGAGAGACACAGTCT ACCTGCAGCCTAATTACTCAAAAGCTGTCCCCCAGGTCACAG

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EST34088 2	62 A T ---	---	GTGGGGCAACAGTGGGAGAGAAAGGGGCCAGGGTATAAAAGGGGGCCACAAAGAGACCGGCTC[A/T] AGGATCCCAAGGGCCCAACTCCCGAAGCACTCAGGGTCTGTGGACAGCTCACCTAGCTGCAATGGCT ACAGGTAAAG
ESTD- GNAT2	56 A G ---	---	GACCTGAGTAGCTCCCTAGTGAGCAAGATGTCTCCGATCCAGGTCAAAACCAAC[A/G]GGCATCA TTGAACCAAGTTTCCGTCAAGACATTGAATTCAGGTAAGTGCATGGTTCCCTAGG
ESTD-HT2	154 G ---	---	GGGCTAAATTTCCGAGCAACTTTGCATAGACTGTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGAGAGGAAGATGTTACAGTTGTCAGAGAAATAAAGGATAACCTGGGGTTTCTGTGC TTTGCTTCTTCACATCCCTGGGAGTTAATAGCTGCAATTTTCAAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTCAAACAAGACACACCTT
ESTD-HT5	149 C ---	---	AACACAAAGCCCCAGCGAGAAATTGAACCTCGCGACCCCTGGTTTACAAGACCAAGTGTCTAACCCCT GAGCTATGGAGCCCTCGTCTGCTGTTGTTTCTCTCTTTCATCTTATAGATTGATGTTATGCTCCTA GCATTCGGGCTACCGAATAGGATGTTAGCTTGAGTAAATTCAGGATATCTCTACAAAATGAAA ACATTTCTGCTCTGTAATCCCTCGAAAAGGTTCT
EST37382 5	124 A G ---	---	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCCACCCCTCTTCTCTCTCCCTTGGA CTTTGAGTCAAAATGGCCTGGACTTGAGTCCCTGAACCAAGCAAAAGAGAAAAGG[A/G]CCCCAGA AATCACAGGTGGGCACGTCGCTACCGCCATCTCCCTCTCACGGGAATTTTCAGGGTAAACT
ESTD- IGFBP1	43 C T ---	---	ACCCAGTGGAGCCCGCTCATTCACCGTCTTGGCAGGAGGTGC[T/CT]GGGAGAAAGGAAGATG TTCCAGGGCACATAGCTTAGTGGAGACTC
ESTD- IGHV4-6	120 C ---	---	TTTACTATTTCAATGGATACAGAATTTGGGAGTCACTATATTCCTATGAACAAAAATTCAATTT CAGTGTAAAGTAATGTTGCCCTACATTTGTGTGAGTGACGGGCAGTGGTGGATCCGAGAGTGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAATACTTCACAAAATACTAATAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	110 A G ---	---	CAAAGTAAGCACCCCAATAAATGTTAGCTATTACTATCATTATTATTATTATTTATTTTGTG AGATGGAGTCTGGCTCTGTACCCAGGCTGGAGTGCAGTGGC[A/G]CAATCTCGGCTCACTGCAAGCT CTGCCCTCGGGTTCATGCCATTCTCTGCCCTCAGCCTCCCGAGTAGTGGGAATACAGGCACCCGCC ACTGTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTCAACCGT
ESTD-IL1B	99 A G ---	---	CCACTTACAGATGGATAAATGGGTACATGAAGGGCCAATAGCCCTCCCTGCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTGTTCTCTGCCCT[A/G]GGAGCTCTCTGTCATTGCAGG
EST74082	134 A T ---	---	TCCAGGGTGGCTGGACCCAGGCCCAAGCTCTGCAGCAGGAGGACGTTGGCTCGTGAAGCATG TGGGGTGAAGCCAGGGCCCAAGGAGGAGGACCTGGCCTTACAGCTGCCTCAGCCCTGCCTGTCT[A/] TCCAGATCACTGCTCTTCTGCCATGGCCCTGTGGATGGGCTCTCTGCCCTGCTGGGCGCTGCTGGCC CTCTGGGGACCTGACCCAGCCGAGCCCTTTGTGAACCAACACCTGTGGG

EST45311	151	C T	---	---	GGCTCCTCTCTCCAAATCTGTCCCTATAGTTTTCCTCTATTAAAGTGAATACATGCATTCITTTAGT GGATAGATGCACACAACACACAGCCATTATGGGGAAGATCCACGTGTGTGGCCATATTGTAACA CATTTTCGCAAAATC/JACCTCTTTTCAITTAACAGCCCTATTCAATGGCCCTTTTCTTTTCAGTA GTACATACACATCTGTGTCAATTTGTTGAAT
EST65258	80	A G	---	---	TGCCCATCAGCGGCGGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAACCCAGAAAT CCAGTATTTTCQJ/GJCCCTCAAATGACAGCCATGGCCGGGGTCTCTGGGGCTCGTCGGG GGACAGCTCCACTCTGACTGGCACAGTCTTGCCATGGAGACTTGAGGAGGGGCTTGAGGTTGGT GAGGTTAGGTGGGTCTTCTGTGCAAGTCAGGACATCAGTCTGATTAAT
EST38216	26	A T	---	---	ATGCAGGATGAAGGTGGACAGGGAGG/JTGAGGGCCAACTGTCTCCAGGGCCTGCAGATGTGG CTGGACTATGGGTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782	149	G T	---	---	ATACTAGTACAAAGTGGTAATTTTGTACATTACACTAAATTAATAGCATTTGTTTAGCATTACCTAA TTTTTTCCTGCTCCATGCAGACTGTAGCTTTTACCTTAAATGCTTATTTTAAATGACAGTGGAG TTTTTTTTTCCCTC/GJAAAGTGCCAGTATCCAGAGTTTGGTTTTTGAACGTAGCAATGCCTGTGAA AAAGAACTGAATACCTAAGATTTCTGTCTGGGGTTTTTGGTGCATGCA
ESTD- KRT10b	183	C T	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGICAGITGTTACCTTTTGGCAATATT AAAGGAAGAAATGCAATTTTAAAGTAAGTCTAAGGTTTTTCCATTAAACCACATTAATCTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGC/JTGCTTTTAAATAGT CTCTGCCCAGATACATCTCCCTATATAAGTTATAACCCAGTATTGATA
ESTD- KRT10a	133	A G	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGICAGITGTTACCTTTTGGCAATATT AAAGGAAGAAATGCAATTTTAAAGTAAGTCTAAGGTTTTTCCATTAAACCACATTAATCTCTA/J GJGAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTC TCTGCCCAGATACATCTCCCTATATA/JGTTATAACCCAGTATTGATA
ESTD- KRT8b	231	C T	---	---	ACCTCACCCCTCCCTTAGCCGTGGGANGCAGGMAATCTCTCCAAATCCATGATCAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAGTGAAGGCCCCATAG GCTGCCTATCTCTCCCGTCTCAGGTTTACCA/C/JGTCAACATTGACACA
ESTD- KRT8a	21	C T	---	---	ACCTCACCCCTCCCTTAGCC/JTGTTGGGAAGCAGGAAATCTCTCCAAATCCATGATCAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGCAGGGCTGACATGAGACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAGTGAAGGCCCCATA GGCTGCCTATCTCTCCCGTCTCAGGTTTACCACGTCAACATTGACACA
EST75099	82	C T	---	---	CACCTGTGTGTAGATCTCCTCAGTGGCCGCTCTACTGGGTGACTCCAAACTTCACTCCATCTCA AGCATCGATGTCAA/C/JGGGGGCAACCGGAAGACCATCTTGGAGGATGAAAGAGGCTGGCCCCACC CCTCTCCTTGGCCGCTTTGAGGTGTGG

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ESTD-LF79	142 A G ---	---	GGGTGATTTTGGGCTCAGTTAATATTTCAAATGTAAACCGTAGCAAAATGCATTGGTATTTAGA AAAAATAAAATTTCCAATATGTAGTGTGTATATACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACC[A/G]GGAGGGCTCCCTTACCACCCAGA
EST35879 9	142 A C ---	---	GAGATCGGTGTGTGAGTTATTAGGCATGTTACCTGTGATTTCTCCCAATCTTGTGGTTCCACCGATG GAACTGCCGGCAAATCCTGACACGTGTGCACCCAGGCTGTACCCAAATAGGTGAACATGGCTTCGAG AGAGTTG[A/C]ACAGATTCTCTGGAAGACAGCAGCGGGATGGGGCAGGAGAGAGCTGCCTGGATGA
ESTD-LMP2	35 C G ---	---	A TACACATTTTCTTACCCATTACCTGAAACGACT[C/G]GCAAACTGGAGCCTTTAGGAATGGAGT TGACCTTCCCCAAAGCCACTATGATAAGCTATTTGGTG
ESTD-LPL	113 C T ---	---	TGTCAGTGTCCCTAGGGGCACCTCACCATCCAGCTTCTCAGCTCTGGCCTGCTCCTGCTGCCTGCA AGGGTTTGGCTTAATTCATTCATATGTCCTTCATCTTTTAGIC/TAAGCTGTGGGGTTTGTGTTG TTCCTCTGTTTGTCTAGTATCTGACTACTTTTAAATTAATAAAGAGATGTATCTAAACAAAAATAG AGATTGTTATCAGAAGTTCAACAACATTTTAAATAATTTTTCACCTG
ESTD-MCC	45 C T ---	---	TTGTCAGGAGTGTGCTGATGCTGCCTCCCGAGCTCTGTCCCTAGC[C/TA]GAACCTTCAGGACAACGTGC AG
ESTD-METH	118 C T ---	---	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCGAA TCTCAGGAAGTCTCTGCTTCCAGGGTTGGTCTAAGTGTGCTGATTAC[C/T]GGATTTTCTGACG ATCTTCACTGCTAGAGCACTGGTTCCTGTTTAGCATGG
ESTD-NF1	25 A G ---	---	ATTATCCAGATGAATTTACAAAAC[TA/G]TACCAGATCCACAGACTGATATGGCTGGT AACATGGACTTGTATATTTGTACAAA. AAAAGTTTATTTTCTAAAAAGAAAAAGAAAGAAA AAATTTAAAGGGTGTACTTATATCCACACTGCACACTGCCT[TA/G]GCCCCAAACGCTTATTGTGGT AGGATCAGCCCTCATTTTGTGCTTTTGTGAACCTTTTGTAGGGGACGAGAAAGATCATTTGAAATCT GAGAAAACCTCTTTTAAACCTCACCTTTGTGGGGTTTGTGAGAAAGTTATCA
ESTD-NFKB1	107 A G ---	---	TGTCCTTAGGCCCCAGCCCTGCTTGCTCCTCCCTGGCTGTATCTT[C/A/G]TACTGCAAGAGAACACA GACAT
ESTD-NPPA	45 A G ---	---	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATATTTCTTTCTGCAGGCATATAGAATTTGGT GGGTTTCTTTTATGTAGGTGATATGGATCTTTTGTGATTATATATAGCAATTTGAGGG ACAAACAGATAGGCAGAAATGGGCTTGAATAGTAGATGCTTATTAAACCTTGGCAATAGCATTG[C C/T]ATCCCTGTGGTTTAAATAAAAT
ESTD-NRAS	202 C T ---	---	GCCACCACACCCACCCAGCAGCACCTCCAACTCAGCCAGACAAGGTTGTGACACAAGAGAGCCC TCAGGGGCACAGAGAGAGTCTGGACACGTGGGG[A/G]GTACGCCGTGTATCATCGAGGCGGCCGGG CACATGGCAGGGATGAGGGAAAGACCAAGAGTCTCTGTTGGGGCCCAAGTCCTTAGACAGACAAAACC
ESTD-PAI1	100 A G ---	---	TAGACAATCACGGTGGCTGGCT

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ESTD+AR	120	A	---	---	CTCTTCAGGAACCAACGAGTCTCTTACCAACACGAGCTTATTGCTGTCGAGAGGTACAAACCCGTAGA
ESTD- Per/RDS	74	A	G	---	ACTTCTTCTAACTGTAATTTAGTTAAAGGAATCGAAACGAGTGGCTCTGAAGACATGGAGATACGCT
EST68308	5	29	C	T	AAATCGACTGGCTTTTCAATAGCTCTGAGGTTTCTTCTTCTTCTGTTCTAGAACGTTTCTTAG
EST54045	6	39	A	G	GACTGGCAGTTTAAAGCTTTCACCTAGGCTTTCGTATACCCATGCC
EST76136	39	C	T	---	ACCTACAGACGTGCTGGATGGTGTGCAACCCGAGGAATCTGAGAGCGAGAGCGGCTGGCTG
ESTD- SPTB	176	C	T	---	CTGGAGAAGGAGCGTGGGAGACCTGGAAAGGCTT
ESTD- PXMP1	88	A	G	---	GGAAAGAGATTAAAGAGCTTGAATTTGGA[CT]AATCTGGTCTTGGAGTGTGAAGAGTTCATGTC
ESTD- s14544	94	G	T	---	TCTGCTGAGTTACAACAGAAATCCTTGTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAAT
EST52908	0	45	A	C	GGAGAAATGAGCTTAAAGGTAAGAAAGTAGTATTTTAA
EST19590	55	C	T	---	GGAAATATAAAATATTTAAATACCTCCATTTTGT[AG]TCCCTTTAGTGAAGATGATACCTGC
EST76136	39	C	T	---	AAAGACATGGCTAAAGTTATGATGTCATGTTGGCAATTTGTTTCTTACAAAATCGGATGGGAAA
ESTD- SPTB	176	C	T	---	TCTGTTAAGTAAGTACTGTTTGGCTTGGAAATGGATTTTAAATGTTGACTTTATCAT
ESTD- s14544	94	G	T	---	ATGAAACATGGTCTTTAATTTATGATATGTTGTTATAGCTATCTTAAAGGGCTCTTTTTTTTAA
EST52908	0	45	A	C	ATGCAGAAAGAGGGGAAAAAAGGAGCGAGCTGGTGGACAAGGTGTTTTCTCAAGGCTCATAC
EST19590	55	C	T	---	AGATTCTGAAATCATGGTCCCTAGAACATTTTGAAGAGGTAAAGTAAATGAAATATAATCTT
EST76136	39	C	T	---	CCCGAGGAATCTGAGAGCGAGAGCGAGGCTGGCTGCTGGAGAGAGCGTCCGAGACCTGGAAGG
ESTD- SPTB	176	C	T	---	CCTTCTGGAGAGTGAAGAGCTGGGCAAGGGCAACAGGTGGAGCCGAGGCGCAGACGACGAGG
ESTD- s14544	94	G	T	---	CCAGGCCACAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCGAACTGAGAAATAGTGCAC
EST52908	0	45	A	C	CCAGAAACGTGGATCTCCCCCTCATCCAACTCCGAAAGTCTGAA
EST19590	55	C	T	---	TTGGGAAGTTAGAGCCTATATTAATACGGAATTAAGGCAGGACACAGAGGCTTAAATTGAAAA
EST76136	39	C	T	---	TATCCCAAAGTTGAAATGTCTCAGTT[CT]CTGTGTGGTTAGATGCAGGATTTATATGATCCGTTA
ESTD- SPTB	176	C	T	---	ACCTCT
ESTD- s14544	94	G	T	---	ATCACAGGTCTCTGGTCTCTGGCCATCATTTCTCTGGAGAGATGG[AC]TGGTGGTCTGCAAGCCCTT
EST52908	0	45	A	C	TGGCAATGTGAGATTTGATG
EST19590	55	C	T	---	AGGAGAAGCTGAGGAGGGGAAGAGAGACAAAGATGACATTGATGAGTGAAGATGT[CT]GGCTCAG
EST76136	39	C	T	---	GATGCCGGAATGAC
ESTD- SPTB	176	C	T	---	TGAAGCTTCTGCCAGCTTGCAATTTCTAGGAGAACC[CT]GCGTCATACCTTTATCTATAGCCTT
ESTD- s14544	94	G	T	---	CCCCTAGGCTT
EST52908	0	45	A	C	TGAACACCCCTGTGGTCCGAGCAGGTGTGTTTCTCTGGAGCCTGAGGAGTTTGTGTCTGTGTG
EST19590	55	C	T	---	CAGTCCCCCGGCAACCTGCTGTGTTGAGCCTGGACATACACCTTACCTCTTGGCCCGGAGAGAC
EST76136	39	C	T	---	ATTACCCACCTGGCCATGTCCCTGGGCTGTTGTGCAC[CT]CTCTGTGAAGACCCCAACCCCTGC
ESTD- SPTB	176	C	T	---	CTCCCCACCCCAAGCCAGTTTCTCTAGCAAGGGCAGGAC

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ESTD-TAT	224	C	---	---	AAATGGTCAGGACCCCTGATCCACAAGAGTGGTACCATTTTCATCAGGGCCCATCAGTTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTTCATTCATCTTAAATGACTTGTGGACAGGATCA ATTTCCCTCTCACCTAGAACGTTTGTACAACTTTCTCCAGTATGGATGGATTATGATGGGGGG GAGAAGCAAAATTTTAAATAGGACCCCATGAGACACATCA
ESTD- THRB	125	A	C	---	TGGGCCCTTCTCCGGCAGGGTAGACTTCTTACTTGGCTGTTGATTTCCAAAGAGAAAGAGTCCCAAG CACACGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAAATCACACAGGATC[A/C]TTCAT CCACACTGGATTGGCCCAACAAGCTGAGTGCAGCCAGGACTCAACGGTCCCTGTAGATGGG TAGTGAAGTTTTCATCTCTGTGAGCTTCTGGATTCTTGTCCCAACCAAGAGAGTCTATGC CAAGGCAGAAAGCTGGTCTCATGGGCAAAATCAATGCTCTCCAGATTTCAG[T]ATCCCCAA GCAGTGCATCCATTGACACATAATAATGCATCCAGACAAGAGGTCATAAATATTGATGTCGTTAAA CATGGGTGTTGATCCATTTTTCATTTGGCCATAGGTCCCTATGGGGATGACA
ESTD-TYR	122	G	T	---	AGTAGTGGATGAAGCTAACCGCCTCTCCTCAGTATGATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACAA AACCACTGGTGAATATAATAGATTGAGTTAATCACTGATTTCTTTTACCTTTTACCTTTCTTCT AATACAAGCATATGTTAG[A/C]ATTAAAGTTCTAGGCATACIT
ESTD- TYRP1	222	A	C	---	AGTAGTGGATGAAGCTAACCGCCTCTCCTCAGTATGATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACAA AACCACTGGTGAATATAATAGATTGAGTTAATCACTGATTTCTTTTACCTTTTACCTTTCTTCT AATACAAGCATATGTTAG[A/C]ATTAAAGTTCTAGGCATACIT
ESTD- VB12	148	C	T	---	TCCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTTCTTCTATTACA GGACACATGGATGCTGGAATCACCGAGAGCCCAAGGTCACAGAGACAGGAACACACAGTG ACTCTGAGATGTCA[C/T]CAGACTGAGAACCCCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148	C	T	---	TCCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTTCTTCTATTACA GGACACATGGATGCTGGAATCACCGAGAGCCCAAGGTCACAGAGACAGGAACACACAGTG ACTCTGAGATGTCA[C/T]CAGACTGAGAACCCCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74	A	G	---	TCCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTTCTTCTATTACA GGACACATGGATGCTGGAATCACCGAGAGCCCAAGGTCACAGAGACAGGAACACACCA GTGACTCTGAGATGTCAACAGACTGAGAACCCCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT

EST58607 0	105 A G ---	---	CTCTGGATGGGTTACAGGTGGCAGGCACAAAGCCAGTCCATCCTGTAGTCATCATAGTTTGGCTCC CAAGTTGCTCTCCTCACTGGAGAAACAGGACAGCCAC[AG]TGGCGGGATGGCCGGCGGAGTTT TGGTTGGCGCCACGGCTGTGGCCTCGTTGTGAACGGTAGCCTTTGCGGTTGCGATGCCTAAACCTTTGT TTCTGGCCAAAGGAGGGGGGGTCCATGCTGAGATGTAGATGCGGCC
ESTD-VWF	36 G ---	---	AGGTAGGAAAGCAAGAGTTGATTAGTGAAGGAGAGAAATGGACCTACCTTCCACACTGTCCTTTGG TCCCCTAGAGTCTG
EST71770 6	189 C G ---	---	AGCACCACTCTCACGTCAGCCCTCAGCACAGATGCTGTTCTATAGGATGACGTGCTGTTTTACAA CATCTCCTCATGAAGAGCACAGAGATTATTTATTCCTGAAGTCCGGATCTATGACTCAGGACAT ATAAATGTACTGTGATTGTGAACAACAAGAGAAACCACTGCAGAGTACCAG[C/G]TGTGGTGGA AGGAGTGCCAGTCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAGG
ESTD- TNFab	152 A G ---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGGAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTGAAGGGCATGAGGACGGGTTTCAAGCTCCAGGGTCTACACACAATCAGTCAGTG GCCAGAAAGACCCCTC[AG]GGAATCGGAGCAGGAGGATGGGGAGTGTGAGGGGTATCCTTTGATG CTGTGTGTCCTCCCACTTCCAAATCCCCCCCCCGGATGG
ESTD- TNFAa	88 A ---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGGAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTGAAGGGCATGAGGACGGGTTTCAAGCTCCAGGGTCTACACACAATCAGTCAGTG GCCAGAAAGACCCCTCAGAAATCGGAGCAGGAGGATGGGGAGTGTGAGGGGTATCCTTTGATGCTT GTGTGTCCTCCCACTTCCAAATCCCCCCCCCGGATGG
EST52418 6	113 A G ---	---	CAAAATTACAGGGTCAACTGCTATGATGTGTTGGAGCCCACTCACCCCTTGGTGGCTACAAGATGTGG GGGAGTGGCCGGGAGTTGGCGGAGTACGGGCTGCAGGCATACACT[AG]AAGTGAAAACTGTGAGTG TGG
EST13586 3	89 A G ---	---	CCCACTCTATTTGCCAGCCCCAGGGACAGAGCTGATCCTTGAACCTTAAGTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCC[AG]GGGCTGGCTTATCAGCCTCCAGCCAGACCCCTGGCTGCAGA CATAAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCTGCTGCTGCC CCGGTCACTC
EST51976 7	123 A T ---	---	AGGCAGAAACTGGGCCCCCATGCGGGGACGTGGAAGGCCACTTGAGCTTCTGAGAGAGGACCTGA GGGACAAGGTCAACTCCTTCTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAG[AT]CTCTCTC CCTCCCTGAGCTGGAGCAACAGCAGGAAACAGCAGAGGAGCAGCAGGAGGAGGAGTGCAGATGCTG GCCCTTTGCAAGCTGAGCTGCCCCCTGGTGC
EST11458 6	140 A G ---	---	CCACTTTGGTAGTGCCAGTGTGACTCATCCAAATGATTTCTCCAGTGTCTAICTTGTCTCGAGTTT CTCTGCCATGTTGCTATTGACGAGCGGACCTGTCCCAAGCCAGATGATTTACCATTTTCCACAGTGT CCC[AG]TTAAACATTTCTATGAGCCAGGAGAGATACGTATTTCTGCAAGCCGGGCTATGTG TCCGAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC

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ESTD- AT3aa	60	C T	---	AGACCTCAGTTCTCTCTGTAAAGGGAAGTTTGTCTTGATCTCCATGGGCCAGCIC/TJAGCA CTGGTCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGACCAGGTGGAGGAAITTTGAAAGGGCA TTGGAATTCAGAGCAAGAGACAGATATTAAAGAGCTGGGGAATGTGG
EST39852 8	106	C G	---	CGGCTTCCTCCAGGTATTGTTGCAGAAGGCCGAGATGACCTCTATGTCTCAGATGCATTCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCACCTCTTTC/G/GGGTACAGAAAGGAGATGCATGAACA GCAGGAACACGTGGAAGGCGCTGTTCCAGTGTAAAGCATGCAAAAGGCCCTCCACAGGCTGCTAT AATACAGCCCT
EST62448 0	112	A G	---	ACCTGGTGTGCTGGTGGTGAACCTGGTCTCTTGGCATTCGCCCTCTCTGGCCCTCTGGCTGGG TCCTCCTGGTGTGGTAGTCTCTGGAGTCAACGGTCTCTT/G/GTGAAGCTGGTGTGATGGCA ACCTGGGAACGATGGTCCCCCAGGTCCGATGGTCAACCCCGACACAAGGAGAGCGGGTTACCC TGCCAATAT
EST36027 2	120	A C	---	AGTGACTTCCAAGGAAATGGCTACCCAACTTGCCTCATGGCCCTGCTGGCCAACTATGCCTCTCAGA ACATCACCTACCACTGCAAGAACAGCATTCATACATGGATGAGGAGACTGG/AC/JAACCTGAAAA AGGCTGCTATTCTACAGGCTCTATGATGTTGAACCTTGTGCTGAGGGCAACAGCAGGTTCACTTAC ACTGTTCTGTAGATGGCTGCTCTAAAGACAAATGAATGGGAAAGACAA
ESTD- COL2A1cc	112	A G	---	AGAATGTATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTCTGTCACCTTC/J/GJGGGTGTTCAAGGTGGAAA GGTGAACAGGGTCCCGTGGTCTCCAGGCTTCCAGTAACTCAAGCATATACAATACTAGCCT TTGGTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD- COL2A1dd	97	C T	---	TGAGAGAACACCTAGTCTCCATCTCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTGCTGGGACCTGGAAACA/C/JTGGACTCTTTCTACTGCAGCAGACAAGACTTA CCCAAGAGAGATTAAITGGCAAAGATATAC/AAATACAATTTTATTTGACCAAACTATCATGGAACA GCATT
ESTD- CPT2	150	A G	---	GCCGCAATGCCCGGAGTTTCTCCAATGTGTGGAGAAGCCCTTAGAAGACATGTTTGATGCCCTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGCAGATGAAAGCTACCATCACTTCTCATCATGAAAAAC TGGGAGGCCGGGCAT/JGJGTGCTCATGCTGTAAATCCCAGCATTTGAGAGGCTGAGGCGGGTGGAT CACTTGAGGTGAGGATTTGAGACCAACCTGGCCAAACAT
EST12274 0	135	A G	---	CCCCCAGTTGACAGCCACTGCTAGACTAAGTTCTTGCTTCCAAATAGAGCCTTACCAAAGTGAT TACATAAAGAAGTCAAGTGGTTTACTCTCATGACCAAAATATCTTCCCTCCTTAGGATGAGGTG A/GJTAGTAATGACCGATGGGTGAGAACTGTCTGTCCACTGGAGGATACTATAACTGTGAAGA TAAATCAAGGCCACAGAGCTTGCCAGATC
EST76807	91	G	---	ATGCTAAGGGGATCGGACATGAAGGACCCCTGTGAGCCGATTGTCTATCTCCAGCGGCCCTGTCTATC CAGCTCACTCATCAATGGGCCAGTCAGGCCAGGCACTGGCTCCGAGGACTCACCAGTGCCTCCCT GCTGCCATGTGGACTGGTGAAGTTGAGGACTTCTTG

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ESTD-SSA1	111 C T ---			TTACATTTGTGGATTGTTCTTTTGGCTGTGCAGCACCTTTTCAACATGATGTGATGCCATTTTGTCCAAAG TTTGGCTTTGGCTGCTGTGTTGGGATATTGAAAGAGATGCTTTTGGCCAGTCCAAATGTCTCTAGTA GAGTTTCCCAATGTTTCTTGTAAATAGTTTCATAGTTTGAGGCCCTTAGATTTAAGTCTTTAATCCATT TTGATTTGATTCTGTGA
ESTD-RYR1	109 A G ---			CTTCGTGACGGGAGGTACGTCCTCCGCCCTTTTCATGGACATATGGATGAGTGTCTGACCATTTCCC CTGCTGACAGTATGACACGCGAGACTTGTCTACTATGAGTGGGGAGCTGTGTGCACTCATGCC CGCTCCCTCTGGAGGCTGGAGCCACTGAGAATCAGTGGAGTGGAGCCACCTGGCTGGGGCCAGCC ACTCCGAGTCCGGCATGTCTACACCGGCGAGTACCTAGCGCTCACCGAGG
ESTD-WT1	70 A G ---			AAGACCTACGTGAATGTTACATGTGCTTAAAGCCCTCCCTTCTCTTACTCTCTGCTGCTGACGAGTGTG CGTGGTGTGCTGGAGTAGCCCGGACTCTTGTACGGTCCGCATCTGAGACCAGTGAGAAACGCC CTTCATGTGTGCTTACCCAGGCTGCAA
ESTD-F2 EST4438 7	100 C ---			GATAAGTACACTGAGGCCCCAGGAGGTATTGCTCTAGTAGCCCCAACTGTGCATGCACGCTTAACCTCT GCACCAAATGGCTCCAAAGGCCCGTAGGGGAAGTGGGGGATCTAGGGGATGGGTAGGAATGGCCC AGCCAGTCCCGCGGTGCTGGTCCCAACAGAGGAGGCCGTGGAGGAGACAGGAGATGGGC TGGATGAG
ESTD-PBDA	103 A G ---			GCAGCCAGGAGCCGCTGCACCATGCCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGA[CT]G TCCTGCTCCGACCTAAGCGGAGAGCCCTCAAGAGCCGAGCGGAGGTGGG
EST12839 3	122 A G ---			CCCTCTCATGCCAGATGGAATTCAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAAGGCGAGGACTAATCCAA[AG]TCTCTACCCGCGAGCTTGTCTGCGCATACAG ACGGACAGTGTGGTGCAACATTGAAGCCCTCGTACC
ESTD-CTLA-4	48 A G ---			TGCAAAACACACAAAATCTTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTTGCT CCTAACATCTATGTAAGTATCTAATGAACACAGCAGCTTACTCCAGAG[AG]TCAAGTCCA AGGCCATTGGCTATCTCAACACTGGTGAGTATCTTGAAGTAAGGGAACCTTGAATGTTATTCAAC TGGATTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACITTAGCTTAG
ESTD-ACE	96 C T ---			ATGGCTTGCCCTTGGATTTCAGCGGCACAAGGCTCAGCTGAACCTGGCT[AG]GCCAGGACCTGGCCCTG CACTCTCTGTTTTTCTCTCTCTCATCCCTGCTCTGCAAAAGCAATGCACGTGGCCAGCCCTGCTGT GGTACTGGCCAGCAGCGGAGGCGATCGCAGCTTTGTGTGAGTATGCACTCCAGGCAAAAGCCAC
EST54419 8	88 A G ---			GATCAAGCAGTGCACACGGGTACGATGGACAGCTCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTACCTGCAGTACAAGGATCTGCC[CT]GTCTCCCTGCGTGGGGGCCAACCCCGCTTCCA TGAGGCCATTGGGGACGTGCTGGCGCTCTCGGCTCTCCACTCTGAACATCTGCACAAAATCGGCCTGC CTTCTGCCTAATTGAATGATATTGTTGCTGTGGGACCTGAGCACTTTTATGGCACAAATGATCACTA TTTTCTTGACCCCTACTAC[AG]ATCTCTGGGAGATGTTTGGGTTTAGCGTGGTCTGATGTTGTCTA CTATAGTCCAAGTGAA

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ESTD-PS-1	99 A G ---	---	---	GGGAGTAAAACTGGATTGGGAGATTTCATTTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAAACACAAACCATAGCCTT/GJTTCGTAGCCATATTAATGGTTTGTGCCCTTAC ATTATTACTCCTTGGCCATTTTCAAGAAAGCATTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGT TTTCTACTTTGGCCACAGATTATCTTGTA
ESTD- B3AR	104 C T ---	---	---	GGCTGCCAGGGTTCGTTGGAGGGCCCTAGCGGGGCCCTGCTGGCGCTGGCGGTGCTGGCCACC GTGGAGGCAACCTGCTGTCTCGTGGCCATCGCCCTC/TGGACTCCGAGACTCCAGACCATTGACCAA CGTGTCTGACTTGGCTGGCCCGCAGCCGACCTGGTGATGGGACTCTGGTGGTGCGCGCGGGGGCCA CCTTGGGCGC
WI-567b	48 A G ---	---	---	TCTCACACTGACCCCTTACCTTCATCCTCACCTCTGCTGGCTTGGTCTG/GJAGCCCTCATCTCTTTA CAGGATCCGCGCACAGCATCCCAACTGATCTGGCTTAGGCTCTTCTTCTCCAATCCAATCTTCAAAAG GCTGCCACTGTGATCTTCCCAAAGGTGATCTGATGCTACCATCTTGCTTCAAGCC
WI-801c	58 G T ---	---	---	ATGGAACATTTCTTCCATAATGAATGAGGTCTCAATCCATTACACATCCCTTCTTCTG/JAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTTGCAGGGGTGGGGCTGTGC ATCTGTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCCAACAGAGAGTTAA CATTCTGCCACCCCTC
WI-801b	58 G T ---	---	---	ATGGAACATTTCTTCCATAATGAATGAGGTCTCAATCCATTACACATCCCTTCTTCTG/JAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTTGCAGGGGTGGGGCTGTGC ATCTGTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCCAACAGAGAGTTAA CATTCTGCCACCCCTC
WI-1099b	76 A G ---	---	---	GAAATTCACCTATACAAGAACTATTTCTCTAATTATTACATTAGTCTCATATTCTGAAATATTAT TTTTTACA/GJTACCCCTTGTATTATTTTGTATTCAATTTGTAAAGAGAGATTACAATATCAGTAACGC TGTTCAATTGATAGTGTATCACAAATGTCTAAATACTTTTGGGTCAACATCAAAATTAGAAAGAAA CTTACAAAGTTTATTGTCTTTATGGTTTA
WI-2529	71 C T ---	---	---	AGGAAATGGCTGATCTCCTGGTGGCTTCATTATAGTAAAGGAGATGTAATTGCTTGATGAGCCTCT CAA/C/TJCTTAACTGCTGCCCTTCAGTCAGTGAACATTTAATGAAGTCTACACAAATTAATTAGTGT AAGTTGTAATGCTGAATAAGCTTGAATAAAGTGAAGAGGTAAAGAGGAGACAACTGTGCTTT TTAAGAAATAGAAGAGTCACTTTCATTAGAAATGGCTTTGGGGATGACAAGTA
WI-10088	205 C G ---	---	---	TAAGGGCCTGTCTTCCCCAGAGGCCCCACGGGACAGAGAAAGCATCTTGATACCCAGGGGCCACAAA TGAGCAATCCATAGATACTACATATAAGAGAGACCTGTACCCCTATGAGGTAACTGAGGATGAAGGA GTGAGTCATATTGGGTGGCAATTAATGACCCAGCCTCTCTCTCAAGAGAGACTTTTACATTTTAGAC AGG/C/GJAGCAGAGAGCAGCAAAAGGAGAAAGGAAGT

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WI-2625	98 G A ---				GGG CAG T C C T G G C T G T A G T G G T A G A C A G C A C T G A A G G A T G G A G A A G A G A G A A A C A G A G C A G A A G C A C T G T G G T A G T T A A C A A G G C T T A T T A G G A [G/A] C A A A T T G A T A C T C C C T G A G G A C T C G C A G A A A T T A C C A G C A G T G G A C A G G G T A T C T G T G G T G A A T T C A G T A T T C C A C T T G C A G G A G G A A A G C C A G C C A G C A A A G
WI-2924	54 G A TAGG	TGACCTTCCTA GTCCTCTCTTA		GCCTAAGTGT AATCAGAGG	TCTGTGTCAATATTCCTCTTTGACTCTGACCTTCCTAGTCTTCTTATAGG[G/A]ACCCCTGTGATT ACACTTAGGGCCTACCTGGATTATTTAGAACAATC
WI-2939	72 G T GTGCCITT	GGCTTGCTCA		CTTGTGAGGG AAGGICTTG	CCATTGTGAGGTTGGTGGGTCACCTTGTTCATCCCTCGCACTCAACAAAGTGGCTTGTCTCAGTGC CTTT[G/T]CAAGACCTTCCCTCAACAAGAATGCTTTCCATGCTCCCGTGTCTTTGAAAAATTCGACT TTATCCTGA AAAACTCAGCTGCAGTGTATCTCCGGTATAAAGCCACTCCTG
WI-3203	99 G A AGACGAG	GGTATGCGGC		TCAAGTATTGC CTTGTGTGG	CTTGCTACCATGCAATTCACAGCATACAACCTCAGTGAATGCCGTAAACCCCATTTATAAAACAT CTTGCCATCGAAGGGTTATGCCGAGACGAG[G/A]CCACACAAGGAATACCTTGAAGTGACTTGGGA GAATAAAGATTTTGGATGGATGAAGCAGAGAGGAGATGCTAAAAGIGA
WI-3473	101 A G GCCCTAGGGA	AAGCATTTTA GCCCTAGGGA		CCTGATGTCAC CAACATTTTCT	GGAAAAAGAAACCTGAAGGATGAGTAGAAGTTAATTGGGAGATAGTTGGTGATAGGCCCTGTTTGGGA GATTGCAGAGAAGGAAGCATTTTAGCCCTAGGGA[G/T]AGAAAAATGTTGGTGACATCAGGGCT ACACACTTTTCTGTATGCTCTTCATCAAA[G/T]GCAGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTTGCTGGCTCCCC
WI-1796b	29 A G ---			---	ACACACTTTTCTGTATGCTCTTCATCAAA[G/T]GCAGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTTGCTGGCTCCCC
WI-1796	29 A G ---			---	AGTCGTCCATCTTCAGGGTCTAACTCTGGATCTGGCCTGCAGAGTAGGAAAGATGGGGTGAGT AGTCACATTAGGTATTTTCCAAATAA[C/T]AAATGCCCTCTGAAAAATATCTCTCCCATGTCCCCTGTC TAAATATAACATTTTCCC
WI-4360	93 C T AAATAA	GTAGTCACATT AGGTATTTTCC		GAGAGATATTT TTCAGAGGCAT TTT	GCTGAGCTTTGTGGCAGAGCCAGGACAATTCAGCTGCCGATTTTAAATAGATTCTGCAGCACTGCAA CAGGAACCAAAAATCAGTC[C/T]GGGTAACCTGAGAGTGGTTTTCACACCCAAA
WI-1959b	87 C T ---			---	GTTGTCCTGTAGCAGACACAGAAGGCA[G/G]AGAGGAAAAAGCCCTTTTGGTCCAGGGGCTTACAC TGAATCCCTCAACAATGCAAGATGAGCTAAATGGTCTTAGAGGTATAATCTAAGTGTGAGAAAAACA AAGGTATAGGGTTTG
WI-1973b	28 A G ---			---	CTTGAGTATCGTGGATTTGGTATACACAGAAATGGGAGAGCTGGAACATAATCCCCCATATACCA AGGGACAAAATGTATCTGTTTCTACAATTATACAGTAGGAGACATTATGTTCCATGACAATGGTAAT TTTTAA[C/T]GACAGTTTTTAATTGAGTGAAATACCATAAAAATAATAATAGTAGCAGCTAATATT TACTGAGCTGTTACTAGGTGCTATAAATAGC
WI-1980b	140 C T ---			---	

WI-2015b	190	A G ---	---	TGTCAGATAGTCGCTCTACCTAGGTGCAGTAGCATGCTAGGAGCTATTAAAGTACACAAATTATGCT ATATATTATACAATATACAAATTACTTGCAGATAGCATGACCATGCTAGTGAACCCACAAAGACTAT GTGTGAATCGTCTATTAGGGTTTGCTATAAACTCTACATGGTCTTTTCCAACTAGGTCATATACCTT CTAATACCATAGAG
WI-754b	49	C T ---	---	GAAGGCACAGGGAGAAGATGGCTGTCTATCTACCAGCCAGGGAGAGAAAGC[C]TACATTTATTGGTAA TCCTATAAGTGCATCTTTAAAAATTGTATTACTTTAGA
WI-754	22	T C ---	---	GAAGGCACAGGGAGAAGATGGCT[C]GTCTATCTACCAGCCAGGGAGAGAAAGC[C]TACATTTATTGGTAA TCCTATAAGTGCATCTTTAAAAATTGTATTACTTTAGA
WIR-1b	56	A G ---	---	AGGCAATCAGACCTACAGAAAGGAAACCCCAATAAAACTCTGTATCGTACATCC[AG]TGCCTG GAGGTGATGCCTCTCTGAGGACATGGAGCTTCATGTTTGGAGCCCTCCCTG
WIR-1	56	A G ---	---	AGGCAATCAGACCTACAGAAAGGAAACCCCAATAAAACTCTGTATCGTACATCC[AG]TGCCTG GAGGTGATGCCTCTCTGAGGACATGGAGCTTCATGTTTGGAGCCCTCCCTG
WIR-3b	72	A G ---	---	TAAATTTAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GAAGT[AG]TCTAAAGTTATTAGCTCAGAGCCTCACACATTCICAGTACTGATAAAACAATAAGCA AAGCTGGTGTCTGAGATAAGA
WIR-3a	69	A T ---	---	TAAATTTAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GA[AT]GTATCTAAAGTTATTAGCTCAGAGCCTCACACATTCCTCAGTACTGATAAAACAATAAGCA AAGCTGGTGTCTGAGATAAGA
WIR-4	47	T ---	---	GAGCCTTTCTAAAAATAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCCTGTCTCACACATGTGCA AGGCAGCAGCAAAATTTGCCAGCTGCC
WIR-5g	209	C ---	---	CGGGACAGAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5f	196	C ---	---	CGGGACAGAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5e	194	C ---	---	CGGGACAGAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG

WIR-5d	191 A ---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5c	177 C ---	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTCAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5b	159 A ---	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTCAAGAGGTTATTAGGACTCAGTTCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTT AGGTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACAC AGGTTTACGTCCAG
WIR-5a	37 A G ---	---	TAACCCGTGAACCTTTGCTCTCCATCTCAGGGAGAACACAGACTTTCATGTTAAGACCCAGAA[A/C] CGCAGCTTGGGGTTGGGCAG
WIR-6	63 A C ---	---	TTCTGACTATT[C]/AAGCATCTGTAGAATATTGAATACATAGTCTTGAGATTGATC
WIR-7	12 C T ---	---	GGCGTCCATGACTATCCTGGTCATTGATTGACTAATGATTCC[TG]/[G]GCCCTTG
WIR-8	46 C T ---	---	AAACAGAAAAATAGAGGTTATAAGGATGGAACATAAAAGTTGTCAGAAGAGGATGA[C/G]CTGAAG AAAGAAATTACTCTCTTTTGACCAATAAATACAATTGGGAAACACTGGAAAAACCATGGCTTGATTACT GACAAC
WIR-2	56 C G ---	---	TGTCCTTGCTTATGCCCTGCTCTTCGCTTGGCAGGATGATGCTGTCATTAGTATTTCACAAGAAAGTA GCTTCAGAGGGTAACCTTAACAGAGT[G/A]TCAGATCTATCTTGTCATCCCAACGTTTACATAAAA TAAGAGATCCTTTAGTGCACCCAGTGAAGTACATAGCAGCATCTTTAACACAGCCGTGTGTTCAAAAT GTACAGTGGTCCCTTTTCAGAGTTGGACTTCTAGACTCACCTGTTCTCACTC
WI-7069	93 A ---	---	GGTCATTCCCTTTTATCTGTCAGGCGCCAGCTCTGACTT[A/T]CTCTCTGTTCTGTCATCTCTCCC CCACATACCAACTCTTCAACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18694	41 A T ---	---	CACACTGTTACACACCTATATTTCAAGTTTGGAAATGC[A/G]TATTTGCAAGCAGCAATACAAAAGTA TTTCATGAAGAATGCATAATCTCTGAAATTTATGAAACATCCCT
WI-18612	37 A G TGC	CCTATATTCA AGTTTGAAA	TTGTATTGCTG CTTGCAAT

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WI-18517	87	C T	CAGGAATCAG CAGCCTGA	TGTTTGGACAA GTGCAACA	TTAAAAATCAACTAGGGCTCACCCCTCAACACCCCTCCATTTGTCAACCTCTACAGCCCTGCATGCC ACAGGAATCAGCAGCCTGA/C/TTGTTGCACCTTGTCACCAACACAACTGACTGC
WI-18668	76	C T	GGCGAAAAC TAGGCAAAA	GCTAAATTAAA CTGCACITTTT GC	CGATTGACAACCTTTTATTTTCAACTTAGGTAAACAGTCCAAATCAGTGTAGATTGGCGAAAACT AGGCAAAAC/C/TTAGCAAAAGTGCAGTTTAAATTTAGCAAAAGGCTCAAGACAGTATGTGGAAAGGAA GGTGAGATTCCCTCCTACT
WI-18680	75	T C A	GCTGTCACTCT AGCATCTGGA	CCTCCTGAATA TACAACGGAGC	TAAACATACGAGTACTGTACACGCAAGCATGCATCCCTTGAGTCTGAGTGAGGCTGTCACTCTAGC ATCTGGAAT/C/GCTCCGTTGTATATTCAGGAGGGGA
WI-18704	99	A C	GGTTCCTCGA GGGTAC	TGAAGGCCCTG CTGG	CACCCAGGCTGTACCCAGGCTTCTGTGCGAGCACACCAACAGGGCAGGTTGGGCTTGAAGGAGCC CTTGAGGAAACACGGGTTCTCCGAGGGGTAG/C/CTCAGCAGGGCTTCAGCTTAAAGTCG
WI-18673	29	A G	---	---	TGTGGCAAACTTGTTTTAAATTGCAAAAC/A/G/ACTTTAATTTACAGCACATTCAATAATGAACCAAC AGGAGAGTTGCTGACTTTGTAAACATATGAATATATAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAAGCGCATACAAGGAAG
WI-18640	121	T C	GTCGTGGGTG GGG	GCAATACCAC TGAAGAGGAC A	ACCAGTCATGTTTATTTGGAGGTTAATTCCTATTAGGATATGAAAGGATTTCAGCAACGATTGAGATT GTGTTCTCAGGAGGGGCTCGGGCCAAAGTCGTGGGGTGGGGGTGCAGAGT/C/GTGTCTCTCTC AGTGGTATTGGGACC
WI-18533b	91	T C	---	---	GGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTTAAACTCCCGAGATTTCCTCTTTATTT TATATTTTCATTTTTCATCCTAAT/C/TTACTGAAGCCATTTCTTTGGTTAACTTAGA
WI-18533a	59	T G	---	---	GGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTTAAACTCCCGAGATTTCCTT/G/CTTTA TTTTATATTTTCATTTTTCATCCTAATTTACTGAAGCCATTTCTTTGGTTAACTTAGA
D11734	83	A C	TCATCTGATAC CTGTTCAGAT TTC	AACCAGGATA AGGCTACAAC ATTT	GAGCATATGCTGTCATGAGGACCTTTCTATCTTACATTAGGCTGGGAACTTACTCTTTCACTGATA CCTGTTCAGATTTC/A/C/AAATAGTTGTAGCCTTATCCJGGTTTACAGATGTGAAACTTT
D49493	159	A T	CCTGAAGGAA TCTGGGAATT	ACTTTCAGGCC AGGC	CAGGACTTGTGTGAGCTGCAGACACAGAGCACAGCTCATGGGCAACATCACTGGGGCCAGAGAG AGCTGTCCGCCAGTGCATCATAGGGGCTTTTTCATTTGCTAGTACTAGCCCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAATT/A/T/GCCCTGGCCTGAAAGTGCCCATCATTCATACCCACTGTT CT
EST10030 7	98	T C	CATTTTGTTC TCTCAAGTCCC	GCAGTGGTGGT ATGGATGA	TATTTTCATAGAGGAGACCTAGGAGGAGGTTGACACAGCACACTGCTCAGCAGATGACTTAAAAATTTT CCCTTAGCCATTTTGTCTCTCAAGTCCCTT/C/TTATCCATACCACCACTGCTGATTG
EST10052 2	24	G A	GCTCACTTCTG GAGGCTG	TGTGGAACCTC AATCTTAGACT TC	TATTTGGCTCACTTCTGGAGGCTG/A/GAAGTCTAAGATTGAGGTTCCACATCTTGTGAGGCGCTTC CTGTTGAGTCAATAACCTGGTGGGAAGTCAATGTGGCAAGAGAGAGGGCTACAGAGAGCAAGAGGAA A

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EST10605 2	118 C G ---	CTCTCAAGTAG ATAAGAGGCA TAATCT	---	GCTAAATTTTC AGAAAGAATT TTGTTT	CTTGGCTAAATCACAGTTCTGTATTCATACAAAAACCTTTGTTTTCTCTGACAAACCTGTACACATAGA AACAAATTTCCAAATGGACAGGAACCTTAAATTTGTGGAGATGCCCATGT[C/G]TTGTGAGACTTAA AAAAAGAAAAAGATCCC
EST11048 0	61 T G ---	ATAAGAGGCA TAATCT	---	AGAAAGAATT TTGTTT	CATGTGTCAATCCCATGATTGAAAGACATGTTGCTCTCAAGTAGATAAGAGGCATAATCTT/GJAA ACAAAATTTCTCTGAAAATTAGCTTATGAACCTCATTAACACTGCAAAACAGAGAGGAGCAC
EST11260 8	101 G T ---	---	---	---	TATGGAGGCCAGAGGAAGTGACACTATATGTGGAAGTGCTGAAAGAAATGAAGTGTCAACACAAAA TTCTATATCCAGCTAAATATCATTTAAGAAATGAAG[G/T]GGAAATGAAGGCAATATCAGATAAA
EST11349 9	109 C T ---	---	---	---	TTTGATGGAGAAATCCGAGGCTGCCAGCATCCCCACCAGTAGATTCTTTGGACGAAGAAAAATCCT TCTGTGGATTCAGCTTACC GCCCTTTCCTCATCTGCTGGT[C/T]TTCCTCAGAGCTTTAATGTCGGT CCTGCTCTCCGAGTCAG
WI- 16632a	71 A G TGGAGCCCT	CCAACTACTT TGGAGCCCT	---	TCCAGCTTTCT CTAAAACTCC T	GAATTCCTGGGTATTAAATAGCGGGTGCCACAGGACACATAGGAAGAGCATCCAACCTACTTTGGAG CCCT[A/G]AGGAGTTTTTAGAGAAAAGCTGGAGCCCCGAAGACCAGTAGTAGGAGGTAGCCAGACCAA AAGGGAGGAAGGAGTGGAA
EST11772 6	74 A G ---	---	---	---	CCAGGAATAAAGAAAAAAGAGTCCAGAGGAAACAGTCTTTGATGTTATGAGGCTGAGACACTACTC TTCCCTCA[A/G]GACTATTTTCATCTGACTATAAGTGAATAAATACATGAAGACTTCAGGAGCTCA
EST11795 3	82 G A ---	---	---	---	CTGTCCATTATTTGTGCATGTTCTTAAAGGCTGTGAAAGATAACTTGGAAATGTGGGAAAC ACATAGATCCCAGA[G/A]ATTAAAGGGGCTGGAAAAGTAGCCCTTAAGAC
WI-16644	42 G A TAC	CAATAAGCAG CTCATTTTGAT TAC	---	ACTTCATGAAT TTTACTTTCATG TATACC	AGAGCAATGGTCCGATCTCAATAAGCACTCATTTTGTATTAC[G/A]GGTATACATGAAGTAAAAATTC ATGAAGTAAAAATTCATTATACCAAAAAGCCCTCCACACAGAACTTTCATGCACCCCTGAGCTATGTGAAC TGAAAAGTAACAGTGGAT
EST12005 9	56 A G CAAAGTCTGT	TTGTATAATA ACACTCAGTA	---	GGCTGGTCACT TCTGGAT	GCCTAGTAATCCAAAAGGAACATGTTTGTATATAACACTCAGTACAAAGTCTGT[G/A]ATCCAGG AAGTGACCAGCCCGACGCTGTGCTATGACCCCTCTGAACCTCCCATTTCCATAGTTTTTGAATC
EST12055 9	32 T C ---	---	---	---	GTGGAAAATTTTTTATCTGTTACGCTTTCC[C/G]ATTATATTTATCTTGTCTTGATTTCAGCACCC CACCCGATTTCAGGCGAGTCTTCTAAACGTGCCCCGTGAGCTGTAAAAAGTCTCT
EST12492 1b	95 A G ---	---	---	---	CCCTTAGCAAAATGACITGGAGTTGTGTTCCAATACCAAGTTACATCTGTTGCCAAAATTAAGCTCTC TTCCCCAGAGGCATTAACTGAGATTAT[A/G]GGAAACGCACAGCAAAATTGACGATGCAGCTTTTAA CCTTTTTA
EST12492 4	25 A G ---	---	---	---	ATCTTGAGGTTTCTGGGCCCTGTGAG[A/G]AAGTGACATCTTTTACTTACCACAGGTCAGGAACCCCTAT AAAGAACTGTGTAGAAAAGATATCAGGTCAGACTTTTTAAAGGGCTCTTATCAGCTCAATAAA

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EST12502 2	52 C G ---			ATAACTAGGGAGAAAACCAACTGGAGGCAAGTCCACAGGTACACATTGTCA(C/G)CAGCAAGTAT AAACAAAGTGGGTTTCGATGAAGAGAAAATGCTCACGGGGAAATGACCAATTTTAAAGGGCCATGTG GTGTCGAGGCGAGTTAGAGG
EST12619 8	105 T C ---			CCAGAGAAAATAGAAATGATCGGTAAAAAGAAATAGGAATGCATATTTCAACTCACGTGTACAAA CAGGTGTTTATTATCCCAATGACAGTGTGCCTGAGAT(C)GATGCATGTGGCAGACGAG
EST12620 0	67 A G ---			TTTTCTCTCTCTCATTTATTGTTCAAAACACTGCTAGTACCAACATGTCCACCGGGC(A /G)TTGAGAATACAATATTGAAGAAGAGTCACTGCCCTCTGGAAAAATCAGAGTATTGA
EST12817 9a	22 C A ---			TTGGGTTCTCCAGGATTCCAG(C)A)CTCGTAGCTGATGTGATGAGGTCTCATCCATGCTCCACGG GTCTTTGGGAGTGACCGGGATGGGAATCCATGTGCTTGGCTACTCCATCAGGTCAITGGG
EST12941 8	23 T A ---			TCTCAGCTTCCACCTGACCTGCA(T/A)CAACAGCCCAAGTTATTTACCAAGAAATTTGTTGCGTTTCA ATGTAGTGTAGCTTTAATACACTGCACITGTTTG
EST12949 2a	52 A G ATACTGTT	GGCTTTAATCA TAACCTAATA	TGTGTCCTGT GGGTCTC	AGGAATTCATGAGGCTTTAATCATAACCTAATAACTGTTAAAAAACACAC(A/G)TCTGTCACTTG CAGAGACCCACAGGGACACACATCTCTCTCCATACATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104 C T ---			ATTTTGTGTTTCTTAAATGAAGCATAATAAACAGTTAAATCTCAGAAAAATCATCTATAGTTGA GTGTAAACCTCCCTAAATCAGTCTTCTAGGGCCACA(C/T)GGAGCAGAAAGCAGCTTCCCACCCAAAG CACCTCTGAAT
EST13117 6	66 A G ---			TGCTGTCTGCATCAGTCTTTTAAAAATTTAATCGCTTTATACAATTGACACCAATAAAATGCACTA /G)TATTTAAAGTTTACAATTTGAGAAGCTGACACGTGTCCATACAGACACACCTCATTTTACTGTGC TTTACTG
EST13121 6	44 C T ---			TCTGCTTTAAAGATTCTTCATAGCTGCTTAGGTTTGTCTTCC(C/T)AGCATATTCAGCTATAATCA CTTACATCCCTCCACAAATATTCCTGTGTGGCCAGGCCAGTCTCCTCAGTGTCCCATGAATAGCC AGTCTTATTTCCACTCT
EST13226 6	74 T G ---			AACTGTTTACTAACAAAGGTGCTTTAATTTGAAAAGCATTTGAGGAAATAAATTAATGAAATAGTCT GGCCATT(T/G)GACTAACAGTCTACAAATTTACATATCCGTCACTCAGATGAGCATATACCAAG TCAGAGGAAACAAACATG
EST13230 6	72 G A AGAGACGC	GCTCAGATGTG ACAGAGA	CCGGCTCCTGT ACAGAGA	GCATCATCAGCGGCTTTTACTGAACCTTACAACCAACTTGOOGCTCAATATGCAGCTCAGATGTGAGAG ACGC(G/AT)CTCTGTACAGGAGCGGTACTGTCTTCAATCCCTTTCATGATGAGGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C TCTCAGGCT	AACCAGATTT TGACAAAAA	ACAAGAGGTT TGACAAAAA	AAAGATATAAAACAACTCCCATCAGTAGCAATACAAAGTTATACATTTTAAACCAGATTTTCTCAGG CCT(T/C)TTTGGATACCTTTAGTAGTTAACTCTCTTTTGICAAACCCCTCTGTATATAACCA

EST13278 2a	51 A G	C T T C A C C G A A C A A T A T T T T A G	C A T A T T C T T G G G T G G T G A G A A	T T C G C A G A A C G T T T T A C A A G C T C C A A A C C T T T C A C C G A A C A A T A T T T T T A G G [A/G] A T T T G A A A T T A T T T C T G T A G T T C T C A C C A C C C A A G A A T A T G A C A G C T T G
EST13282 0	99 A T	C C A C A C A T T T C A G T C C A A G A	G A T G G A A A A T T T G A G G A A G G T T	T G C C T G A G A A T C C C A C A C A T T T C A G T C C A A G A [A/T] A A C C T T C C T C A A A T T T T C C A T C T C C C A T C A G A G G
EST13290 9		C A A T T T T T A G A A G T T T G G T T T	A A A T C A C T T C A T G G A A A T T T C A	A G C T A C T C G C A A G C A A T T T T T A G A A G T T T G G G T T T C T T [A/G] C T G A A A T T T C C A T G A A G T G A T T T T T T T C T G T G C T T A A C T T C A G T T A C T T A A G A C C T A A A A G A C A A A G T G G T A T C A C A T C A C A T A T T T T G T A T G T G G G C T T T T T G
EST13518 2	45 C G		---	G A A C A T C C T C C A G T A T T G A G G T T A A A A T G A T T C A G C A T T T A [C/G] A C T T T A A A A A T T A C C T C A A T G T C C T G G A G T C G C A T A G T T T A A A A T G A C T T C T G C A C C T T C C T T A T A A C C T T G A T T G
EST13522 8a	66 A G		---	C A G G T T G G T A T T C T C A A C T A G G A G C T A T T T T G C C C C A T C C C C A C C G C A G T G T C T G G A G A C [A/ G] T T T G A T T G T C A C A A C T C G A G A G G T G G T G C T A C T G G A A T C A C T G G G T A G A G G C C A
EST13568 6	69 T C		---	C T T T A A G G A A G T G A C C A G A T C C A A T G A C C A A C C T G G T T G A G A G C C A T T G G T C T A G G A G T A G A A A [T/C] G C A C A C A A G G A A T A A G G G A G A A G G A G G T T C G G T T A G T T G A G G G A G A A A G T T G G A A G C A T T T C A A G C T A A G T A A A T G G T
EST13785 0	101 C G		---	A A G A T T A C G G A C C A T A A G A A C T G C C C C C G A C C C A C C A T A C A C A C A C A A T T T A T A G A C A G G T A A A A C C A A C T G A A A G G A A C A A A G T A A T G A C T T T C T T G A A C A A A [C/G] T G A T T A C G A A A G T G A A A G G C T A C A G G G T G A T T A C T A
EST14038 1	25 A G		---	C C T A A C C A T C T G T A A C C C G A G C C C [A/G] C A G T G A C C G G G A C T T G C T G C T T C C C C A T C C C A G C C C T C T C C T A T C A G C A T C C G C T A A G C G T C A G T C A G C A G G T G
EST14083 7	23 A G		---	C A A T G G T G T C C A T G T G A A C A T A [A/G] A C C T A T T C A T A A A G T T A A A A A T A A T C C C T T C T T G C A A T C A C A G T G C A A A G G C A T G A G G G T G A A A G T C A T C T G C T A A A A T G A C C G A A C A G A G G A G G T A G G A G G
EST14221 5	42 T C	G C A T G C T A G A C A G A G G C A T T	G G A C A A G T C A A A A T A T T T T T A A A G A	A A A T C A A T G C A T T C T T G G C A T G C T A G A C A G A G G C A T T A [T/C] T T T T G A A G A T C T T T T A A A A A T A T T T T G A C T T G T T C C C C C T C A C A C T A T T T T A A A T T G T
EST14812 2	50 A G A T A	C A A G T C A G C T T C T A C A T T C T G A	T A A A G A T T T A C T T A A A T C C C A T T A T G T A C T	T T C A C T T A G T A C C A A G G A T G C C T T T C A A G T C A G C T T C A C A T T C T G A A T A [A/G] A G T A C A T A A T G G G A T T T A A G T A A A T C T T T A G A A G T C C C G A G T T G C C T T T T C T A A C A T T T T C A T A T C A G G T G A A A A C A A T T T T T C A T A T G G G T G A T
EST14815 3	128 A T A T A T A C T G G T T	C A T C A C C C A C C G T A C T G G T T	C G G G A A A A C A G T A C C G G A A	T T T G C T T C G G C A A T A C A T A G T G C G C A A T G C A G C G T G A G T T C G C G C C G T C T C C C A C T G A A C C A G T A A T T C A C C A G A C A A T G G C G C A C C A C T T A A A T A A A C T T G C C C G T C A T C A C C C A C C A T A C T G G T T [A/T] T C C G G T A C T G T T T T C C C G T A

EST15420 6	109	A	---	---	---	TTTAAACCCCAAGACTTGTAGATGTCAGGACTCCGATCATTTTCTCTGCCTATAGCTTGGATATCTTA ATCTCTCCCTTTTGTCATCAATAATCATATAGCCAAGGGACT[C/A]GGAATTTTGGCTGCTTCAAGTCA TTCCAAACCTCTCAGG
EST15700 6	48	G	C	GGA	GGAAATAGCTGA AACAGAGATA TTATTCTC	GTCACCAAGCCTTTTATTAGACGTGAAAGACAAAGACAAACAGAGGA[G/C]AGCAGAGAATAATA TCTCTGTTTCAGCTATTCAGGATGTTATGCCAATTATCCAGAGTCCCTTGATCTGATGTAGTA
WI-16739	57	G	A	CACAAGC	GATAGTTGATG TTCATTATTCC CTATAA	AAGGATTGAAAACATACCTAGATCATATAAATTTGTGAAGGTTTGCCATCACAAGC[G/A]TTATAG GGAATAATGAACATCAACTATCCTACAGCTAAACCTAATGAAGACCAAAATTCCTCCCAAGGT
WI-16782	96	C	T	CACTGAAGG	CTTCTATCTTT CTGTCTCTCCA TC	CTTCTCTCTTCTAGACGTGGAATACACACGGATACAGTATCTGGAGATGTAGCAGCTGGCTCTGAC CATAAATGGTGGGAGTCTCACTGTAAAGG[C/T]GATGGAGGAACAGAAAGATAGAAGAAGTTTGGGGT GCTGATGAAATTTGTGGGG
WI-16783	64	A	G	-	TCCTGAGATGT CTTTACCTGA G	AAAAATGTAAACCTTAGAGGTTGCCTCTTTTGTGCACCTTTTCTGTAGATGTCTTTTACCTGAG[A/G] CTAATAAGGATTGAACCAAGCAGTATTTTAAATGGCAAAAGTCCAGATGTAACCTCGAGT
EST15948 2	58	T	C	---	---	CAGGACTTAAGGTCAATTTTGCCTGGAAGACTTTAACTAAAGGTGAGGCAACATAGGA[T/C]TGTGA CAGCACCACTGGACCAAGGAGTGTGAAATGTCACACTAGCTGCCAGCCCTTTTTCCTGGC TGCTCTGCCTCCAGAGC
EST16088 8	89	G	C	---	---	GGTTTGAAGACGCAGCTTATCTCCACCTGCCACTGGGATTCTCATTTTGAGAGCTGTTTGTGACGC TTTTCCAGAAAGGCCGCTC[G/C]GGGTTTCTGAACCTCTATGGGCAATTTTAGAAT
EST16089 9	96	C	T	---	---	CGTCTGAAGTTTCTTTTATCACAAGTCACATCAATCCCTCGGGCCCCCTGCTCAAAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTCTC[C/T]AAGAGCCATCCCTGCCCTTTCTTTGCT
EST16100 1	24	C	G	---	---	ATCCAGCTGTGAAGGGACAGGAG[C/G]GTAACACACAGTCCATTATAAGGGGTGTGCACATTCCTCA GGGGCTCCAAATAATGCAACATTTTCACTCGTCCATGCTGCTGATAGTTTCATAGTAAAAAAGTC ACTCCAGACAGGTTGGCTC
EST16104 9a	83	A	G	---	---	TTCTTTTAAATAACCCACACACACCCCATGACACTTCCAAATTTACAGAGCAAAAAAGTGATTTCAG CTGGTTCTCTCCAGGA[A/G]TTGGCCCGAAGCTGGCTCAGTTCACCTCCAGGACCTCAGTC
EST16118 0b	119	T	C	---	---	ATGGTAAACAAATCAGTTCAGGTTTTTCTGTAACAAATGATCCCTTTGGTCTTTCCCGTGGCAGT CTCCTAAACAACTAAACCAACCCCTCTACGTCTAATCAGTCACCTAAGATA[T/C]CAGGTGGCAAGT CTTTCACA
EST16118 0a	32	C	G	---	---	ATGGTAAACAAATCAGTTCAGGTTTTT[C/G]TGAACAAATGATCCCTTTGGTCTTTCCCGTGGC ATGCTCTCTAAACAACTAAACCAACCCCTACGTCTAATCAGTCACCTAAGATATCGAGTGGCAAGT CTTTCACA

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EST16151 2	53 C T ---			AGCCAATTCAAACGAACTCTATCAAAACACACAAGGGCTAGAGGAGAGATT[C/T]AATGAACGT AAATAATTCAAGGCAATTTTGTATCTAAAGCATTTTGTAGCTTACAAAGGCATGAATGAGGTGT GGTCACGTTTTGTATAGGA
EST16182 6	54 G A ---			CATTGGTTGGGTAGGAAAGATAGTAGTGCAAAATAAAATGGTAAACACAGCAG[G/A]AAATGGAA TTATAGCTTTCTTTTCATATAGGGAATTGAATTTATTACTGAGGTGATAGGCAGAAGTAGTA
EST16183 2b	59 A G ---			GCAGGTAAACTGTGGTTCAACACGTAATTGTTCTTTCATAAAGAAAGAAATATCTAGTTG[A/G]GTAG AGGAAGGCACGTGCTTCTGGCCCTCTCTGTTTCATATTTTATGTCACGTGCTCTAACGTGGGCCGTGT GCAAGAGATCTTTGAGA
EST16198 4a	28 G A ---			AATCTTAGGCTCTGGCTTTCAAAATCA[G/A]TACAGACAGATAAGAGCTTTAAGTATTTTCGCATTT CCCCAGAGGAAAGTCAGCATCATATAACCCACATGGGTACATGCTCAGGCACATGGTGTC
EST16229 2c	52 T C ---			TGTGAACCTCGAATTCGTTGTCCAAGTCTGAGTCACAGTTTCATTTTGGGAGTT/CJCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGCAGGATACTCCACTAGCTGATTCAGACAGGCAGAGGCTGCA
EST16229 2b	45 T C ---			TGTGAACCTCGAATTCGTTGTCCAAGTCTGAGTCACAGTTTCATTTTGGGAGTTCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGCAGGATACTCCACTAGCTGATTCAGACAGGCAGAGGCTGCA
WI-16816	124 A G TGGGTTA	GGAGCCATTGT	GCCTAGATTTT GTTCAGGACAG	CAGACTTTTCTCACACCTCATTTGGCTGGAACCTGGGTACATGCACATCCTTGAACATATCATTTGGCAA AGGGAATGGGTATCAAAATTTGCTTAAGGCCAAGCAGGAGGCCATTGTTGGGTTA[A/G]ACTGTCC TGAACAAATCTAGGCTC
EST16269 5b	49 G A ---			GCACCTCTCTGTGGCTTGCTCTGCCAGCTGCTGCCAGTGCCACAG[A/T]GGCTAGCCCTCATGG CAGAAGCATTTTAGCCAACTCTGGTCTGCTCCACTCTCTCTCTCCGCCGCTGGGGCTCACCACC TCTTCTCTCTCAATC
WI-16824b	83 G A ---			GTCACCCCGAGCCAATGCTTCAGGAATAAATGATGGTGTGCTGCAGCTGTTCTTATGAAGAAGTCAG AAGCTGATAAACGTGG[G/A]CTTACACCTTAGCAGCGATAGTTTCCGGTCCCAAGTGGGTGTGGA GCCTTCCATTATGGGAATA
WI-16824a	47 T C CAGCTGT	TGATGGTGCTG	CAGCTTCTGAC TTCTTCATAAG AA	GTCACCCCGAGCCAATGCTTCAGGAATAAATGATGGTGTGCTGCAGCTGTT/CJGTTCTTATGAAGAAGTC AGAAAGCTGATAAACGTGGCTTACACCTTAGCAGCGATAGTTTCTGGTCCCAAGTGGGTGTGAGC CTTCCATTATGGGAATA
EST16445 3	96 T C ---			TTGCTTTTATTAATCCAGAACGGCATGCTACAGATACTGTACAGCATGAACATTTATTATTACAAA AATGGCTTCCAAACCAATTAAAATGAACTT/CJGGAAATAGAGCATAAAACGGAAACAGTAACATCA
WI-16857	47 G A A	CAATAAGCA GCTAATGGCA	TGTGAATTGGG AAGACCACT	TATAATCCATCTCTCAACACACACACAAATAAGCAGCTAATGGCAAT[G/A]CTAGTGGTCTTCCCAA TTCAAGAGACCTGTGCTTCAAAATTTTCTCTGATAATGTGGAGAAATCTGCTCTTTATGTA

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WI-16879	79 C	T	GATACAGGCC ATAATTTCCCA	C AAGGCTTCT AGAACTAGAGT CC	AGACAGGTCAAACTCCTAGGGATAAAGATATAAATCCAGACAGCATTATTTCCAGATACAG GCCATATTTCCCA[CT]ATAGGACTCTAGTTCTAGAAAGCCCTTGGGGAGAACAGGCCACCCAG
WI-16882	99 A	G	GAAATGCCA CGTCTCTGAC	GACACATGTCA GGTAAATCGC	ACATGAATGGCAACCTCTTAGTGGGAGAGACAATTCTCCCTTTTACCCAAAGGTTACTCTGAC AAGGCTATGAATGAATGAATGCCACGTCTCTGAC[AG]GCGATTACCTGACATGTGTCATCTCCCT
WI-16888	70 G	A	GCTAATTTGG GCAGGTTC	AATGTTCTGAA TTGACCAAAAT TAA	GTAGTAAATGTTCACTACCTACCCGGGGAGAGCAAGAACCATGGAACGGTAGCTAACTTTGGGCAGG TTC[G/A]TTAAATTTGGTCAATTCAGAACATTCCTCAAT
WI-16905	75 C	T	ACTGGCCTGT GTTGTTCA	GTCTACTCT TCTAGGCAGTG GG	TTTGTGTTTGTATTGGCTCCCAACATCAGAACATAAGTTCCATGAAACAGGAACCTTGGCCTGTG TTGTTCA[CT]CCCACTGCCTAGAGAGTATAGACA
WI-16910	74 G	A	AAGAGTAAAG ATGGCGCTAG AA	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTCAGTATGTCTTAAGGAGGTTATATTCGCTATGACTTTCATCTCAGAGAGTAAAGATGGCG CTAGAA[G/A]GTATCTGTATAGAAACGATACITTCATTTGGGCCTGAACCCAGTGAAGGT
WI-16918	93 C	T	CAGCCATTAA CACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAGAAAAATAAACTACCACCATTCCTCTGCTACCACAGAGCACATAAATCTAGGAATTTGAC TTTACTGCAGCCATTAAACACCCAGCAC[CT]GATGCCACTTCTGTATCAGGAACCTTAACGTGACAACC ATGAAAGGTCTCTGAAAG
WI-16947b	127 A	C	GGAAAGCAGA CCTGGG	ATGTGATTGCC CGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAATAGCCCTGGAGCACAGGATT TGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAGCAGACCTGGGG[AC]CCA CGGCAATCAGATGAGATG
WI-16947a	58 C	G	CATGGAATA GGCCTGGAG	GCCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAATAGCCCTGGAG[CT]GACAGG ATTTGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAGCAGACCTGGGGACCA CGGCAATCAGATGAGATG
WI-16966	43 T	C	AAATGCACAC TACATAACAA CCTAA	TGCAAGTTATC AGTATAAAAA CTCATATT	CATTTGTTTACTTTAAATGCACACTACATAAACCCCTAAT[CT]CTTAACCTTGGTCCAACCTATT AGTATACTAATATGAGTTTATATCTGATAACTTGCAATGCCATTAA
WI-16995	55 T	C	GAGCAGTAGA GACTGAGGTA AATAGTATT	CATGTTGATTT CCAGCGGT	TTGAGTGCCAGACATCAAGCATAGAAGAGCAGTAGAGACTGAGGTAATAGTATT[CT]CJACGGCTGG AAATCAACATGCCCTCTCTCTGTGAAGTTGTCAGCATGGAGCTGAGAGGCTGAGTCAATCT
WI-16992b	60 T	G	---	---	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAGTACACTGTG[AG]CCCTCATCTGAGATGTG TAGGACTGTAAAGGAATGTTTGGGGTTAGGAA
WI-16992a	46 G	A	AAGCACCAG AAGTACACTG TC	CACATTCCCTT ACAGTCCCTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAGTACACTGTG[AG]CCCTCATCTGAGATGTG TAGGACTGTAAAGGAATGTTTGGGGTTAGGAA

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WI-17010	23	T C	TTCACAGGA AAAGCCATG	AATAATACGGT GTTTGAATGT CA	ATGTTTCAACAGGAAAGCCATGTCATGACATTCAAAACACCCGTATTATTAGAAGCTCATTTAAT TGTTTAATGCAGACAAAAATCAAGGCTAACTAAAGCAGATCCAAATGACCCAGTGATCAACCTAGA GGTCCACG
EST171.7 9b	74	C T	CACTCGGCAC AGACAGAGT	GGGAGGCGAGG GGTG	ATTCCGCTCCAAACAGCATCCAGGCCGGGCATCTCCCCACGATTTTATAATACACTCGGCACAGA CAGAGTCCTGGAGCCATGGGGCACCCCTGCCCTCCCCAGGCTCCCTAAGTAACAACCT
WI-17040	94	T C A	AATCTCTTAT CATCTCAAGCC	GGACTATGGCT TATTCAGTGAT G	CACGCGTTCATTAAATTTGGTACAAAGCATGAACACTCAGGACAGATTGGCACAATACATGCAGTTC GAGAATCTCTTATCATCTCAAGCCAGTC/CATCACTGAATAAGCCATAGTCCCAGTCTCGTTTTTCC AAATCTTCTCATATTGT
WI-17044	47	G T G	GCCAAGGGAT TAACGTATAG	GGGGATCCOCT TGTTTAAGA	TTGTTTGTTTTTTCTCCTCTGCCAAGGGATTAAACGTATAGGTC/GTCTTAAACAAGGGGATC CCCCACTTATAGCTGACAGCAGCTGCAACCACTGACTCTCCTGCAGAAATGGCAGGGAATCGAAT CAAAAAGAAAAGCAAGTG
WI-17021	62	T A ACTC	TGGACTTGTC GCCTATAACT	TGTAGAGTTAG TGGCAGCTGC	GCATGTTGGAGCAGATCTCCATGGTAAGCCAAAAGTGGACTTGTCAGCCCTATAACTACTCTT/A/G CAGCTGCCACTAACTCTACAGGCACAGTAACACTTATACAGGAGCAGCATGCCAAAAGTGCCTGG GAGTGCCCAATAAAATCAA
WI-17065	90	T C CTT	CCAGAAAGGA AAAGCATAAA	CCCAAGAGAC AATGAAATCCT	TGTAAAAAATGTAGACATGGGGAAAAAACATTCGTAAATCAACATGTGCTGTTTTTACTTCCGGTA CCAGAAAGGAAAAGCATAAACTTC/CJAGGATTTTCATTGCTCTTGGGT
WI-17066	32	A C T	TGTACAGCCA ACATCACTGTT	GAGATGTTGAA AATGTTCTGGA A	TTCTATAAGGTTGTACAGCCAAACATCACTGTTT/CJATTCAGAAACATTTTCAACATCTCAAAAAGA AACTCTGCACCCATTAGCAGTCACTCCCTGTAGCTTCCCTCATAGGCAATGGCAACTGCTGATC
WI-17074	86	T G ---			TGCTGACTGTCATGACTTAGTAAGGCCATCAGAGGTTGCCAGAACATCTACTCAACTGTCCAAGCAT AACCTCCTACACAGGCCCTT/GJCTACATAGGAGTATATTTGGCCAAAGACTCACCAGTAGAAGTGATT
WI-17104b	108	T C ---			CAGATGAGAACTCATGCTGGCTCATCTGCAAGCTTCTGATGCTTTGGAGCTTTCCCATTCATTCCA AATCAGAAAGCAGTCAAGTGGCCCGTGGTTCCAGACGGCTTC/CJCTCTTTTGTAAAGAAATTA
WI-17114a	37	T C	TTTCCATCAAG GACTTTGTTT	TTGTATTATAA ATAGCAGAGTG AAGAGAC	AGCGTCCAACAGATGTTTCCATCAAGGACTTTGTTTT/CJGTCCTTCACTCTGCTATTATAATAC AAGCTACCTCCCAAGGCCAGATGCTTAAGTGCTAAAAGAAAGACTGCAGCCACAATCAGAGTTACAT GGGA
WI-17150	76	T G CTCTT	GATGAAATTC AGATAGTCTTC	TTCTCAGAATC CTGGAAGATAT G	CGTGGCTGGACTAAGTGCTCTTCCATGTGGACACATCTCCACTGAACAGGATGAAATTCAGATAGTC TTCTCTTTT/GJCATATCTCCAGGATCTGAGAAAGGCCCTCTTGTCTGCTCTAATTT
WI-17163	43	A G TAACGTT	CATTCTTTGT AAAATAACAA	CAGATCTTGT TTTTGCCTT	GAAATCGAATACGTCCATTTCTTTGTAAAAAACAATAACGTTT/A/GAAGGCAAAAGCAAGATTCTG TAAACCAACATTGAAAAGGGGACACAGGGAGGGGAGAGGAAAGGCCAGATTTTCAACGGTTT CCTCCACATCTGCAGACAAA

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WI-17178	127 T C	GGATCCCTCA	COCTCAATTTT	AGCAATGTCCCTCCAAATTCATTAGCTATGATGAGTTATCAGTTTCATTTTCAGAGGGAATTACTGG
		CGAGGAGC	CAACTGCTTC	GGCGAGGGGGTTTAAATATCTGTGATGGGTTTAAATTCAGTGAGGACTCCCTCATGAGGAGGCT/CJAGAA
WI-17180b	81 C G	---	---	GCAGTTGAAAATGAGGG
		---	---	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAAATCCTGCACCTCCCAAGTCTCGTGCACAG
WI-17180a	47 T C	CACAAAAATA	TGGACGAGAC	GGAGTC
		TAGAGATCC	TGGG	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAAATCCTGCACCTTCJCCCAAGTCTCGTGCAC
		TGCA	---	CAGGCTTCAACAATACCAACATCTTGCCCATTTTGTTCATTATCCGACCCACACTGACAGATGAG
WI-17156	54 G C	TGTTCTCTAAA	CAAGAAATAT	GGAGTC
		CTTTAGATATC	ATATTTGATTC	TGAGGTAGCAGGGCATTTCTAAGAAATGTTCTCTAAACTTTAGATATCTCCCATTCJTTCCACAGA
		TCCA	TGTGGAA	ATCAAAATATATTTCTTGTTGGAAATTTTAAATGTTCTTAACATATCTGCCTACCACCTCAAT
WI-17149b	79 T C	---	---	TAATATCTTG
		---	---	CAGCGATTAAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACATCTCATGCACGTGCGTGGAA
WI-17149a	48 C G	CAAGGTTGA	CCACGACGTG	ACCCAAATGTCA/TGCTGTATGAACACTACAAAGGATGGGAAAGAACACATTTCTCTCACA
		AGGAGGAACA	CATGA	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACATTCJTTATGCACGTGCGTG
		---	---	GAAACCCAAATTTGTCATGTATGAACACTACAAAGGATGGGAAAGAACACATTTCTCTCACA
WI-17197	67 G A	GCAGAAAGTAG	GGTGAGGTGGT	ATTTTGCTATGTTGCCCTGGGCTGGACTCCAGCAATCTCTGCTGCCTCAGCAGAGTAGTGGGGCTACJG
		CTGGGGCTAC	GCATACC	/AJGGTATGCACACCTCACCTGCTTATCAGTTTCGTTTAAAGAAATTTGACTTTTAGATGCGCA
		---	---	TGATTTTCAGTACTTTTCTCCCTTGTCCCTAGTTTTCJTTAATTTCTCAGTGGGACAAATGGACAA
WI-17198	38 A C	TCCCCCTTGTC	TCCATTTGTCC	ACCACTCTCTGTTTGAATTTGAATACACAGATACATGCAAGATATCTTACAAGAAACAATGCACATCC
EST18753	27 C T	CCTAGTTT	ACTGAGAAAT	TTC
		CTACCCAGGCT	GGATCGCATGA	TCGCTATGCTACCCAGGCTGGTCTCATTCJTTACGGCTCATGGGATCCCTCTGCTGCTGCGTGG
		GGTCTCAT	GCCTGA	GATAAGACACAACCTGCCACCGGCTGCCCTAGGAGTAGTCTTAATGCCCTGATGGTGGG
WI-17108b	74 C T	GCCATTCAGTC	AACTACGATTT	TTATTTTAAACATAACCAGATGCACCTTGGTTTTTTACATTCCTCTGGTTGCCATTCAGTCTCAAAGT
		TCAAAGTAAA	ATCATATGCTC	AAACACJCTJGGGAGCATATGATAAATCGTAGTTTAAAGGAAGCCATAGCACTTACAGAGT
EST19067	41 A G	---	---	ACACAAAATTTACCATCGTGACCAATTTAAGGGTATAGTTCAJGJGTGGCATTAAGTACATTTCAACT
		---	---	TTTTGAGCAACCCGCCATCACCATTTCATCCATCTCCGTT
EST19067	40 A C	CGTGACCAATTT	AAAAGTTGAA	ACACAAAATTTACCATCGTGACCAATTTAAGGGTATAGTTCAJGJGTGGCATTAAGTACATTTCAACT
		AAGGGTATAG	TGTACTTAATG	TTTTGAGCAACCCGCCATCACCATTTCATCCATCTCCGTT
EST19125	28 A G	TTC	OCA	CTGTTTCTCAGAGATGACACTGCCAACA/JGJTCACAGATTTGCATACATAACAGTTATGTATTGGC
		---	---	TATTCACAAATTTACAGTAGTGTTTTCTCTCTGAAAAA

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EST20824 8	115 T G	AGTCGGGAGT GCTGATTG	AAGATTTTATC TTGGACCCGA	GTGTGAAGCCGGAGTTTATTATTATTCAATCAGTCTCTCTGAAAACCTCAGGGATTGAGGTTTTTA AGGATAACTTGGTGAGTAGAGGGCCAGTAAGTCGGGAGTGCTGATTGT/GJTCGGGTCCAAGATAAA ATCTTAGG
WI-17347	50 A G	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGTGCTA	TTGGTTAAATGATGCCCAGATGGGGTCACATCCTCAGAACTTCTCAGCCT/GJGTAGCACAAGTGG ATGCTTGAAGAACTCAGTCTTGGAACTCAGACAGCAATGGAGACGGGATGTGAGTGGGACCA
EST21904 b	128 G A	TTCATATGGCC ATTTTAATAA GTG	GGCAGGTGTTC AGAAAGCAT	TGATTGTGGTCTGGGAGCAGGTGGGCAGTTCAGTGAGGAGCAGAGGAAAGTAGACGCAGTAGAAAT GAGACTGGAATCAATAGAACAGAAAAATGTACTAGGCTTTTCAATATGGCCATTTTAAATAGTG/GJA/T TGCTTTCTGAACACCTGCC
EST22111 3	82 T C T	GAAGATCTGT CTGGCATTCCT	TGGAAAAACA GCCCCAC	CAAACAATGTAGACATAAGGGAAACAAATTCAGAGAGCTCAAGTCACCATGTTTGTAAAGAGAAGAT CTGCTGGCATTCCTT/GJGTGGGGCTGTTTTCCAAGGCACA
EST22197 2	78 T C	AATTATTCTGC TATTCCTGCCA	ACCATGAAGG ATGGGT	GTTTAAATGATCACTCACCAAAATCCACAGGAGAACTTTAAATGTTTACAAGCACCAATTAATCTGCT ATTCCTGCCAT/GJACCGCATCCTTCATGGTAGAGTATCACAAAGTAAAGTTTCTGGTTGTTTCATC TACTTAAAAACCA
EST22311 9c	92 T C	---	---	TTTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATATACATAAAAAATCCACCACCTGTAAACAG TAGCATTCATGGTTTTTACTCTAT/GJGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9b	54 A G	---	---	TTTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATATACATAAAAAATCCACCACCTGTAAACAG TAGCATTCATGGTTTTTACTCTAT/GJGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9a	41 T C	GGATTAGATC ATCTTTTAT	TTGAATGCTAC TGTTTACAGTG G	TTTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATAT/CJACATAAAAAATCCACCACCTGTAAACAG CAGTAGCATTCATGATGGTTTTTACTCTATTTGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22319	19 A C	---	---	TCGAGGAGCTCTGAGGAGC/GJ/CACCAAGGGACGTGTGTCGCCAGGGCCACCGTGCAGGGCAAGTGTG GTCCAACTCCTTCCTCCCTTTACAAAACTCCAGCCTCACCCACACAAACACTGGCTGACAGGGCTTCT TAAGCCTTTTTTAACGT
EST22433 c	103 A G A A	AAGACATGTT CACCAAGTGA	CAGCTTCAGCT TAAGTGACAGA AGTTTCAGTTT	GATGTTAATGACITTTCTTTGAGATATGATGGAAAAATATTCAGGTACACATGGAAGACATGTT CACCAAGTGAACCAATCTAACCCAGAAAGCTTTACC/GJGTCTGTCAGTTAAGCTGAAGCTGAAAT CTGGGAGCTTGACATGCTG
EST22657 9	71 A G	AAATGGATCC TTATCTGCACA	GCATGAATTT T	TATCCATTTCAAGAAAAAAATGACTTAAAAAATACAAATTTCTATCCAGAAATGGATCCTTATCTG CACA/GJCCATTGAAGAAAAAAATTCATGCAAACTGAAACTATGCTTT

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EST22993 5b	71	T C	ATCCTTTTGT TCTACCCCC	TTGCTGTAA TTTGAAGTAA TG	GCCTTTTATTGCTCCTTTTAAACATCAAATGTTTATAACACACATTTGATCCTTTTGTCTACCCCCA ATTTC/CATTACAGTCAAATTACAGGCAATATAATAGGCTAACAGAAIGCTTGCAATTT TTATTTCTCAGCTTACCAATTTGCTACTTATATCTCTGTACAAGGTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTTAAATTTTATTAATCTTTGCCTTT/AJATGGTTTGACAGTTTGTCCTTTCT T
EST23021 0	108	T A	---	---	ACAGAAATTTAAACATGCAAGTTTCATTTACATTTACCTTTGCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAACTTAGGCAAAAGCCATTTCTTIG
WI-17387	55	C G	CCTTTGCAGAT TGAAGAAAA	GCCTTTGCCTA AGATTAATAGT AACTACT	TTTTTGGCTTGTCTGCAGAAATAGATGAAAGAGAAAAATATACCCAGATACTTTGCTCACTCTCCCA AGTGCACTAGGCAATGTAAAGCTCCAGAGGCAG/C/C/GCTTACAGGAGGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG
EST23669 1	101	A C	AATGTAAGCT CCAGAGGCAG	CCTTCCCTCC TGTAAGC	AAAGGCTGTAGTTTGTGTTTGTGTTTCTTTCCTTTC/GJATTGATGGGATTTTAAAGTGCATATAACTGAAG GCAAGTCCAAAGGCTAGAGAAAGATATGAGGCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA
EST23733 9	31	T G	GGCTGTTAGTT TTGTTTGTGTT	TGCACCTTAAA TCCCATCAAT	CTGACAGTCCCTGTGTGCGGGGGTGTCCATGTGGGTGTGTGTGAGTGAGACATTTTACTCGCTCCC GTCCCGCCAGCCCTT/GJTCGGCCCTGCTCACTGSCCTTGGTACATTTGTATTTCTGCTTGGTTGAAA TACCATCAGCCTTCC
WI-17470	83	A G	GTGTCCTAGC TAATGAATGC	AATTATTATT TGCAGGCAATA CTC	TTTTTAACGAAATCTCACTACTGCAAAATGCATTGTGTCTCTAGCTAATGAATGCAIT/C/JAGAGTATTG CCTGC/AAATAATAATTGAGATTCTATTTTAAAGAGCTTAGAACAGTACATGGTGCATAG
EST25356 3b	95	C G	---	---	TCCTTGATACAGGTAACCCAGTTTGTACATTTATTCAGAACTTCACTGTATCTTCAAGTTTGTAT CAGCATCTCTGTGGAGAAAGCAGTGTG/C/GJATAATGTCAACATCAGGATTTCTTTTT
EST25356 3a	26	A C	---	---	TCCTTGATACAGGTAACCCAGTTTGTACATTTATTCAGAACTTCACTGTATCTTCAAGTTTGTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT
WI-17581c	99	C T	---	---	GGGTGACGCTCCAGAAATGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCAACACATT ACTACCAGTTATTGATAAT/CJGATAGAACCCCACTAGGCGCAATTTACATTGACGCGTCATGC
WI-17581b	86	T C	ATTCAACATT ACTACCAGTT ATTGCGCCT	CGTCAATGTAA ATTGCGCCT	GGGTGACGCTCCAGAAATGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCAACACATT ACTACCAGTTATTGATAAT/CJGATAGAACCCCACTAGGCGCAATTTACATTGACGCGTCATGC
WI-17596	86	A G C	ACTTCCCTGTG TAAACACTCC	CATTCTTATAG CTAGAAATCGA CAATAT	GTGTGCTGGTAAATGGATAATAGCAGTCTCTCATCTCTGAAGGGTGGGAAGTAGGAGAGGCCCTACT TCCCTGTGTAACACTCC/CJGJATATTGTCGATTTCTAGCTATAAGAAATGGGGCCCACTAAGTGGGTC

WI-17623	46 T C ---			---	TGTGGTTTAAATTTCCCATATAATTAATGGTGGGCACATTTTCGCATGTGCTTACTGGGTC ATTTCATATATCTTTGTGAAGCATCTGCTCCAATCTTTTGCCTGACTTTGGAGTTTITTTGGT
EST26419 1b	46 T C ---			---	ATTTCATACAGAGATACAAAGGCAACTATGTGCAGCAACAATCTGA/T/CJGGGCAGTCCAAACTTCT TGGGAGGAAGTAATTCATGGTAATGTTCATGATGGCTGTTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGATG
EST26419 1a	35 C A AG	ATACAAAGGC AACTATGTGC		CAAGAAGTTTG GACTGCCC	ATTTCATACAGAGATACAAAGGCAACTATGTGCAG/C/AJACAATCTGATGGGCAGTCCAAACTTCT TGGGAGGAAGTAATTCATGGTAATGTTCATGATGGCTGTTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGATG
EST26780 5	69 G C ---			---	TCAGCTTAAATTTAAGGGACATGTAATAAAGATGCATTTGACAGGACAGCAGACTAGTTCAAGC AG/G/CJAGGTTAGACCAGTAACAACCAACCAAGAAAGCAAGTGTCTGTTTCCATCTTGGCTTTACCA CACTTACAAACTGATACCC
EST26900 7	39 A G ---			---	TACTTCAGTTTAAAGGCAATTCACACAGAGACTGTCTC/A/GJGAGACGGGCACAGAACAGACACC GTAGAAACACCACCACCATGCATGACGGGAAGCAGAG
EST27152 1	101 C T ---			---	CAAAGGATTTTATTTGTTCCCTAAAAAGTAAATCTAGAAAAATAGCAACCCACTGCAAGAAGAGTT CTATACTAAACATTTTCAATCATCTCTCTCT/C/TJTTACATGGTGTACTCTTTCATGTACACAT CATCGGAACACAGACTGA
EST27504 0a	33 G A ATTT	GCATTTGCAA CAATTTAATA		GCTGGTGTGAT GCTACTGTAAAT G	TTTTTGCATTTGCAACAAATTAATAATTTATC/G/AJCATTACAGTAGCATCACACCAGCAGTCAAT AATGCCACTTTAGGCAAAAGTCTTTCAGTATTTCTGTACACATCTGTTAACAAGAACCCCATACATT GGTAAATTCATCT
EST27662 4	51 C T CTCCAGTCTTG C	CACATTTCTGTT CTCCAGTCTTG C		TTATGAAATG GCTTATGTAAC	ATCTTAAAGGACCATTAGAAAAGGCCAGTCACATTCCTGTTCCAGTCTTG/C/TJAGGTTACATAAG CCATTTCCATAAATTCATAGCCCTTCTTCTTAGAGTAACACACACTCTTGTITTAGGAATGTTT
EST27788 3	100 A G ---			---	ATTTTATTAGGCGGTACAATTCCAAGGTGTAAGGGTGAAGGAAGGCGAAGGCGAGGCAAAATACAT TATTGAGCTGAAAACAACCTTTACATTCAGGGAC/A/GJGCTTCCAGACAAGCCCATGTAGAACCCAGCAT GCCTTGGGACTGTGGAT
EST27828 4	58 G A AGAACCCAC C	GGAAGTCATC AGAACCCAC C		GTGCAGAGAGG TACTCCAAGTA C	TCCTCTAAACCTTCTCTGTTGGATCCCAGTGACGTGGAAGTCATCAGAACCCCA/C/GJGTACTT GGAGTACCTCTCTGCACCAAGATAGCTGGCTGATTTTCTGCTCAGTCACAATTTTACTTGAA
WI-18369	58 G A ACAATC	AATAAATTTT AATCTGTAC		TCAAGAAGGCC TTATCCATT	TAAAAATTTGAGATACATTTCCCAATGTAAACAATAAATTTCAATCTGTACACACAATC/G/AJAAATG GATAAGGCCCTCTTGACAAATTTCTGCCACCTCCGTTTAACGCATCAGAACTCAATCTTA/CIC TCCCGCTTCCAAAAGCTTTATTGGCAATATGCTCTA/T/CJAAAAGAATGATCAATCTGTGCTCT AAGTCAATGGAATGAAGAGCTGTGTCAGGGACACACCACCGCTGCTGAAGGAGACTGCTGTTGTG TCCACCCTTATTTCATAG
EST28036 4	37 T C ---			---	

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EST2483 7	31 T A	GGAGTAAAG GTGTTCTTCT TTAAA	TTTCTCGCATT TATTTTATAC CA	CATTTGGAGTAAAGGTGTTCTTCTTTAAA[1/A]ATGGTATAAAAAATAAATGCGAGAAACATTAAAG GGAGATGTACAGACAACAGACGAGACATGAGTTTGTCTGACTGTGACACATTGGTGAAA AGAAATGGTCTAGTAATCGTTCCAGGATTTCCGGTATGGGCCCTCCCTGTCT[1/C]GGACACTGCCAACCC CACAGCTGGAGGGGCACCTTAAGGCACGTCATTTTGATTAGA
WI-17724	50 T C	TGGGCGCTCC TGTC	TGGGTGGCAG TGTC	TGAGCCTGGGAGAAAGACCACAGAAAGTGAAGTGCTATTAGTTACATCATACCAAGTGTACATACTG TT[1/C]CACATGATTTATGGCTGTGTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGCA
WI-17730b	68 T C	---	---	TGAGCCTGGGAGAAAGACCACAGAAAGTGAAGTGCTATTAGTTACATCATACCAAGTGTACATACTG TT[1/C]CACATGATTTATGGCTGTGTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGCA
WI-17730a	39 A C	GACCACAGAA GTGAAGTGCT ATT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGAGAAAGACCACAGAAAGTGAAGTGCTATT[1/C]GTTACATCATACCAAGTGTACATA CTGTTACATGATTTATGGCTGTGTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGCA
EST29041 5b	53 G A	GGAACAAACA CATTAAAGCAT CA	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTTCATGAGGAACAAACACACATTAAGCATCATTTGTCACCT[1/G/A]GCTAACTCCT CAAAATCAACAATACCCCTTTATTTTAGCCATGAAAC
EST29128 4	58 A G	---	---	CTTTAGAAGGACACCAGTCTTGTGGACTTAGGGCTAACCTATTCCAGCAGGTGCC[1/A/G]TTATTT TCACITGGTTACGCTGTGAAGGACCGTTTCCAAATGAGGTTACAGTTCACAGGTTCTGAGCAGACATGA GTTTGTCTGGGACACT
EST29912 3	103 C T	TCTGCCAGCT ACAGGCT	GCCTAAGTGTC TCATTCTCTG T	ATTATTAGGTATCTGCTGTGGGGTGGGGTGGGAGATTGTTGAGATACTGCAACAGACACAAA AGCAAAGAAAGAAACATTTCTGCCAGCTTACAGGCT[1/C]ACAGAAAGAATGAGACACTTACGCGATG GCCATGATACACAGCAGTGA
EST29936 8	121 G C	---	---	TATTGGTATGCTTAGGGAAGATTCTGATTTAGAGATAITTAATCTTAAAGTTAACTACCCATGAAA TTTAAACCTTCTGTACTGGCTTCACTGATGAGGCAGTAAACTACATAGGGATAAA[1/G/C]AGCTCAGTA TCTGGAATCATGCTTCTCTG
EST30223 2	99 A G	---	---	AAATAAATACATCATGGGGAATGGGATATCCATCCCTCAAGCATTTATTTTGTAGTTACAAGCAA TCCAAATTACACTCTAAGTTATTTTAATATTC[1/A/G]GGAATTAATTTCTTCTAGTTCAATCTTTGGGA GG
WI-16260b	86 G A	---	---	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAAGACCCAGA GTTTCACAATATAGGTAGGAGTACAGGCTCACCTTCCCTTCCGTTCCGTTGAGAACTTCGTGGGAC
WI-16260a	59 G T	TGAGGTGGATT CAAGAAGAAA A	CTACCTATATT GTGAACTCTG GGT	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAAGACCCAGA AGAGTTTCAACAATATAGGTAGGATACAGGCTCACCTTCCCTTCCGTTGAGAACTTCGTGGGAC
WI-17835	30 G A	ACAGGAAATA TTGTGCTTTCT TG	TGGGGTATAGG AAACAGGC	AAGAGAAACAGGAAATATTGTGCTTCTTG[1/G/A]GCTGTTTCTTACCCCAATATCATAGAAT GTTGTTGCTTCTATAATGTTGAGCTTCAAAATCTTTTGTCTTAATCAATCCAAATGAATTACCTGAAT TTCTCCTCTTGTTCAAA

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EST31951 4	87 C T	GGGTGTCCAG CCAACA	CCACCAAAAT CACCTCC	ACAGCCATTATTATGTTACTTGGTAATATCAGAGACTGAAACATTTTCACTCTTTTAGCAATGACA TCGGGTGTCCAGCCAACA/C/TGGAGGTGATTTGGTGGGAATTCATTATCACAATTTATCT
EST31968 8b	95 T G ---		---	CGAATTTGTCCTCTTATTTTGTGATTCAGTAATCCATAAAGATTTGGGGGGGGTACTATAAGT GCATTTTATAAATGGGATTTTCTGCTT/GJAAGTGGCCACTGATTCCTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCC
EST31968 8a	75 T C T	GCGGGTTACTA TAAGTGCAATTT	TGTAAGAATCA GTGGGCAGTT	CGAATTTGTCCTCTTATTTTGTGATTCAGTAATCCATAAAGATTTGGGGGGGGTACTATAAGT GCATTTT/CJATAATGGGATTTTCTGCTTAAC TGCCCACTGATTCCTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCC
EST32063 2	103 C T ---		---	TCCATGGATGAACAGACGCTACCATGCCACATCCCACTCCCTCCGACCAGATGTCGTGGCCAGAGC TGGCTTCCCTTCCAGACCTAGCTGGCTTTGTAGT/C/TGTTGAGGCCCAATGAAATAGCAAAACGCAC AGTCATGTAGCACTCGG
WI-16303	65 A G ---		---	AAGGCTTTCOAAGCATTCAAAGGCACCTTGGGTGTTGTGCTCTAAGTTTCTGGTCACTGCAGCCCCC/A/G JTCTGATTAGGGAGCACCCCAAGCCAGTAACAATATGTTCTTGCAAG
WI-17800	29 C G	GGGAGCACAA GAGAACTCA	TTTCTACAAT TAATCCCAGTC TT	TGGACATGGGAGCACAAAGAGAACTCACT/C/GJAAGACTGGGATTAATTTAGGAAATATTTACACAG TTTCCACAAGTCAGAAGAGCTAATCCCAACCCCTGTATCTGGAACATACACTGCTGCCATTTTCTGC CCATGAAGGGAAATACCC
WI-17857	34 T G C	CCTAAAGTCTG GGATGACTTTC	TTGGCTTAGGT TCTACTTGATG T	AAACTGTCAATTCCTAAAGTCTGGGATGACTTTCCTT/GJATTCATCAATAGTAGAACCTAAGCCAAT TCAGAATCAGAATCCCTTTTGCCATCAAAATCCAGCTAACTCCAAGCTGAATTAATGTTCAATCT GTATCTGATGTAGTTAACCATGGCCTGTCATGATTATATTGCTATAAGGAAGGGAACAAAATCTTTA TAGTGTCCAAAGATAATTAATTCCTGGTTTAAATCTTTGCCAGCAAAAGCAAAATA/T/A]CCGACTGAC TGCCTCTAGTCTGTGATC
WI-17860	121 T A	TTTGCCAGCAA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	CAGCAACCTTTTTTTTGTATAGCCTACTTCTCAAAATTTGT/TATTTTGTGATTAGTGACAACG GGGGAATCTACAATGCTCACATCACAGTAACTACCA
WI-17866	43 A T	TTTATAGCCT ACTTCTCAA	CCGTTGTCAC AATCACACAA A	GAAAAAAGTCAAATGTGTTCCCTTTATGGGTGATGCCACCATGATTGCCTCACACAAGCATGATC AATCGCCACGAGA/G/A]ACTGGATGCCAAAGAGTATGG
EST33301 4c	80 G A ---		---	GAAAAAAGTCAAATGTGTTCCCTTTATGGGTGATGCCACCATGATTGCCTCACACAAGCAT/G/A] ATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGG
EST33301 4b	63 G A ---		---	
EST33460 1	44 G A CA	AGCGTGGTTTT CAATACTAAA	CTGTATTTATT GTTAAATATTT GCATTGTT	CTATCCAAAGATATTTATTGCAGCGTGGTTTTCAATACTAAACA/G/A]GTAAACAATGCAANTATT TAACAATAATACAGTGATTAAATAAGCCATGGCATATCCAGTTGATGTAATACTTTTGCAA

WI-17904	50 A G	AAAGCATGAC AATAAAATGA ACAC	CGCTTATGTTA ATAGTAATTCC CG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACATAAAATGAACACAC/GTACGGGAATTAC TATTAACATAAGCGATAACATCAAAACATCTGGTAAATGCAGTTAAACACAAACACAAATGA
EST34149 5	69 A G A T	TGCCAAATAC TCAAGTGTGA AT	AACACTAGCG AGAACAACTA ATAAAATC	GTITTTCTTTGAGTGACACAAGCTTGTTCATTTTGGAGAAATGTGTGCCAAATACTCAAGTGTGAA TJAGIGATTTTATTAGTTGTTCTCGCTAGTAGTTTGGTATCTATGAAAAAAGCAGCTAGTTTCAGC TTACAAATCACACAAGT
EST34343 8	95 C A	GGACCATATG ATATATAACT CCTAAAGC	---	TGGGAAACATAAAGTTAACTCAAGATATATCCAGTCTTTATGTTACTAAACATTTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCTC/AJTACAAAGATTAAAGAACTTACCATCAAAACACTTC CAGTGCATCAA
WI-17982	98 C T	GGACCATATG ATATATAACT CCTAAAGC	CAGAAATTATG TGATAATAACT CCTTCC	GGTACACAATTTTAAATGGAAGGAACACAGGTATGTTGAAAGAACATCAGTACAGCTGGAGACAGG GAGGGACCATATGATATATACTCCTAAAGC/CJTGGAAAGGAGTTATTATCACATAATTTCTGGGC GCTACAGAAGTTTTCATCA
WI-17993	118 A C	---	---	CTCAGTAACCTCCGGTGATAATCTGCCATTTATTGATTTATTATGATAAAACACCTCTCATTTGTA AAACAGCTAAGGTGACATCTCCAGACCCCAACCACTGCCCCGTGTAATGT/CJCTGCTGAGAGTCC ACATTTTGGAAATCCAAAT
WI-17996	84 A G	GTAGAGGCGA AGGGAACAG	AGGCACATGGG CAGC	CCCATCCAGAAACCCAGTGTGATGGTGGAGCAGCATGAAACAAACATCTCCCAGGCCTCGCAGT AGAGGCGAAGGGAACAG/A/GJGCTGCCCATGTGCCGTCTCTAAAGACGCCACCCTCAGGTTGATGT CACCTGTGGGAGACGGGT
WI-17136	33 C G	---	---	ATCTTTATAAAACACCATGTCCCTAAAATGT/C/GJATTCACATATATGCACACCTTCOGATGTAT AGGACACTGATCAAAAAGACAGAGAAATGTGCCCT
WI-18041	24 A C	---	---	GCCACTGAAAAAAGGTGCTCTTCC/CJGJTTCTAACCTCCCTGGACTCCCTCATTTGGAACCTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTAGACITTTGCTGTATTTTAAAGGCAGTGTGATGCTCCAGGAT TCAAACTACTTAATCA
EST35164 8a	57 A G	CACAGCCCTGC OOC	CCCTCTGGATT CTGAATCTCAA	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGCCCTCAAGCACAGCCCTGCCCC/CJGJCTTGA GATTCAGAATCCAGAGGGTGTCTCAGTCCCTTGGTTAGGTGCTTCTGTGACATTTCCCTCTTG
WI-18052b	67 A G	---	---	AGCGAATGAAATGCTACATAGGCTCCCTGAGTCTTTTCATGTACGAATCTTGGTTACACATCTTAGJ A/GJACAGCAGAGCTGCCCTGAGGGAGGGTTGTGTTTAAATGTCGTATGCATGCTCAGCACAGTGTCTGGC ATGGCCCATCCATGCTTT
WI-18052a	50 T C	CCTGAGTCTTT TCATGTACGA ATC	CTCAGGCAGCT CTGCTGT	AGCGAATGAAATGCTACATAGGCTCCCTGAGTCTTTTCATGTACGAATCTTGGTTACACATCTTT AGAACAGCAGAGCTGCCCTGAGGGAGGGTTGTGTTTAAATGTCGTATGCATGCTCAGCACAGTGTCTGGC ATGGCCCATCCATGCTTT
WI-18054	46 G A	GGGAGTGGG GAGTAAAA	CGTCACCCCTGC TTCCA	CTGTTGTGCTGAGAACAGAGGGGTCAAGGGAGTGGGGAGTAAAGJAT/GTGAAGCAGGGTGACG CATGCAGGAGTCCAGACAAAGACGGGTGATTGTTGCTCAGGTTGTAGCAACAGAGGTAATG

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WI-18064	54 G A	GTAGTGCTA AGCTGTATTC	CCAGTGGTATG ATTGTGACATT C	CAGCTGCCAATCATCTCTCAAAACCCGTGGGAGCTGCTAAGCTGTATTTTCAGAG[G/A]GAATGTCAC AATCATACCACTGGGGAGAGAGTAAGCACAGTGCTTATTAGTGCCAACTGGGGTACCTGGGAG GCAGAAA
EST35347 2	97 T C A A	GCATAAAATT TCCAGTTGGT	CCCTCGGCACC TGCT	TTAGCACCAATTCTAGTGGAGCAGGATTCCTGATCATGGGGTGAATTTTGTGTATCTGGGCTTCAT GGGATGCATAAAATTTCCAGTTGGTAAGT[C/J]AGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGG CAGGCA
WI-18070	28 A C G T G T A T	AACCCACTAC TACTCAGAGT	AAAACTAATA AGAACTGGA GGTTTT	AAACCCACTACTACTCAGAGTGTGTAT[C/J]ATATTACACATGAAAGATATAATCTTAGAAAAA ACCTCCAGTTCTTATTAGTTTGATATTTCTGTACTCAGAACATTTTAGGTTGCAAGGATATAA
WI-18080c	80 C T	---	---	TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCTCTTTGTAAATTAATACTACTATGCCGTG TTTGACTTTTAT[C/J]TCTTATGTAAATTGAAGCCAAATGCATGTTAATCTCTCTCTTTGGTGAT
WI-18080b	65 G A	---	---	TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCTCTTTGTAAATTAATACTACTATGCC[G/ A]TGTGTGACTTTTATCTTATGTAAATTGAAGCCAAATGCATGTTAATCTCTCTCTTTGGTGAT
WI-18080a	41 T C A G T C T C	GCAAATATCA ATATCAAACT	CAATTTACATA AGAGATAAAA GTCAAACA	TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCTCT[C/J]TGTAAATTAATACTACTATGC CGTGTGTGACTTTTATCTTATGTAAATTGAAGCCAAATGCATGTTAATCTCTCTCTTTGGTGAT GTGGGCATCCTATAAAAAGCAGCCATGTGTGAAACAAATGATATGCACAGAAAGCATCTTCT[G/A] TGGCTTGTACACGGGTTTCTTTCAAGAGGAAGATGATCAGCCCTCCAGCTTCTGCAGTCTAGC TTAGGAGAGGGTGTGAA
WI-18086	63 G A	---	---	AACTACATAGTATGGTCCCTGGCTTAGAATCAATGGGTAAAGCCCTTTAGTGACCTTTTGGTATCCC TTC[C/J]TTTGGTATGAAAGACAGACACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAGGGTGAG TCAGT
WI-18115b	71 C T	---	---	AACTACATAGTATGGTCCCTGGCTTAGAATCAATGGGTAAAGCCCTTTAGTGACCTTTTGGTATCCC TT[C/J]CTTTGGTATGAAAGACAGACACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAGGGTGAG TCAGT
WI-18115a	70 C T T	TTAGTGACCT TTGGTATCCC	AGAGGTCTGTC TTTCATACCAA A	TTTTGAGAAAGCACTCTGTAAGGCAAGGATGCATTCAAAAATGGCTTTGAGGATTAATCTTCTCTTTA GGTAAATTGCA[G/J]TAAGAACAAATAAAAGCATTTTAAAGTCCACTGCCGCCTTAGAAACT GGCAAAATATTTTACATCACACCTGGAATCTGCCCAAGCTTTCCACTATGAAGGCAATCGTAGAG TGTGCAGGAGGAAAGGTGTTATCCAAGCAGCCATCTTTCCGGAAGCTC[J/G]TGGAGCACAAAGCAGA ACTCGGTGGGTAGAGTGA
WI-18169	115 A G	CCATCTTCCG	GAGTTCTGCTT GTGCTCCA	TGAAAGAGTCTGACACAGCGGACACT[G/AT]CATAAGTGGAAACAAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAAATGAGCTGGAGACATTAACTCTGGCGA
WI-18190b	26 G A	---	---	

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WI-18190	62 G A	...	AAATATATAC AACACTCCCTT	CGTTTACCAT TTGTTAAGCTT TTG	TGAAAGAAGTCGACACAGCGGACACTGTCTATAAGTGGAAACAAAGGATGAAGCTAAATCATGGA[G/A] GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGATGAGCTGGAGACATTAAATCCTGGCGA
WI-18181	100 A C	CAGATC	AGCAGAGTTC CTGCCCTC	CCTCCCTCTCT OCCCC	GACAGTGAAGACATTGAAACACAAATACAAACAAACATTAGGAACAAAGAAATGTGTAAATCCAA TGTGTGAAAAATATATACAACTCCCTTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAACGTA TGTGTTCTTGAAC
WI-18215	78 G A	CTGCCCTC	AGCAGAGTTC CTGCCCTC	CCTCCCTCTCT OCCCC	ATTACATACAGACATTCTCTGAGTACAAACTAGGGGACAGGTATTTTACAAAAACAAATAGAGCAGA GTTCCCTGCCCT[G/A]GTGTGCGGGGAGAGAGGGAGGATTTCAGCATTTTGGTGGAGTATGTTAATT CCCTCAAGTTAATTCCTTC
WI-18232	60 T A A A	TGGTGTGATT GTGATACACTT	AAATAAAGGT TTTCAGGGGTT	AAATAAAGGT TTTCAGGGGTT	CATTTCCGAAATCTGATAGTTAAATATCCCGTCGGTGTGATTGTGTATACACTTAAG[T/A]GAA CCCTGAAACCTTTATTTTGAATTTGAAGTTTTCCTCAGAAACTGGGCAGAACTTTTCACATTCTG AC
WI-17892	76 T C A C A	GGAAACTTG AGTTGAGATC	CACAGAAGTG AATAGACTAGT GAGACA	CACAGAAGTG AATAGACTAGT GAGACA	TTTAAAAATGCTTAGATTTTCTCAGTATTTTATCAATAGTGTGTAAAGCTGGAAACCTTGAGTTTGAG ATCACATA[T/C]CTGTCTCAGTAGTCTATTCTCTGTGGGCATTTCGGCAGAAAGTGGC
WI-18242	30 G A A A T C G T A A C A	CCCCAAATGTT AATCGTAACA	GCTAACACTTC TACTGTAAACAG CTTTC	GCTAACACTTC TACTGTAAACAG CTTTC	AATATCCCCAAATGTTAATCGTAACATACT[G/A]GAAAGCTGTACAGTAGAAGTGTAGCAAAAAT TGGATGCCACAACCTTATCTCACCATTCTTCAAGCAAGTGAGGGTCAGAATGTTTCTTGCCCTATATC TGCAAAAGATCGAACAAG
WI-18266c	119 C T	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATC[Π]ACATTTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124 T C	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97 C T T T C A A A	AAATAGGAAA TAIGGACTATC	TTTATGCATCA TTTGIGCA	TTTATGCATCA TTTGIGCA	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGCAAAATGATGCATGAATCCACATTTTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73 A G A A	GCTGTGAGCTA TTGTTATTCA	GGAGAAAAGG GAGCAGAAGA	GGAGAAAAGG GAGCAGAAGA	CTGAGCCTCTTGGATATGTGGTTTAGTGTCTATCATTAAATTTTGGAAAGCTGCAGCTATTGTTATTC AAAT[A/G]TATCTCTCTCCCTTTCTCCTTTTCTGGGATTCTCATTTCGCAATGTTTATA
WI-18330b	66 A G	AAACATCTACAGCTGTCTTAGGCCATCCTGTAAAGAAATCAGGGATAAGAGCTGAGGAACAAGAGGG A/G]TAGTGGCAGTGAGTCAGGACTATGCAAAACCAATAAAATAAGAACATAATTTTGTGTTGAT TCACA

WI-18330a	49	G A A A G A	TCCTGTAAGA AATCAGGGAT	AGTCTGACTC ACTGCCTACA	AAACATCTACAGCTGCTTAGGCCATCCTGTAGAAATCAGGGATAAGA[G/A]CTGAGGAACAAGA GGGATATGTAGGCAGTGAGTCAGGACTATGCAAAACCATATAAAATAAAGAACATAATTTTTTTGTTGAT TCACA
EST37564 5	85	T C A G A	AAATTC AAGC CATCTACAAA	CTATGGAGGCC TCAATGAGA	AAATTAGTTAGCCATAACAGGCTGGAAATTGCTGGTTAGAATACTGCATGTTATTTAAGCTAAATTC AAGCCATCTACAAAAGATTT[C]TCTCATTTGAGGCCCTCCATAGGCTGCAAAACACATCAAAAGGCAATTAC TGTACTGGAGAGGACTGAG
WI-18327	104	G A T T	AACAGCTTT CGTTAGGCTAG	CGCATACAATG GCTCAGC	CAAAGGGATTTTATTACCTACAACAAGTAAGGAGGACAGCTGGGGCAGTTTCCCAAAGCAGTACCTC CCAAACAATGGTGAACACAGCTTTGTTAGGCTAGTT[G/A]GCTGAGCCATTGTATGCGGAGGCAGA GT
EST37624 6b	102	G A ---	---	---	GTGGCAAGAGCAGCTAAACACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCACGCTGATGG CCTGCAGTCTCTGCCGTGCTTGGCTCTCTGGACG[G/A]TTCATTCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
EST37624 6a	58	C T ---	---	---	GTGGCAAGAGCAGCTAAACACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCACGCTGATGG TGGCTGCAGTCTCTGCCGTGCTTGGCTCTCTGGACGGTTCATCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
WI-18357	89	C G GCATCAA	CCAGCCCTTA GCATCAA	AAGGACTCAA AGACTGAAGAT GA	AATGTTTTAAAGTCTTACCCTGCTGAGGTGGCCATGAAGCCAAAGCCCATGGAGAGACATTTTCAGA TAATCCAGCCCTTAGCATCAA[C/G]TCATCTTCAGTCTTTGAGTCCCTCCAGCCAGGTCCTCAAGCTT GTGGACACAGACAAAGCC
WI-18012g	117	A G ---	---	---	TTTTATCTGGGTCAGCTCCTCTTAATGCCCCTGAAGGTCATCTCCTTTCAACTTTCCAGACTTTGGAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTTCGTGA[G/G]GTGTTTCCCTGATACA CGCTGACGTTTCGAGGG
WI-18012f	113	G A ---	---	---	TTTTATCTGGGTCAGCTCCTCTTAATGCCCCTGAAGGTCATCTCCTTTCAACTTTCCAGACTTTGGAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTTC[G/A]TGAAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112	C T CCCT	GCCACTTTTG CCCT	TCAGCGTGTAT CAGGAAACA	TTTTATCTGGGTCAGCTCCTCTTAATGCCCCTGAAGGTCATCTCCTTTCAACTTTCCAGACTTTGGAAG AGATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTTCGTGAAGTGTTCCTGATACAC GCTGACGTTTCGAGGG
WI-18012b	46	T C ---	---	---	TTTTATCTGGGTCAGCTCCTCTTAATGCCCCTGAAGGTCATCTCCTTTCAACTTTCCAGACTTTGGAAG AGATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTTCGTGAAGTGTTCCTGATACAC GCTGACGTTTCGAGGG
EST38390 4	75	A G C TCTGCATTG	GCAAAAAGGA CTGATTAAATAA	GCTAAAAGTCAG CTGATTAAATAA ACTTAA	CATATCATAGCCAGATCTACAACCCAGAGTAATCCCATGGTTATGTACATGGCAAAAAGGACTC TGCAATTGTA[G/A]TTAAGTTTATTAAATCAGCTGACTTTAGCATTTGGAGATTATCTGGAT

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EST38512 7	91 T	TGACGATGCC AATACTTCG	CACTGCACTCT GGGAAGC	TAATAAAACTGACCCAAATTGGTAAACTGTCTCTGGACTGAGAGAAACAATGAAAAATCTGTAAAT ACCTGATGACGATGCCAATACITCGT/GJGCTTCCAGAGTGCAGTGATAACTGTTATAGCC
EST38519 0	24 C T T	CCTGCACCTCC TAAAGATCT	TCTGTTAGGAC TTGGGGA	CCTGCACCTCCTAAAGATCTTTT/CJTTCCCCAAAGTCTAACAGAAATGGTATATCTCTCTGGAAAA AGATGAACGTCATCAATGGATTGTGCTGCTCTCGTTTCAGCTTTGATTTTTTGTGCTTGAACACCTTG TCCTCCCTGCTGATTT
EST38575 1	66 T C A A	GAACATCCCA TGTTCTGTTT	AGGGAAGTA GTATAACACAT AAGAGA	AGTGGTCAATGTAAACTAATGGGGACACCAAGCCTCAGGAAGAACATCCCATGTTTCTGTTTAA T/CJTCCTTATGTGTATACCTTCCCTTCTCTTCTTATACACATAGATTTTCCCTAATTGCAGC CCA
EST38616 9	101 C G C T T C	CCTGCTCCGOC	GAGGAATGGAT GGTBGC	CCATCTAGGAGGCTACCTGAGCTCTGTGCTCCAGAGTGGTGCTCACGCCGCCGGGCCCGTGG AGTCTCCGGGCCGCCCTGCTCGGCCCTT/CJ/GGCCACCATCCATTCCTCCAGGGG
EST38652 8	59 T C C A T T T C A A	TCTGAACTGGG CAATTTCAA	TTGCAAAAATG AAAGGAAAAA	TATAGTAGGTACTTTCTCTGCTGCAGCAGGAATTAATCAGTCTGAAGTGGCATTTTCAA/T/CJGCGTG GTATTTTTTCTCTTTCATTTTTCGAAGTAAAAAATCAT
EST38654 5	42 T C G T T T A C A	AATGGTCATTT TAAATATCA	CAGTGATGGTC CTTAATCTTCT ATC	CTCAAGCTGAGAATGGTCATTTTAAATATATCAGTTTTACATAT/CJAGATAGAAGATTAAAGGACCAT CACTGAGGTCACATAGCTCAGAGGCAGATTAAAGATTGGACCCAGGCGGTTGGTTCAGCATATA
EST38707 9	75 A G ---		---	GGATCCTCACTCACCTGGACAGCCTGAGAAAGGACATCCACCAAGACCTACTGATCTGGAGTCCCA CGTTCCCG/WJAGGCCAGCGGGATGTGTGCCCTCTCTCTCCCAACTCATCTTTCAGGAACACGAGG ATTCCTGCTTCTTGAAAA
EST38759 2	86 A G G T G A T A T G G	TGCTCCCTGA GGTGATAGG	TCACCATCGTG GACTTAAGG	TGACCTTGATTTCTTCACTAGAGGGGAGAAGAAATCACCTACCTTTTGGATGCCCTCCACTCTACTTGT CTCCCTGAGGTGATAGG/WJGCTTAAAGTCCAGCATGGTGACCTAAACTCAGTTTAAATTTCTTGCC TAGCAGCACC
EST38775 1	40 T A C	AATCAATAGG AGAGGATTGG	GGCTTTGCTCT GAATTCAAA	GACTCTCAACCAAGAGAAAAATCAATAGGAGAGGATTGGC/T/AJTTTGAATTCAGAGCAAAAGCCCT CTTACTGAGAGGTGAGCCCCAGCCCCCTCCAAATGCCCTTTTCATGAGTTAGGATCTCCTAAAGTGGTAC AAACAAACCAACATGGTGG
EST38815 4	91 C A C A	TGTTTATGAGA ACCCATTACA	GCTGACTGGCA CATGCTTT	CACCCCATATTTGACCAAGGGATGAAGCCTAGCCATGCTTTTCACTTATGTGTGTTTCAATCAACAG TGTTTATGAGAACCCATTACACA/C/AJAAAGCATGTGCCAGTCAGCAGATTCTGTAAATAA
EST38858 4	98 C T T G A C	CACGAGTAA AAGAAACTCA	GGAGCGAGTCC AAGGAGAA	TCCTTACTGTGCTTACAACCTTCTCTCCAGTTTGGGGTGGTTCCATATTTGTTATTTGTTATTA TTCAACACGAGTAAAGAAAGAACTCATGAC/C/TJTTCTCCTTGGACTCGCTCTCTCCCCCAATCTCGAT ACCGACTGCACTGTG
EST38865 2	72 T C T G T G A T G C	GCTGTAGAATT TGTTGATGATGC	GGAAGGACGG AGGACACAG	CCCTTAATGGATTTTACAGCTCATCTGAGTCTCTGCTGTGTTCTCTGAGGAGCTGTAGAAATTTGTGCG ATGCT/CJCTGTGCTCTCGGTCTTCCCCAAATGAGCACATATGAGGGCAGGCAAGAGCATGCTGGA TTTGTCTTAGTTGTTAA

EST38878 9	47 T C	AAACATCATT ACTAGCCTAG ATCCTAA	CCITCAATAAA TCTCATGTCTT CA	CCAATGAGAACCAAGTAATTAAACATCATTACTAGCCTAGATCCTAAAT[C]GTGAGGACATGAGATT ATTGAAGGGAAATCCTCAATTAAATATGAACATTTCTTGAGAAATGGGAAATTTGAAACATTCC TTATTCATATGTCATCTACACATTTCTTTATTTTATTTTGTCTTCTCAATATCGGATTGTTGC TCATGAGAAATAATGGCTGAGGGAGCTGGCAGCGCAGTCTTCTCA[G]C]GCTCCCTGGATAGCTAAAT TTA
EST38882 6b	113 G C	---	---	TTATTCATATGTCATCTACACATTTCTTTATTTTATTTTATTTTCTCAATATCGGATTGT TGCTCATGAGAAATAATGGCTGAGGGAGCTGGCAGCGCAGTCTTCTCAGGCTCCCTGGATAGCTAAAT TA
EST38882 6a	35 T C	TGTCATCTCAC ACATTTCTTAT TTTT	CGATATTTGAG AAAGTGAAAA CAA	
EST38909 5	47 A G	GCACAGCATG GCTAAAACG	GGTATTTGTTG ATTCCCATCTT T	GCACATAACTAACTTTTCTTTTGTGATTGACACAGCATGGCTAAAACG[A/G]TAAAGATGGGAATCAA CAATACCATTTGAAGATATGGAGCAAGAGAACTCTACATACTGCTGGAGGGAATATAAAAT
EST38911 9	85 A G	GTGAGGGAA ACTTATAACCT CAC	TGTTGTTTGT GAAACAAGCG	AACTGATGGCAGTGAANAACACTACACATCAAAACTTAGGAAATGTGGTGTAGTGTGGTACGTTGAG GGAAACTTATAACCTCAC[A/G]CGCTTTGTTTACAAAACAACAGCAGACACAGAGATTTCCAACTC CAGCAATGACAGGCTAGGG
EST38955 5	30 G C	TGAATTCCTT GGTGG	CACTGCAATCT CACCCC	TAAACATTCCTCAATTCCTTGGTGGG[C]GCGGGGGGTGAGATTGCAGTGCCTCAAGATAAA TATCACAAATATATCAAAACTTCAAAATGTCTATGCAATTCACACACTGACATGAGCCACAAACAT CCTTTCACAGGGACTGTAC
EST39002 0	42 G A	GGACCTTCGG TGACC	CTGGCAGGGAG CCTG	CCTGCTATGATGCCTGGGCAGATCCCGGACCTTCGGTGACC[G/A]CAGGCTCCCTGCCAGGGCTTGG CCCCTGACCGGGCTCCCCAGCTCGGCCCTGACTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST39004 8	79 T G	GGTGGTAAGG CCTAAGGAAT	ATCTCGGCTGG CGC	CACGTGGCCCCAAGTTCCGGGCTTCTCAGTCTGGATGGCTGTGGAAAAAGCTTGGTGGTAAG GCCTAAGGAATTTGAGGGCAGGGGGGATGCCGCCAGCCGAGATGGTCTGTAAAGCCTGTGGGTC AAAGACCTAACTTCTGGA
WI-16398	90 T C	TCCCTATTATT CCATGATATT TCA	GAATGGTTTGT GAAAAATATA TTGATAT	AAAGATAATGTCATCACAAACGCAACATATAGAAAACATAAAAGAAAAATAAGTATCCACCCTAAAT CCCTATTATTCATGATATTTTCA[T/C]JAGCAACTAGTATATATATCAATATATTTTTCACAAACCAT TCAGTTACAC
WI-16403	69 T C	CCITTTGCTCT AATTTTAAAC ACT	TAAGGGCTAAT TCCCTATATAA AAAG	GGTGTCTTTTCATGATTTTCTCATTTCTCATGAGTTTCTGGTCTTTGTCCCTCAATTTTAAACACTT T/C]CTTTTATATAGGGAATTAGCCCTTAACTGGTACATGCTGCCAAAAATTTCTCTCCAGTT
WI-16406	24 C T	GCTTTAATGGC TACAGAAAGA AGG	CCAGAACCAG ATGTGTTTAAA AA	GCTTTAATGGCTACAGAAAGAGG[C/T]GGTTTATTTTCTTTTAAACACATCTGTGTTCTGGCAGC AAGTTATATTATGCAATTTAGAGCAATAGTGCCCTGAA

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EST39236 0b	57 C G	TCATCTGAGA ATAAACTTCCT GTCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCTTTTATTTCATGATTTGTTTCATCTGAGAAATAAACCTCCCTGCTCTAAATTTCCAA[C/G]ACTATGTT TAATGTATGACTCAGTACCTATAATGAGACTGGAAATATATACCTGGCAAATGAATGAGGTGCTC TTT
EST39294 4	63 G T	CCTGAAACAG GGATGCC	GCACAAATTA ACATAGTACCG AGAA	CAAACAGACCTTTGGTTTGAGCTCACCTGGTGACAGGAGACTCCCTACCTGAAACAGGGATGCC[G/T] TTCTCGTACTATGTTTAAATTTGCTGAGCCAGCAACCTCGAGTTACCCGGCTTTTACCCACGCC AGCTCTGCTGTCTGCAT
EST39366 2	72 T C	---	---	AGAAACATTTCTGTGATCAGAGGAAAGATGTATGTAGAAATCAGAAATCAGAAATCTGACTGAATTCCTAAA ATCTAT[C/J]ACACTGAGAGGAAATGGAAAGAAATGTTTGCATAAAAGCTTTTCCCTGACTCTCA GAGGGGTTCAGA
EST39371 9	86 A G	CATTGGATTA GGTGAGAGG	TGATTTGAGAC ATTTCACATTT TT	AAAAGCTGTAGCTGGCAAGTCAAAAGTTATTTTATGTGTGTAATCCCAGTTGAGCATTTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAATGTGAAATGTCTCAAATCAAATGCTTCTCTTCTAAAGATTA GACATTGCCCAACCTGC
WI-17177	23 A G	---	---	ACAAGTGACATATCCAAACCAACC[A/G]TCCATCCCCACCTGTGCCCTATTTCTTCTTGTTCTTT AGAGCCTTTTTCAGCTATTTCTGTGAAGCAACTGCACGAGGCCCTCCCCGTACTCCTCCCCCTGGAA G
EST39428 8	31 C T	GCTCCCCACA ATTTTGATT	GGTCCCTTATG AAGCCACC	AGGTCTCTGGTGTCTCCCAAAATTTTGATT[C/T]GGTGGCTTCATAAGGGACCCAGGATTCGCAAT TTCTGGTGGGCGCTAGGTAATTTCTGTGCTTTTGGTCCACAGAGCACAATTAAGAAGATCAGGTCT GGCTGTTC
EST39430 2	45 A C	GGCAGAGGAA TAACTGATGTT	CAGGGGTGGG GTATTG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAAATGAATGTT[C/WC]CAATACCCCGACCCCTGA CCCAGTACCTTTCCCTCAGGCCAGGCTCCGGTGGAGGATGTCCTGGG
EST39446 7b	117 C T	CTACTGACAT AGGACTTCA	TCCTGGAAAC TGACATAAAC	AAAGCCCTGTAACTGAAGCTAGACAACGTCACCTTTGGAAAGAAATAACAGGAACCTATTTATAT ACGTAATCACATTTTACCTGCTGCTACTGACATAGGACTTCAGAGTAATA[C/T]GGTTTATGTCAGT TTTCCAGGATTGTTCTCCC
EST39465 2	80 A G	AATGCAGGAG GGTGGC	CAATCTCGGC CCTCT	ATGGTGTCAATTAGAGGGCCACAGGGGATGGGGAGTAAATAAATAACATAAACGAACCTGAACAGAAA TGCAGGAGGGTGGC[A/G]AGAGGGGCCAGATTGGGTGTTACGGGCAGAGAGGTGGAAGACCAG
EST39501 0	81 A G	AAAGATTCT GTAGACATCT	CACCTGCAATT CTGAAGGCT	TGCTTACAACCCATAACCATAGGCCATGTGTCAGACATTTCTTGACCAAGCCCTAAAGATTCTCTGAG ACATCTAACATTAG[A/G]TAGCCTCAGAAATGCAAGTGCAGTTCAAGTCAACCAATTC
WI-18387b	84 A C	---	---	CACAAATGGGACTGCTGAAGAGTGACAGTTGGACCTTACCTTTGGTGACCCCATACATTTTGGTGCA CATGCTTTAGCCATA[C/J]CATGGTAACATTGACTATGGAGTCTTGGAAGGTGTAATGTGCGGATG GCTATGTAGACATAAAGA

WI-18387a	57 A G	CCCTACTTTGG	GGTAAAGCATG	CACAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACIAGTITGTG
EST40601		GTACCCCAT	TGACCACAAA	GTACATGCTTTAGCCATACACATGGTAAACATTGACTATGGAGTCTTGTGAAGTGTAAATGTGGGATG
9	78 A G	GCGTGGAAACCT	TTCTTGAAGA	GCTATGTAGACATAAGA
		GAAACAC	AAGGCGTC	TCCCAGGATGGTTTATTCAAAGCTGTGGACGGTGAACATTAAGACGAAAGAGGTGACTCGCGTGGA
		AGTGATCAC		ACCTGAACACIAGIACGCCCTTCTTCCAAAGAGGGCTGTGGCGATCAGGCCACTCAAGG
EST41935	32 A G	ATCTTCAGGAT	GCACACCCCTTC	TCCATTGAGTGATCACATCTTCAGGATAGGTAGJATGAACAGTGTGAAGGGTGTGCTCATTTTCTTC
		AGGT	ACACTGTTA	AGCTGTGAGTAGAGGAGTCTTCCCGAGAGTAGCAGTTGTGA
		CATTCTGGTCT	AAAACGTGATTT	
EST43091	28 C T	TTATTTTGGG	GTAAACATG	ATGTCATTCTGGTCTTTATTTTGGACA/C/TGTAGCATGTTTTAACAAATCAGTTTTTCATAGGCAA
		CA	CTAC	CCTTTTGAACATCAAAAGAAATACAATATATTTTCACAAATTCICATCACTGTAAATTC
WI-18420c	108 T C	TTCCATTAAAC	AAATTCTCAGC	AGAGAGACAACAAGAAGAAATAGGGGAAATGGGAAGAACAGACAGAGTGAAATTAAGCAAATCTTGGA
		AGGAAGTTTC	ATTGCTATAAG	TTCCAGATTCCATTAAACAGGAAGTTTCTCAAAAAAATCAAA/T/C/GCTTATAGCAATGCTGAGAA
		C	C	TTTCATAGGTACTTCATGGGA
WI-18420a	38 C T	GAATAAGGGA	CCAAGATTGC	AGAGAGACAACAAGAAGAAATAGGGGAAATGGGAAGAA/C/TJAGAGTGAAATTAAGCAAATCTT
		AAATGGGAAG	TTTAATTTAC	GGATTGAGATTCCATTAAACAGGAAGTTTCTCAAAAAAATCAAAATGCTTATAGCAATGCTGAGAA
		AA	TC	TTTCATAGGTACTTCATGGGA
WI-18425b	101 T C	AGCTGATCAGCTGTGTTACTGTGTTTATGTGTGGCCAGGGAAGCCAAAGATCAGACACCCCTGTC
		CACCTGTCT		CTAGACAGATTCA/C/TGCACACAACAACAGGAGGTGGGGTCAACACGGGGGAGAGCCAAAGAC
		AGACAGATT	CCTCCTGTGT	TAGGGC
WI-18425	81 A C	A	TGTTGCA	AGCTGATCAGCTGTGTTACTGTGTTTATGTGTGGCCAGGGAAGCCAAAGATCAGACACCCCTGTC
				TAGGGC
				AAATTGAGGTCCGGGTGGAACATAAAAGGAAGAAAGAAAGAAAGTAAATCAAGGGAGGCCAAAGTG
WI-18449	129 C T	AAGTGGGACT	CTCCCTGACT	GGAAAGCTGATTGCTGATCTAACGTGCTGTCCAGTTCCCTTTCTTTGGCTTAAGTGGGACTA/C/TTC
			GTATCCAGA	TGGATACAGTCAGGGGAG
WI-18457	120 T C	ATCGCTTCATTGAAGCCTGCTTAATTTCTCTCAGTCACTGGTGGCCCAAGACATTATTTTATTTCTT
				AAATGTCCAAATATCTGCTGATCTGCTGTTGTGTCACATTGGGGCCACAG/T/CJAAATAGGCTAAA
				AGGCAGTCCCACTGCT
WI-18462	39 A G	CCACAATGGC	TTTAGGCTTTG	GGTGCTATAGCTGCTGTATACCCACATGGCAGAGGTGAJAGJTAGAAACCATCTCAAAGCCTAAAA
		AGAGGTGA	AGATGTTTCT	TATTTACCATACATCCCTCACAGCAAAAGTTTGTAACTCGGGTTAGGGACTCCATTGAG
				TGAGGACGTGTGACAAGCTCCAGAGGGTGGGGCCGGGCTGAGGGTGGGGTGGGAGG/C/TGGT
WI-18476	60 C T	GAGG	GCACGATGGGA	CAC/TCCCATCGTGCCCTGGCCGTCCCTCCACTCACCCACACCTGGCCAGTCCACGTTGAGGT
			GTGACC	

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WI-18491	109	G A	AACAAATGGT AGTGGTATT	CGTGTGCATTT TCITGTAATCC	CTAATCAGATGAATACATGGAAGGGGTTAGCACAGTGCCTAAACACACAGTAAGTAACCAACAAAT GGTAGGTGGTATTAACTATTATTAAATCCAGAAATGAC[G/A]GGATTACAAGAAAATGCACA CGT
EST50757 b	79	C T	GAGCTCGAGG CTGCTTCT	ACCTTTCACCC GCCC	AGCCCCCTCCACTCCACTCTGCTTCCACAAGTCGGCTCCCGAGAGCTCGAGGGTCTCTTTTATAT GTGCAGGGGC[C/T]GGCGGGTGAAGGTCAGAGA
WI-17675	103	T C	GGACATTGG ATGGTGACTT	GGGGAACCAAC CAGG	GATCTTGGAAAGCACTAGAAACTAAACATCTTCACCAGGTGCTGAAGAAAAGTGTCTTCGTTTTAAT TGCCAAGCAGGGATGTGGACATTTGGATGGTGACTT[C/T]CCTGGGTGGTTCCCATAGATTACCCAT TGCTCTAATGGTGCTA
WI-16543	67	G T	AGATAAACTA CATTTGGGTTT	GATTTCATTT ACAGGGGACTT	GATCCATTACCTAGGGTAAATTCCTGAATGTCAAAACAAAGAGATAAACTACATTTGGTTTTGGT G/TJAAGTCCCCTGTATGATGAATCAAGAAATCCCAAGTCTGTCTTGCCACCCATTTAATACGTATT TTTGTTAAGGCTGAAGTT
WI-17687	107	C G	GCCAAAAGG TTGGGAA	TTACTTTTGT CCGACCAGCA	ATCTGAGATGGAAGAGTTTCATCCCAAAACCATCTCCCCCTGACCCCCAGTCCATGGAAAAATGTGTC TTCCACAAAACCGTCCCTGGTGCCAAAAAGGTTGGGAA[C/G]TGCTGGTCCGTACAAAAAGTAATT G
WI-17690b	79	A G	AGGCATTTTC TAGCTGTGTT	CAAGAGTTATG GGTCTGAATC	ACAACATGTGAAGAAGATATGTGCTTTACTACAGTGGAGGATTTTCTAGCTGTGTTGATTT GGCTTCCCCTAT[G/G]GATTCAGGACCCATAACTCTTGTTCTCACTCATCTGCTATGCTGCTG ACAACATGTGAAGAAGATATGTGCTTTACTACAGTGGAGGCAATTTTCTAGCTGTGTT[G/A]A TTTGGCTTCCCTATAGATTCAGGACCCATAACTCTTGTTCTCACTCATCTGCTATGCTGCTG
EST51717 b	128	C T	GCGGAAGACA GTGAGCTGTT	TTGAGGCAATA ATCCAGCTC	GATCCAACTCAGTGTCACTCACTATCCAGATTAT[C/T]GAAGTGGAAACCCCTCCGACCC TGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCGGGAAGACAGTGAGCTGT[C/T]GAG CTGGATTATGCCTCAAA
EST51717 a	39	C T	---	---	GATCCAACTCAGTGTCACTCACTATCCAGATTAT[C/T]GAAGTGGAAACCCCTCCGACCC CAATGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCGGGAAGACAGTGAGCTGTTCGAG CTGGATTATGCCTCAAA
EST53012	97	C T	TGGTCACTTG GGGCC	GGCTCTGCCA GGCC	TTTCCAGGTGACAGGTTTATTCCACCCCTTCCATCCCATGGCCACCCAGGAGGAGGAGACAG GTGTGCTGGAGTCTGGTCACTTTGGGGCC[C/T]GGCGTGGGCAAGAGCCCACTGGGTTTACATCTCTGT GGGCAGGTGTGGACAC
EST53349	96	A G	TGTTGAAAGC AGTCACAATG TAC	CATCTGGATAT CTTGTCAACATT TT	AAACTGCAAATAACAAAACAAACAGAAAGTCCAAGAGGCTAAAGTCTAAGCTATAATTACACATG AAGTATATGTTGAAAGCAGTCACAATGTAC[A/G]AAATGTGACAAAGATATCCAGATGTTTAA TTTCGAAATGTCTCCATGACTTGACAGACTGAGAGCCAGCCAGCCAGGAGGAGACCTGCAGAACT TAAACAC[A/G]GAGCATTTATTGTTAGAAAGGGCAAGTCTTACACTCAAAATAGGTTTTAACATGAAC ACATTAAGGGGAGATGGCC
EST53389	74	A G	CA	C	

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TIGR- A003P30	117	C G ---			ACAAAGTTCAAAGGAGAACTTCCTTTGTTTAAATGCAGCTGTCCTCAGAAAGCCTGTGATTTCTTAGGA AACCATCTGGGTTTAGCCCATTAGAAAAATGCAGTTTAAAGCAGTGTCA[C/G]ACTGGCTGCCTGAA GGTACCTTGGAGATACT
TIGR- A004S34	156	C T A			GCTTGCTTTTATGTTAGGTTCCGGGGAAAGAGGGGCTGACAAACCCGACAGACATCTGGACACCAGC AAGGGTCCAGGGGAGGTTGCAGAACTTCTTTGCTCTGGCTAACAGTCTGTGATGTGACAAATAGCCA AACCTCCTCATTCCTATAA[C/T]CTTTAACAAAAACAGTTAGCTGTTTACAAAAACAGTTAGCTGTT TACA TG
TIGR- A004T44b	97	A C ---			AACAACAGTGTAACTTTAACAGGGGATGTTAAAGGTAAGAGTCAGGAAGATAAACCCAAATGAT TGAGTATGATAAAGAAATTTTGCAATGGCGATT[C/A]AAATAGAAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TIGR- A004T44a	69	G A TGA			AACAACAGTGTAACTTTAACAGGGGATGTTAAAGGTAAGAGTCAGGAAGATAAACCCAAATGAT TGA[G/A]TATGATAAAGAAATTTTGCAATGGCGATTAAATAGAAAAACCTATAAATGTAGAA:AAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TIGR- A004V08	60	T C GGCATTCTCTT			CCTACAATCCTATAATATGCAAGGGTGGGAAGGATGCAGGAACACAGGCATTCCTTTA[T/C]GCC TTTTGTGGGAAGGATCAATTGGTGCATGCACCTTAGGGGACAATTTGGGCAGTAGCTGTCAAAATTC AGTAGCTGTCAAAATTTCAAA
TIGR- A004V26	125	A G ---			TCTAGCTATAAGACCAGATTTTAAATATCTAGATATAGAATTATCCAGAAATAATCTATTGAATTGA CTGATTACAAAATGTTAACAGCTGGATAAACGGTAAATATGCATTATCTTCACATGA[A/G]AAGGT TTCAGTTTATAAATGCTTAAATACTGTATCTATTGCTTAAATACTGTATCTATTGG
TIGR- A004V28 a	29	A G CGATCTC			CCAGGCTATAATGTTGGTGGGATCT[C/A]GCTCAGTCAACCTCCGCCCTCCAGGTTCAAGCAA TTCCTCGCTCAGCCTCTTGAGTAGCCGGGACTACAGGCACCCGCCACCTAACTAATTTTGTG TATTTT TAGTAGAGACATTGTAATTTTAGTAGAGACAGG
TIGR- A004X20	25	T C G A			TAAGTTTTCCTTCTCTCTGTAGGA[T/C]GCTCCATGTTACAGTCAACTATAAACACATGGCTCATGT TCACCTCTGGGCTTCGCTTCAGAGGAGTTTGATATTTTGGAAAGTGGTACCTTTGTTCTGTGCTTTTCA GACCAACCCGCTCTTTCATTCTTCAAGGCTTCCTTCCAAAGGAGTTAAATCATCATCATGTCCAATC ATCATCATGTCCCT
TIGR- A004X30	26	T C CCAC			TTTTGAAATCTTAGAGTAGAACCCAC[T/C]ACTCTAGTAATACITTTGTAATAAATAAATAGTTTT AAACACTTCCATAAAGAAATTAGGGTGCCAGCTCCTTGATTTCCCCCTAGGGATAAAGATAATCCAT GTTAGGGATAAAGATATCCATGTAC
TIGR- A004Z04	102	T G ATGCAAACT			CACGGTATATGCTTATATATAGGTATATATACAGATCGTACACAATATATTTAACAGTTTGACATG GGGTCCACAGTACCTTCATTTGGGTATGCAAAAC[T/G]TTGCTTTTCATGAAATTTCTAATTATAAGG ACTGTGCTTCTTCATATTCATGGACATTATACAAAAATACAGTCTCTTTAGTGATTTAAGACGTC TCCTTAGIGATTTAAGACTG

TIGR-A004Z19	85 C T	GAGAACAACT GCAGCATTTT	AAGATGGTCAT CGGGAAGA	TAAGTGAGACAAGTTATTGGAGGAGCTTGACACCCCTCTCTGCCCTAGCTTGAGAGAACAACTGCC AGCATTTTTTCTTTTC/TC/TCCTCCCGATGACCAATCTTTTGGGCTGGCGGCCAGGCCCTGGGTGTC TCCCATATCGCTGCTTTAGTGAGACTGAGGATCTGGTATAAGGAACAGATC
TIGR-A004Z42c	89 C T	TTGGGGGAGGT AGGAGACT	CAGGGCTGCCG GTGC	GTCTTAGCAGAGGAGATAACTTTGAGGGACAGCCCCCAAGGCCAGGTAGCCTTCAGGGGCGGGCA GGGTGGGGGAGGTAGGAGACTTC/TGGACCGGCAGCCCTGGCTCCAGCTTCATCATCTGTGTCTCTT CATCATCTGTGCTTC
TIGR-A005D17c	81 T C	---	---	TATGGACTGTGTAGAAATATGATTTGGACAAGAAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGCTTC/GTCTAGATCTCTTGGCCCTCTGTGCAGGATCTCTTCTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTACGACAGICAAACTCTTACGACAGTCAAAACAC
TIGR-A005D17b	79 G C	GGGAAACCC AGCAAG	GAGAGGCCAA GAAGAATCTAG AC	TATGGACTGTGTAGAAATATGATTTGGACAAGAAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGTC/GTCTAGATCTCTTGGCCCTCTGTGCAGGATCTCTTCTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTACGACAGTCAAACTCTACGACAGTCAAAACAC
TIGR-A005D44	97 G T	TTAACATTATT GAACTTAAAA CTGTTACAC	TTGCTATTAT TTAAAGCCAA AAAA	CATCAGTAACATATACACAATTGGTTCATCAACTGAACCTTGCCTCCAATATATTTCTATACAATCTT AACATTATTGAACCTTAAACCTGTTACACTTC/GT/TTTGTGGCTTTAAATAATAGACAATGATTTTTG TCTATTACTTAGTGATAGACAAAGTGATTACTTTGTTAGACAAAGTGATTACTTTGTTAC
TIGR-A005E31b	27 G A	---	---	GGAGTTCAAAATTTATAACCAAGCCCTTC/GA/CTCACAGCTGTACTGGCTAGGCAAGCTTTCCAGAC ACAAAGCCACCTGCCTGCCATGTGGATAGTACTCTTTGCCCTGCTTGCCTTACAAAGCCACTTCTAT TTCATACCAATACCTTCTATTTCATACCAATAAG
TIGR-A005E39	182 G C	AGTAAGGTTA CTGCACCTTAC AGAG	---	CTCAGTGTAAAAACTTTGTTTAGGGAAAAAATAAATCCAAATGGATATATGGGAAGAGAAGTG CCAGGCTGGATGGTCTGAGACAGAA/GACCCCTTGGGCTCCTTTATTIGTCTTTTCAACAGGACC CCACAGATATTGCGGTATGTCATGAGGACTGGGGATGCTCTCTATTG/GC/GGATGCTTCTATT GCTGAGTTTGTATCTTAGTAAGGTACTGCACCTTACAGAG/GTCAATTTCCCTGATTTAGGA AGCGATGCTAATGGGTATTGCATAGGTGTAAGTATAAATGTTGATTTAAGAGAAATCCCAACAG CTTGGTATAAGGCAGAAAAATAAATGGTATAAGGCAGAAAAATAATAG
TIGR-A005E42a	42 A G	CACCTGACTCG GTGCTTTAC	CCTGGCTGTG AGGTAATGT	ATGACAAATGATGATGATTAGCCTACCGTTTTCGTAAGCACCTACTCGGTATCAGGCACCTGACTCGG TGCTTTAC/GG/TACATTACCTCACAGCCAGGGTTGGCAATGGTCAITTTTGACAAATGGTCAITTTG ACAC
TIGR-A005E46	76 A G	GCAGGGGTGA CGTATGTAGA	GGGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAA/TC/TGCTTAGGGTGTCTCCCAACAGAGCAGATACTTGAACCG ACTCAATTCCTGTGTAAAGACACTTTGTCTGCTTACGGACCTCCCCAAAGTGTGCAGAGTTCTAT ATAGGATGCTGGATTAGTTCCTTTGATATTGTAAAAATCCCCCAAGAGCCGATATGAATCTGCCC
U20979	24 C T	A	A	

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X57830	106 GC CT	AGTGAACCA ACGATCATAT	CATTGACAGAA TAAATGAGGC A	GTGGCAACTGTGGAAGGCACACTGAGCAAGTTTTCACCTATCTGGAACCAATATGAGATTGGA AAAAATTAGACAAGTCTAGTGAACCAACGATCATATCTG[C]TATGCCTCATTTTATCTGTCAAT GAAMGCGGGTTCAATGCTACAAAATGTGTCTTGAAAAATGTTCTGACAGCATTTTCAGCTGTGAG CTTC
X74070b	72 T G	CTTTTAAAGAA ATTTTGTTTA TGGATC	GGGCTTAAAAA TATTAGAGATC TAGATT	AACCTGAAGAAGTTACTGGGAGCTGCTATTTATATATATGACTGCTTTTAAAGAAATTTTGTATTG GATC[T]GIGATAAAATCTAGATCTCTAATATTTTAAAGCCCAAGCCCTTGGACACTGCAGCTCTTTT CAGTTTTGTCTTATACAAATTCATTTTCGAGCTAATTAAGCCGAAGAGCCCTGGGAATCAAGTTT GAA
Z48804	44 CT ---		---	ACTGCCGAAGTGTAGCGGCCCCCAACCTTCTCTCATCACAG[C]TTAGAGCTTCTTCCCAGAGGG CCTTTAGGATAGGAGAAAGGTTTCATGCACACACGTGTGAGAAATGGAAGAGCCCTCCAGACCACT CTACAGCTGCTCTAGCCTTAGTTGCCACTAGGAAGTTTCTGAGGCTGGCTGTAAAGTAAGTGTAAAG TCCA
D28513b	133 A G ---		---	ATGACCAAGCCACCACATTTAGAACTTTGGCTGCCCTTGGAAAGTCCAGAGCTGGATCTCTCAGCTCC CGCCCCAGAGGGTCAGCACTTTGGACATGGCTCACAAGCAGTTTTTGTGACTGCATGAATGC[A] GJTGCGGTGCAAGCATGAACCTTGTTTAAATCAAGAGGCTTACATAATTTTAAACCAGTTCTGTCTTC AGCTGTACATA
D29833b	85 A G ---		---	CCACTCCATCCTGATGCCCAAGTTATCCACAGCCTCCTTCCCGACCAAGACCCCTATCCACCTGGACC TCCATTTTCCCTGTAA[A]GJTTCTCCAACCTGATCCTACCCCTCCCTACTCCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCAACCAACCAAGACACCACTACCCCTTGTAACCTACTGCTTCTGCTAC
D29833a	21 A G ---		---	CCACTCCATCCTGATGCCCA[A]GJTTATCCACAGCCTCCTTCCCGACCAAGACCCCTATCCACCTGG ACCTCCATTTTCCCTGTAAATTTCTCCAACCTGATCCTACCCCTCCCTACTCCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCAACCAACCAAGACACCACTACCCCTTGTAACCTACTGCTTCTGCTAC
D31762	82 G A ---		---	CTCCCTGCCTCCTCCTCCTGCTGATGCTCCGCTCAACAGCCGAAACCTGCTTGGCAATGGGGG GAGGGGCGTTTC[G]A]CTTTTCTCTCTTGCGCTTCTCTTATTTCCACAACCACTTCTCAATAAA GCCAAAATCTTCTCTTCTCCCTCCTCAGGCCACCTCCTGCTCCTCCTGCTGCTGGCTTTT CTGGA
D37931	64 T C ---		---	ATTATCGGAGTGGTTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTGAGCTG[T]C] CCCAGGCTCTGCTCCTCAGCTCAITTCCTACTCTTTTCTCTATATAACTCATCTTATTAATACATT GCACCAAGAGATATGGAGACATAAACCTGTAAATGAATGAGGCTGGGCTTTTCTGTAAATAGCTTCC TTT

D63807	101 C T ---	---	---	CAGGAGGACTTCAGTGCAGTATCCCTGCCCTTCAGTCTCTTTAGAAATCACATCTGTGTTCAATCC ATTGTTAGAGGGAGTGATTTTCTGTCCAC/C/TAAGAGGAGACTTTTGTTCACAATTTGGATGCAC AATGCAGAGGAGTCTCTCCCTCCCGTCCGCTTCGGTGGTGGAGGGTGAACCTGTGCCAGATGAC
D90145	21 T C ---	---	---	TGGGAACATGCGTGTGACCTC/C/JACAGCTACCTCTCTATGGACTGGTTATGCCAAACAGCCACA CTGTGGAGCTCTCTTAACCTAAATTTAAATTTATATACATTTAGTATTTTATAATTTATTTTGAT TTCACAGTGTGTTGTGATTTGTCTGTGAGAGTTCCTCCCTGTCCCTCCACCTTCCCTCACAGTGTG TCTGGTG
EST14035 1a	59 T C ---	---	---	ATTATCACTCTCAAAAATTTGGTGTGTGTGTTTAAGTACTTCTTATTTATGAGCCCCCT/C/JGAGGA CCAGACATGTTATTAACAAGCCCCCTTATATACCATCTAAT
EST16668 5	71 C T ---	---	---	GCATTTTAAAATTCACATTTGAATCATTATTTACTATTTATGATGTTTACATAACAATTCAGTATCATT ATG/C/TGTGATTTTCAGATGTAGGTCTGTCATCACTGAGCACTTATCT
EST16904 7	57 C T ---	---	---	ACAGACTATGCCAACTTATAATGCTTAACTTTTATGATCAATAGTAATAAATTACAC/C/TJGAGATA TTCACACTTTATTAATAATAGGGTTTGTGTAGATGATTTTCCCAACTGTAGGTTAACAT
EST21863 9	49 A G ---	---	---	TTTTAAGTACGAGGCACTGCTGGAACAGGATGAAACTGTACACCC/C/JGTTACTACTTACTC TTCACCTCTTCAACTGATCCCTTAAAGACTTCTACTTAGCAAA
EST21885 6	80 G A ---	---	---	GGCTGTAAGTAGAATCAAAGGTTAAGAACAATTTATGCACCTTATTCACAAAACATTTACTGAGCATA CTAGGTGCTGGGAG/C/JGTGACAGTGTAGCAAAAACACAA
EST22623 8a	26 A G ---	---	---	ATTTAGTGCAATGACAAAGCCCCAA/C/JGAGAACAGAGGATCAATAAGATTGAAATGTATTACC TTCATATAAGTATACGAAGTTTAAACACAAGTATGGGAGT
EST22644 2	98 A G ---	---	---	AAAATGATTGAATTCAGCAAGTACATTTATGATCTATCTACATTTTAAACAGCACTAAAAATAA AAATTTTAAAATGATTATCCATTATTTACAG/C/JGAAATGTGGAAGATGGCTTTTAAACCC
EST23587 1	31 T A ---	---	---	CCCTCATTTATTTAAAAGACGGACATAAAAAT/C/JATACACAAAAAACCCCAAGTCACATTTTCAG GAGGTAAAACCTAAAAGTCTGATATGAAAATATGGTGG
EST24246 7	106 T C ---	---	---	AAAGATCTGGCATTATTCACATCAATCTAAATATTTTGTAAATTTTCCATGAGTATTTTTTCA TGCCCAAGCATTTTAACTATCATTTTACGCTAAATACC/C/JGAATAACCCATAGTTACAGAATTGG GTCTGTGTAACCTCAAT
EST24308 3	45 A G ---	---	---	TAGTTTAAATTTCTGAACCTTTGGCTTATAAATTTTCTCAACTT/C/JCATTTAAAAATGTATCAAT GCACCTTCTTCAGTAGTACCACATGAAAATATAAACCTCGTTC
EST24435 6	73 G A ---	---	---	CTTGAACCTCTGGCTCAAGTGGTACGTCGCTCAACCTCCCAAAATGATCGGATTACAGGCATAAG CAGCC/C/JGTGCCGTGACCCACATTTCTTATCCGATCTGTTGATGGACATTCAGGTTGTTTC
EST25089 6	25 T C ---	---	---	TATTTGTGCATTATCAAAATGGTTA/C/JAGTTTTCATTTAAACCTGTAATGATTCTCTATGTATAAA ACAGCTTTGAAGTGTAAATGTAGTTTCCAAATCGTTAGTTAATGCTACATT

EST25476 9	33	G A	---	---	AATGATCTTTATTTTCAGACCTGCTCCTAAAA[G/A]CTTTCTCCTCCTCTAAAAAACCAACACACA AGAGGTCTCTGTGCTGCTTTCCATGGACTGTGGCGCTGTGGACTTGGACCGTCTGCTGA
EST26183 2	70	T A	---	---	AGATAATGCATTAGAGCCTGCCCTCATGTATCTTGAATTAACTTTGTAAAGATTGATCTCTAAATAAG ATT[A]ACATTCGGGGTACTGGGAGTTAGAACAAAC
EST27231 1a	28	T C	---	---	AGAAAAAAGGTGCTACCGAACTCATGT[C]GATAGCGCTTTCTTTAGGCACATATTATAGCATTT CAGATGAAAGTTCTGTAATCACACACACACTGTGCCCTTAACAACAACACGGTGACTCTGA
EST27816 5a	26	T C	---	---	CAACTCAAGGTACAAGACAATTGCATT[C]TAACATTGTTATAAATAAAAGGAACATCAGATCAAT CATTAAAGGGCTCCAGAGTGAACAGCATCTTCATAACTCCATGTT
EST28588 0	78	A T	---	---	GTTTAATTGGCGTATGTTCCACAGGCTGTACAGAAAGCATGATGGCTTCTGGGAGGTCTCAGGAA ACTTACAATCA[A/T]GGTAGAAGGCAAAAGAGAACGAGGCATCTCTCCATGACCACAGCAGGAGG AACAGACAGAGGAGGGGGAT
EST30226 5	25	A C	---	---	TACTCACACCGACATACATATCTCA[A/C]GTAGAATTAGCTATACTGCATACTAACTTCATTCTAGT AGGGAATATAAACTACTGAACAAGACAGACTTGCTAACTTAAACAAGACAGACTCATTTCCCTTTGA G
EST30935 9a	59	C G	---	---	AGCTATGGTAGAGCAAAATCCAGTGGTGAATAATCAAGAACTCTAAAGTTCAGTAGAGA[C/G]AGGT GTTTTGAATGTCAAGGAAATCACTGAGGTAGATTTGGGATTACAATAAGACAGCTGCCCTGTGAGGT CATAAGAGCTTTTGTGAGG
EST32515 7	25	G A	---	---	CCGAATATAAGGAAAAAATGGTGGC[G/A]TGCCCTCTAAAAACCTGTTGAATAGAATAATGGCCAAAT ATTACAGTTTCTCACTTCCCTATGAATACTGGCACTGTTTATTTTCATGTTTATATGTGAGTTTCTATGC ATAAAAATCCCAGTAAGA
EST33274 4	27	T C	---	---	TGCTTTGTTCCCTCCAAATCCTAAAAT[C]GTGTGCTTCAAGAAAAATCGTGGAAAGGACTTTGAA TACGAGTTTGTAACCATATTCAGTATTCCTTGAATACAGGTTTCAGATACTATGGAGATGATACCATT GGACTAGGTA
EST33352 7b	75	C G	---	---	TACACATTATTCAAGAGACCACCTGACATGCATCTCTCCGAGAATACATTCGTCCTCTCTTAGAGA AGTTTAA[C/G]GCACATAGTATTATTTACTAAGAGAATATCTCTTGGTGTCATATCTAGGGG
EST33424 1	126	A C	---	---	ATTTTCCCACAGCAGAAGTATTTATTGTGCTGAATCAGGTAGCAGGGAATGAATAGCTCTTGG GAACCAGTACAGAATGTTCAAAAAGATTTACAATCTCAGTCAATTACACACTGAGCAAC[A/C]AAA CAAGGTGTTGAATCCTCTT
EST33488 7	90	A G	---	---	CCTTTGGGGGAGTTTAAAGCCAGAATGTGACAAAAGTCACTTACAGGAAGACTGGAATGTAGCCATAG TTGAACTCTAACATCGTCTATAG[A/G]ACCAATTTCCCGTCTCCAGTTAGGTTCTAGGCATACTAAGCT GCTC
EST33508 1b	45	C T	---	---	AAAAACATGCTATTGAACAAAACTTTTTTATAAAGAATAAGTTG[A/C/T]TGAAAAGCAGTTTTTAAAT AACATCAACTCAAAAATGACTTTTAGAAGCCAAATAA

EST33508 1a	36 A G ---	---	AAAAACATGCTATTGAAACAAAACCTTTTTATATAAGAA/G/JTAAGTTGACTGAAAGCAGTTTTTAAAT AACATCAACTCACAAATGACTTTTAGAAGCCAAATAA
EST33863 4	77 C T ---	---	ACAACATAGGACTGGTATTCTTGGTTTTGAAAAAATTATGTGTGCCACTTCCTATTGTTTTAAAAAATGA TCATTTAAAC/C/JTCTTTGAACTACAGCCTGAATCCCCC
EST34739 3	97 T A ---	---	GAAATATCCTTCCCAGTGGCAGGAAGTGAAGACTCCAGATCAACCAAGGTGGACCTTTTCGTTGATGA GCTGATAGCTTCTAGGCTGTGGGGAACCTC/T/AJGGTGCCTTACAACCTCAACTACTGCAGAAATTCCT TGTTGTGCCTCATAAACA
EST34792 6b	104 A G ---	---	ACCTGACTGCTTTAAAAAGCTCTTTGTAAGCTGACCGTAGCACAGATCACGTGGCATCCACTATCAATA CTCATAAGTCTAATTTATCTCCTCAGGATGTTCCCTGA/A/GJGATTACAGGAATTCCTTAGTCTTATTACA AAGATTTTGTGCTGTG
EST34835 9b	93 T G ---	---	GGAAATGTTCCCTTTGCAACAAAGGTACGTTTATCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGGAGTCTATGTTGCTTTCTGGT/GJGGCCTTAAAGAAACAGACAAATTTGTGCTAAAGAT
EST34835 9a	82 G A ---	---	GGAAATGTTCCCTTTGCAACAAAGGTACGTTTATCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGGAGTCTATGTT/GAJGCTTTCTGGTGGCCTTAAAGAAACAGACAAATTTGTGCTAAAGAT
EST35230 0	93 G T ---	---	CACAAAGGTCCACTTTACTTACATGAAGGAACATAAAGGCATGAGAAACAGTCATCTCAATAAATG CAAGACATGAGCATAAAGAGGTTCTC/GJGCCCTTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337 9	33 C T ---	---	TCTTTTCAAAATTTTGTAGTAGGCATTTAATG/C/JTATAAAATTTCTGCTTAGGAATGTATCTGCT ATATCTCAGAAGTTTGGGCATGTTGTTTCCATTTTACTTAGTTCAGAACTTTTCAATTTTCATCT
EST35708 9	32 C T ---	---	CTGCCCCAAATTAACCTTTAGGCAAAATGGAA/C/JTAGACTTACTGTATGGGACATTTTTAAAAAG ACAGCTTAGTAATATGTTTCATATGCAGCGTGTGCTTCCCTCTCTGAGGTGGCACCTTTCCCTGTTGTG ATGTGCAAGTGIGGCT
EST35747 9	51 C G ---	---	ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCACAAAGGCTCCA/C/GJATGTTAAACGT TTCCC/VACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTGCCCTTCCAGTAGGGTTGAGATT G
EST35751 9	89 C A ---	---	TGGTCCATTATATAAACTGAGGGAACAAACGGTGCTGACATGGCAGACATTTATTTCAATGGAGA AGTTCCCTCCCATGAACCAAGA/C/AJCTTGCTCATGATAAAGTGGAGACAATAAGAAAGCCAGGT ATATAATTAAGGCCTGTGA
EST36301 4	93 C T ---	---	CACCTGTTCAATGTTCACTGGGCTGCTATCTGTGGGCTGATGCTTACCAAGTGTCCAGCCTACAGC AGTCAGGAGGCGAGCCATGGCCCTG/C/JGCTGATGGAGCTTGTAATTTAGCCCCAAACTGATCTTCA GAAAGAGGTACAACAAA
EST36519 0a	33 G T ---	---	GCCATCAGCCCCACAAAGACATGACTACCAACGC/G/JGGCCCCCTTGACCCCTACTGGCCTCAGCAC CTAAGACTGGACAACCTTTGTACCTAATGACCGCCCACTGGCATATACTGGCTGGCCTCTTCTCTGT CACAGGGGTCTTAGTCGT

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EST36620 6	50 G A ---				GACITTTATTAGATAAGGGTTTCGGCTACCCCTCAAAGCTCTCAGGACTGG[G/A]GCTAGGGTTTAAGG AAGGCTTATTTAAATATGGGAAATAAATAACAAAAGGGCCACACCCGATGCAAAAGACTTT
EST36690 0a	89 C G ---				CCTGTGATGTGCATGGTGCCTGAGCAGTCGTACTTACTATGCGTCAGACAGCTCACGTATGTCAGGA AAGGAACTCTGGGATTCTCTA[C/G]AGGGGACATATCACACATATTCTAAGTCACTGTGTGACTCGG CTTGAGCAAGTCATTICA
EST36729 9	62 C T ---				GAGACAGAAGCCCATCGTTAAATGAGGTTAGGCCCTCTCTCTAATATACATGATTGACAATG[C/T]A TATTAGCCAGGTAATGCACCTTAGCTACCCCTGGACAATGCTATCAAGTGTGGGAAAGGGAG
EST36823 6	103 A T ---				ACTGCTGGCCGATGATTGGAGCTTGAAA-AACTACCATGCCAGATCTCCACCCAGACCAATTAG GTCAGTATCTCTGGGGTGCTATTCAAGCAACAATT[A/T]TCTTTTATGTTCTTAAGCTCATCATGAG TTAA
EST36987 4	126 C G ---				ATGATCGCTTATGTAATTTGAGGGCGACATGGGTAATGGGAGATACCCACAGGACCTGTAAATATT TAAATAATATTTAAACAGCTGATCAGAGGCTAAATTACAACCTGACATTTTGATGCAGTTT[C/G]GTTA GGGAATTAAGACAATGCAG
EST37054 3	88 T C ---				GGTCTCACTCTCTGCCAGGACGGTTTGAACCTCTGAGCTCAAGTGACCCCTCCACCTTGGCTTCC GAAAGTGCTAGGATTACAGG[T/C]GTGAGCCACACACCTGGTCTTGTTTAAAGTAACCACTGAA C
EST37269 3b	105 T G ---				AATAGTCTATGGTACGGGCCCGTGGGATGTTAAAAATTGGGATTTTAAATTAGATTGGAACATG CAAAACCAGCAAAATTTCTCAGCTTATATTTTGAAGTC[T/G]CAGGAGAAAAATGGGGTCC
EST37284 2	93 G T ---				AAAAGACCTTTCTCAAGCAGTAAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCAAGAA GCTCTCTGGATAATGTCACCTCTAGGA[T/G]TAAACACAGGTGTTAAACCCTGAGATAGCAACCCT CTTGGCTTGTGAGGAATA
EST37315 2a	90 A G ---				AGATGGGGTCTTGTAGCTTGTCTGGGCTGAACATAAGATATCTCTCTGCCTCAGCCTCCAGGTTAGT TGGAACATATAGTAGGAGTATCT[A/G]CCCTGCCCTGCTAGAACTTCAAGTTTGTATGGGCAAAATCCA CCCCAGAGGACAGGACAA
EST37374 1	45 C T ---				CCTGCCATGATAATGTTAAACATATCAAGATCTCTCTCAAACTT[C/T]AAGGGTGAAGGCATACC ATTCCATTTTGTGAAATATCTTCCATAGCCACACACATTTTTCAGGCACCTCTAGCTACTACA CGA
EST37376 8b	101 G C ---				GTGACATCATGCTCTTCAATGCCCTTTCAATTAAATAGTAGTTGAGCGCTGGGGCTGAAGTCAGACT CTCTGGGTTCAAATCACAGTGTGTCTCTGCA[G/C]GCTGTCTCAGGCAAGTTGCTGACTTCTCTG TGTCAGG
EST37376 8a	41 T C ---				GTGACATCATGCTCTTCAATGCCCTTTCAATTAAATAGTAGT[T/C]TGAAGCGCTGGGGCTGAAGTCAG ACTCTCTGGGTTCAAATCACAGTGTGTGTCTCTGAGGCTGTCTCAGGCAAGTTGCTGACTTCTCTGT GTCCAGG

EST37378 9	63 T G ---			ACACACAAAAAATGGTGGCAGAAAAATCTGGAAGATTCTAATAACCTCAATTTCGTGAAAAAC[T/G JAACATGCCCTCAAAAAAGAGGGGAAAAACITTAACAGAAACACIGCTGACATGATTAGCTT
EST37452 4	46 G A ---			AAGACATAAATCTGCAATGAATCAGTTATGAAATATTAAACCTCT[G/A]CTTCTCAGGAGTGACAC TAATCATGGTCTGGAAGCTAGCCTATCGCATTTTAAACACCCCTTAATCAATGACGTAGAA
EST37613 6	34 A G ---			CTAGGCATGGGGCTTTACAGTCATTTATTACCG[A/G]GTCATGAATTCATTAATAAACACACAGCGAT ATAGCAATGAGCAAAACAGACCCCTCCCCAAATACCCCTGCGTTCATGGATCTTCCATTCTAA
EST38025 4	56 T G ---			TTATTGAGTAGTACACTGTGGCCAGAACTAAGCTTTACATGTTTATATCACTTAT[G]TTATCTCA ACAATCTTGAAAGGGTGGTATTATTTCCCGCTTATAGGTGAAGACTCIGAGGTTTCAGAA
EST38068 6	57 C T ---			TCTACCAGGTCACCAAGTATCTGTATATGCTTTAAGTGGCATTTTCATGTCACCTA[C/T]CGCATGG AAGAACGCTCTCTTTTAAATCCCTAACTCTCTTCTCTGGAAGACAGAACGTCACAA
EST38420 6a	100 T C ---			TAAATCAAGGCCCTCTTTCATTACCAAAACAAAAACAAAAAGGGAACAAAAATACGATGGGAGAGG GAAGAGATGATGCCGAAGTGTACCTGACTGAC[T/G]CTCCCTGCAGTGCCCATGGTCCCGTGCCCT TATTCACTCTCTCTCTCA
EST38950 5	25 T C ---			TTTATTTGCAAAAGTAAGCAGCCGGT[C/T]GGTCCCTGGATTGAGGTGAGGAAGACATTACTTCTCTG CTGGAATACTTGGGACTTACATTTGACACAGGCTAAAGTATGGGATGAGAGAGGAACAAAAAGCTT ACAAACAAGAGCAGCCA
EST39053 6	90 T C ---			TTTTTGTACTCTGTAGCCAGTCATTAATCTGAAGTTTAAATATATCATTTTATTGGGATGAGATCA TAGTCTTTACACAAATGCTATG[T/C]AAACAAGTTACTGAATATTTTCACCTCGTGGAGTTG
EST39331 1	70 G C ---			TCCTTCCTGCTCTAGCACTCAGACCACCAAGAAAGCCCTGGAAGACCAAGCCATGGAAGGAAAGTA TG[C/G]GTGTTTAGGGAGAGCTGGCACCTGGCCTCTAAATCTCCCTCTGCCATTGACCAGATGGGT GCCTTTGGATACATCACT
EST40544 7	31 C A ---			GTCACCATTGACCTTACATAGTGGCTCTAGT[C/A]ACCTATGAGGCACTAGAACTCTATTGTACTTCT CACTTTATCACATTAGCTATCGAAGTTTGAATTT
EST40548 4	37 T C ---			TTCTAATAGCATGCCCTGTGACAGGGAAACTAAGCTCT[C/T]CAAAATAACTGAAACTAAATCTGTA AGATAAAATGCTGGAATTTGAGAAGGCACATGCCTTTTGTAGTTTTCTCCAGAGGCTCAAGGTGTTCT AATAATCTGTGGGACTCA
EST40549 1	42 A G ---			TGTTTCTCTAGAGAACCCCTGTGTGATACACTACGCATGCACA[A/G]ATAAAGTCACATCAAGACTAA TAATCTAAATGTTAGTTGTTACCACCATTTCTCACTTTGAACCTAGCTCCCTGCAAAAGCACCTTCTA CCCTGCACCTTTTGGGGAG
EST40579 1	81 A C ---			TGTGAATTACACATCAGTAAGGCAGTTTACAGAAATTTTCTTCTTACCTAAAGCTGTGCTATCTGTG AGCTGGTGGAAA[A/C]GGACTTGGAGACAGCGATTAAATACGGAACAAGGCTCTCCAGGAAG
EST40584 3	68 A G ---			TTGTATGGTTGTAGGAATTTGGGAAGAAATATCTGTGAAGGAAATTTGCCACTGTAAATGCACACCC A[A/G]TCTGTACTCTCCACAATATCCTATGTTTTAAGCT

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EST51340	51 G A ---	---	GATCAAACTGTATTGCCAGGCCAGCTCCTGAAGAACTGTGAACATATGAAC[G/A]TCTCAGCCTAGA AGGATAATGTGACCTTCAATTTGCACACCATCCATTGTCTCTTTCAAACCTAAGAGCCTCTCTAAGCTA GATAGGCCAAGGATTATT
J04162	134 T C ---	---	CATGGGAGTAATAAGAGCAGTGGCAGCAGCATCTCTGAACATTTCTCTGGATTGCAACCCCATCAT CCTCAGGCCCTCTCTACAAGCAGCAGGAAACATAGAACTCAGAGCCAGATCCTTTATCCAACTCTCGA[T/C]TTTCCCTTGGTCTCCAGTGAAGGGAAAGCCCATGATCTTCAAGCAGGGAAGCCCCCAGTGAGT AGCTG
K01506	63 T C ---	---	CTGAACCTCAGCTGCCCTACAACTCCATCTCAGCTTTCTTCTCAGTTTCATGTGAAAACACTAC[T/C]C CAGTGGCTGACTGAATTGCTGACCTTCAAGCTCTGCTCTATCCATTACCTCAAAGCAGTCATTCCCT TAGTAAAGTTTCCAAACAATAGAAATTAATGACACCTTTGGTAGCACATAATATGGAGATTATCCTTTC ATTGAGCCTTTTATCCT
L18877	69 T C ---	---	TGAGTCTGAGCACGAGTTGCAGCCAGGCCAGTGGAGGGAGTCTGGGCCAGTGCACCTTCCAAGGCC C[T/C]ATCCATTAGTTTCCACTGCCCTCGTGTGACATGAGGCCCATTTCTCACTCTTTGAAGAGAGCAG TCAGTATTGTTAGTAGTGAGTTCTGTCTTATTTGGATGACTTTGAGATTATCTTTGTTTCTGTTGGA ATTGTTCAAATGTT
L31848	36 T C ---	---	GGTCCAGAAGCCTCTCAGCCAGGAGGAGCTGCCCTGGAAGGGACCTGAGCTGGGGACACTGGC TCCTGCCATCTCCTCTGCCATGAAGATACACCATTGAGACTTGACTGGGCAACACACAGCGTC.CCCAC CC[G/C]CGTCGTGGTGTAGTCATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGGTTGTGACCCCTCT CTCCTAGAGACCTTGAG
L38517	137 G C ---	---	ACTTGAGAAGCAGAGCTCGCCACCTTCTGGAGGCCACTGTGATGATGAGCCAAGCAATTTGGAGCCA AGTTGAAGGGACAGGGCAACAAATACAGTAGTCTTTCTTTGTATTTGTATATTTGJCGCCTGA AGATCATCCCGCAAGGCAGGCTGGAGGTGCCGGTGGGCTGTGTTGCTGGGATTTTGTCTGTGCTGG GAG
L39059	123 T G ---	---	CAAAGTTGTCTCCTGCCCATGAGCACCCACAGTCAGGCCCTTGAAGGGATCTCTAGGGAGACAACAGC CCTGTCTCAAAACTGGGTGCCAGCTCCAATGTACCAGCAGCTGGAATCTGAAGCGGTGAGTCTGCAT CTTAGGGCATCGCTCTTCTCACACCACAAATCTGAAC[G/A]TGCCTCTCCCTTGTCTACAAATGTCT AAGGT
L41268d	173 G A ---	---	

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L48728b	111	T C ---	---	---	AAGTGAACAGAAAGCAAGATGGATTGTTCTCTATAAAAGCACATAGTTATGTTTACTGGTATCGT AAGAAGCTGGAAGAAGAGCTCAAGTTTTTGTTTACTTTTCAGAA[T/C]GAAGAAGCTTATTCAGAAAG CAGAAATAATCAATGAGCGATTTTAGCCCAATGCTCCAAAAGCTCATCCTGTACCTTGGAGATCCA GTC
M18079	52	G A ---	---	---	GCGCACAGTCCAAAATACAAAATTGGACAGAAGATCTATATTGTACCAGAAGCT[G/A]TTTATTTCAACC CCATCAAGTATAAAGGTTACTGATTGATTGGTCTTTTATAAACAATTGGTATATTTCCATTTCATGCCAA AGCAAAAGAAGTAAAAGCTAA
M19169	113	T C ---	---	---	TAGGATCTGTGCCAGGCCATTCCGACAGCCACCCACCTCCACCCCTGTAGTGTCCACCC TGGACTGTGGCCCCACCTGCGGAGGCTCCCCATGTCCTGT[C/G]GCCAAGAGACAGACAGAG AAGCTGCAGGAGTCTTTGTTGCTCAGCAGGGGCTCGGCCCTCCCTCCTTCTCGCTTCTAATA GC
M21539	114	T G ---	---	---	TCACCTCGTTCCACAGCTCCACCTGCATCTTCATCAAAAGCCATCCAGGGATACACAGGGAGCTTCT TTCCCCCTTAGCCTGTGATCTGCCCATGATGATCCCCGACAGCAAAA[T/G]GTTTCTTTCTGAGGCTG CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAAAGGAAGTCTCAGCTGTACCGGCCCTTTCAGAGCT TCTCTTGGGTGC
M26041c	173	A G ---	---	---	CCTAGCATTATTTCTGGCCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCACCTCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATATTTCCCTGACTTC CTGATTTTCTTTTCTCA[G/G]GTGTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041b	157	A G ---	---	---	CCTAGCATTATTTCTGGCCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCACCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATATTTCCCTGACTTC CTGATTTTCTTTTCTCA[G/G]GTGTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041a	45	C G ---	---	---	CCTAGCATTATTTCTGGCCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCACCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATATTTCCCTGACT TTCTGATTTTCTTTTCTCAAGTGTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M63967	57	G C ---	---	---	TAAGGCAGCTGTCAAGGAGGCCAGTCACAGTCCAGCAATTCACAACCACCTTGAC[G/C]AATGCT TGCCAAGCTGTTTTAAAGCCCAAGAACACCCCTTCTTTGTTCCAAATTAACCTTAGAAGAAACCCCA CAAATAAGCAATTCAATC
M81695	34	G A ---	---	---	ACTTACTTACCTCACCTGTCAAGGTGACGGGA[G/A]GAACCACTGCACACCCAGAGAGGCTGGG ATGGGCTGCTTCTCCTGCTTTGGGAGAAAACGTCTGCTGGGAGGGGCTTTGTCTTGTCAAGGTTC CAACTGGAAACCCCTTAGGACAGGGTCCCTGCTGTGTGTTCCCCAAAGGACTTGACTTGCAATTTCTACC T

U06641d	166	CT	---	---	CTCCTCCTTATTTTCAGCATGGAGGTTAAATGGAGGATCTCCTTTCTGTGACAAAACATCTTTC ACAACCTTACCTTGTAAAGACAAATTTAAAAAGATCTTTTCACAACTTACCTTGTAAAGACAAAAT TATTTCCAGGCTATTTAATACGTACTTTAG[C]/TJGGAAATTTATCTATGCAATGATTTTAAAGCTA TGAAATACAAATGGGGGA
U09607	39	TC	---	---	GAGGCCATTAGAGGGTCCCTACTTACAGGAACACCCCAAT[C]/GACATTGCAATTTGGGGGGCTCCCG TGGCCTGTAGAAATAGCCTGTGGCCTTTGCAATTTGTAAGTTCAAGACAGATGGGCATATGTGCAG TGGGGCTCTCTGAGTCCCTGGCCCAAGAAAGCAAGGAACCAATTTAAGACTCTCGCATCTTCCCAAC CCCTTA
U09608	82	TC	---	---	GAGCAGAAGGCAAGAGCGGCAAGATGAGTTTGAGCGTTGTATCCAAAGGCCCTATCTGGAGCCTC GGGAAAGTCTGTGCT[C]/ACATCTGCCCGCCCTTCCAGCCCTTCCCCAGCCCCCTCTTGTCTTC ATTCAATCAACAAAATTTGGC
U10694	20	CG	---	---	GTGACATGAGGCCCATTTCTT[C]/GJGCTCTGTGTTTGAAGAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCATCTCTGGTTCCTTGCTATTGGGTGATTTGGAGATTATCCTT GCTCCCTTTTGGAAATGTTCAAATGTTCTTTAATGGTCAGTTTAAATGAACCTCACCATCGAAAGTTAA TGAATGACAGTA
U13877b	162	TC	---	---	AAAAAGGACTCTGGTTCAAATCCAGGTTCCATTTTGCTATCTTTGTGACCTTGCACAAAGTTGTTAAC CTCTTTGTTGAGAAATTTCTCCATGGAGTAACAATATCTAGTTGGGAGGATTAGTGAAGTTACATGT AAAGCACAGAGGAAACAGCCCAAGAGAT[C]/JTACCGTGGTCTTACTAAAGTACATATCCTAACTTGG GGTTTACCTTCAGCA
U15555	187	TC	---	---	TTTCTGCCACTTTCACCTGGTTTTAATAGCCAGCCAGTCATAATAGTAGAGGAATCAGTCAAGCAA AAATGCTTTGGAAGAAATTAATAAGCAATGCTGAACATCAGGAATTTAGATATCCGTACAGAGAGT TCCAGTAAAAATTTATGAGTCCACGACCCCTTTTCTAAGCAGTCTGGTCCATG[C]/JGGTCTCATAC CTCATATGCAGGATTCATTCA
U17077	122	TC	---	---	TCCAATTATTGGTCCCCAAAGCAGCTTCCAACGTTTGCCATCTGGATGACAAAACGGAGATCCACT AAAACGTCCACGGGATTAAACAGAACGTCCTTGACAGACTGAGCGATGACACCACACAT[C]/JTGTGTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAGCTTTTCTTTTCTGGGAAACAACTGTCCTTGG AATTA
U18543	58	TC	---	---	GCACATGCAGAATAGACTCAGCCTATGTCTGATTCCAGCTGGGTAGTTCTAGAACTTT[C]/JAGAAG CTCCATCTTTAATGTTTTTATTGTTATGTCCTCCCTCCCGGCTCCACCTAAATTTAGAGCTTTAAA AGATGCACTGCCCAATAGGACACACGATGGTGTAGCTGAAGTTTGTATTAGCAATTAGGCACCTCC AAGGCTTTAGTAGAGAGAGCC

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U25975b	164	C A	---	---	TCAC TGCTGTGGCCTCATACTCTTTTCCATTTCTACAAGAAGCCCTTTTAGTATATGAAAAATTATT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAATGACTATTCTCTG AAGACAACCAAGAGAAAATTGCAAAAAGAC/AJAAAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAAGGAATTGTGGACTGA
U25975a	143	C G	---	---	TCAC TGCTGTGGCCTCATACTCTTTTCCATTTCTACAAGAAGCCCTTTTAGTATATGAAAAATTATT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAATGACTATTCTCTG AAGACAACAC/AJAAAGAGAAAATTGCAAAAAGACAAAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAAGGAATTGTGGACTGA
U25997	61	A G	---	---	CAGGAGAGGTTATTCACAACCTCACCAACTAGTATCATTTTAGGGGTGTGACACACCA/AJGJTT TTGAGTGTACTGTGCCTGGTTTGAATTTTAAAGTAGTTCCTATTCTATCCCTTTAAAGAAAATT GCATGAAACTAGGCTTCTGTAATCAATATCCCAACATTCTGCAATGGCAGCATTCGCCACC. ¹ 3CAAAA TCC
U28413	29	C T	---	---	ATTCTGACAGCTAAATTAGCCCTAAATG/C/TGGGTAATATTTTCCATGTTTTAAATGAGGTT AATATTTGCATAAAATCTAAACAGACTTCTGTATAGTTATTTAGTCAAAATGTGTTCCCTTGATCC CAGATGTTGTGGCCTGGGAAAGCCCTCATTTGCTACAGTACAAGTAACACAAGTCGTTGTACCTCAGTT G
U30884c	89	A G	---	---	TAGGGGTAGCATTTAAGATTGAGGAGTCATTAGCAGTGATGATTTTGGGACCTGCCGTATAATCTGTT CTTCTATCCACGTTAGCCA/AJGJTTGTTCTTGATGAATCTATATGAGTATAGAACACACAAATCTAT TGACGGGAAGTCATTAGAATGGCTTGATATCTGATGGCTTGAACTTGCCCAACAGTTGAACACAAAGT GCTGTCA
U30884a	34	A G	---	---	TAGGGGTAGCATTTAAGATTGAGGAGTCATTAGC/AJGJTGATGATTTTGGGACCTGCCGTATAATCT GTTCTTCTATCCACGTTAGCCAAATGTTCTTGATGAATCTATATGAGTATAGAACACACAAATCTAT TGACGGGAAGTCATTAGAATGGCTTGATATCTGATGGCTTGAACTTGCCCAACAGTTGAACACAAAGT GCTGTCA
U31216b	78	A G	---	---	GGGACAGCATATGTGGCACCGCCTCTCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAAACA GCCGTGTCATCA/AJGJCCCTCACAATAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTTCAGATA CCAGCACCAAGACCCCTTTACAACGTAGAGGAGGAGGATGCCACGCCGATTGCTTTAGCCCGCC TGGTAGCCCTTCCAT
U31216a	70	G A	---	---	GGGACAGCATATGTGGCACCGCCTCTCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAAACA GCC/GJATCATCAAAACCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTTCAGATA CCAGCACCAAGACCCCTTTACAACGTAGAGGAGGAGGATGCCACGCCGATTGCTTTAGCCCGCC TGGTAGCCCTTCCAT

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U31416c	76 GA ---	---	---	AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCAC[G]CCACAAATCTGGTGCCTCTCTCTGCTTACAAATGCTAGTCCCACTGCGCTGCT GGAAGAAACACACACTCCTTTGCTTAGCCACAGTCTCCATTTCACTTGACCCCTGCCACCTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68 CT ---	---	---	AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC [C/T]TCTCACGCCACAAATCTGGTGCTCTCTCTGCTTACAAATGCTAGTCCCACTGCGCTGCTG GAAAGAAACACACACTCCTTTGCTTAGCCACAGTCTCCATTTCACTTGACCCCTGCCACCTCTCCA ACCTAACTGGCTTACTTCCT
U37519a	78 CT ---	---	---	ACGGGTACACAGAGAAACCTGAGTCTAGCCATGAGGGCTTATGCTCCCAACTCACATTTCTCTCC AGACCGCAGG[C/T]TCCCCCAGCCTCAGGTTGCTGGAGCTGCACATGACTGCATCCTGCCTGCCAGG GCTGCAAGCAAGGCTTCTCTATCTGGGGAGGCTGCTCGAGAGAGGCCGAGAGGCCGCGAGAAC ATGCCAGGTGTCC
U37690	54 AG ---	---	---	GACCACGCTGAACCCACCCACCGCTGTGCTGACCATGGGCCCTGAGCGTCTTGA/GJCCCCGAATTC ACGAGGCTGAGGCATCCGGAGCTGGCGTAATGCCTGGCCGCACTGTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAAGGCTTT
V00540	39 TC ---	---	---	TGAACCCGTTTCAACATGGAAATGATCTGATTGACTAAIT/CJACACCAGTCCACACTTCTATGACT TCTGCCATTTCAAAGACTCATTCTCTATAACCCAGCTGAGTTGAATCAAAATTTTCAGATCTTT TCAGGAGTGTAGGAAACATCATGTTTACCTGTGCAGGCACTAGTCTTTACAGATGACCATGCTGAT A
X15943	106 AT ---	---	---	TCAAGAAGGTGACTGCCCTTGATGATGGATGGGAAGATGAATGACTGGTTTTTACTGGGGTGTA AACCACCTGAGCCTCTCTGAGACCATGIGGTTTTAAAT/VTAICCATAGGGAAGGTACCCACAC CAGTATCTGAGTCCAGTAGCTAAGACCCCTAGAATTTGGATTCACTCIGTTTTTCAIGTCTCTCT GTAACCCCTGAGATCATCAG
X52011b	148 CT ---	---	---	AGGAAGATCCCAACCGACCCCTCCTGGCCTAATCCTTTAGATTAGGTCACATTACATTAACTTAGGA ACCCAGACCGAAAAAGTTGCTGAAAGGGAGGAGACACATTACAAAGAAAGTTGCGAAAAATTCG AAATCTGTTGTGCA[C/T]GCTCAAAATGAAAACGGCTTCGGCTTTTGGGCTTTTATTTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT
X52011a	118 AC ---	---	---	AGGAAGATCCCAACCGACCCCTCCTGGCCTAATCCTTTAGATTAGGTCACATTACATTAACTTAGGA ACCCAGACCGAAAAAGTTGCTGAAAGGGAGGAGACACATTACAAAGAAAT/CJGTTGCGAAAAAT GCGAAATCTGTTGTCACGCTCAAAATGAAAACGCCCTTCGGCTTTTGGGCTTTTATTTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT

X54741	24	A G	---	---	CAGGCCACCTGTCTTCTCTCCACAG/GTGCACAGCTTCTGAGTCACCCCTCTGTCCAGCCAGCTCCTGCACAAATGGAACCTCCAGGGCTCCAGGACTGGGCTTGCCAGGCTTGTCAAATAGCAAGGCCAGGGCACAGCTGGAGACGATCTTGCTGGCAGGGCTGGGCTTGTCGCCAGCCCCACCTGGCCCCCTTCTCCAGCAAGCAGTGC
X54869	99	A G	---	---	AAGCATTTGCGTTACAGTGCATCAGATACATTTTATATTTCTTAAATAGAAATATTATGATTGCATAAATCTGAAATGAATATGTTATTTGCTG/GATACAAAAATTTCTAAATCAATATTGAAATAGATGCACACAATTAATAAGTACAGACATCCTAGCATTTGTGCGGCTCATTTTGTCTCAACATGGTA
X66924	147	G A	---	---	GCCGTGCTGACACCTCCAGAACGAGTGTCTGGGCGGCTTCTGCTGGACCCCGGGAACTCTCTGCGCGAAGCCGCGAGGATGGGCCCCAACTTGCCTGCCACTTGACTTACCAAAATCCCTTCCTGGAGACT/GAAACCTGGTGTCTAGGAGCGAAGGACTGTGAACCTTGTGGCCTGAAGAGCCAGA
X78032	62	T G	---	---	GAAATGTGAAGAAATGTGACAAAGCCTTTAAGCGGTTGTACACACTTGATTTGTATATAAGATAA/TG/TCTATCTGGAGAAATCTCCAGAAAGTGTGACAAATGTGACAAACATTTAAATTAATCTCATACCTTAATGACAGGAAAGCATTTATACTTGAGAAAAATTTGATAAAGAAATGGAAGATCAATTAATATCTGCTCATATCTTAACATCAGCGAGTT
X80026	25	T C	---	---	CTCAACCCATAACCTCAACCACATCTT/CJTATCCTCCACCCACATCCACCACATCCACCTCCATCCCAAACCCATCTCATCCCCAACTACAGCCCCAAACCCAGCCCCAGACTAATCCACAGCCATCCCCAACTCATCTCATCCCCAACTGCAGCCCCAAACCCAGGGCCATCCCCAAACCCATCCCCAAAGCCAAACTCAACACCATCC
X80197b	99	G C	---	---	ACCCAACTCAAGTCCAGGCCCCAGGCATCTTCTGCCCTGCCCTTGCTGGCCCATCCAGTCCAGGCGCTGGAGCAAGTGTCTAGCTACTTCTCTT/G/CJACTTTGAAAGACCCCTCCACTCTGGGCTCACTTTCTGTGTATCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCTAGAAAG
X80197a	28	A G	---	---	ACCCAACTCAAGTCCAGGCCCCAGGC/GJCTTTCTGCCCTGCCCTTGCTGGCCCATCCAGTCCAGGCGCTGGAGCAAGTGTCTAGCTACTTCTCTGCACTTTGAAAGACCCCTCCACTCTGGGCTCACTTTCTGTGTATCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCTTAGAAAGGGACCCACAGTGAOCACAAGTCCAGCAGGGAGGGCGGCCCTGCCGTGTCGGTGTTCCTTTT
X85106	150	G A	---	---	CAGCCCCGAGAGGTCTGACCTGGGGCTTCTCGAAGCTCACTGGGCACGCTCCCCGCCGCTCTCTTTCTCCCAAGC/GAAACCAAATGGCCCCCTTCACTCGCGTGGCGAGGGCGGGGGCTCTTCAGAGC
X87160	128	T G	---	---	ACCACGACCATGGTCTAAGGACATGGATCGGGTGCCCCCAGACGTTGTCACAGGGGACCCCTCTGCCCCACTCTGGGCTTTTCAGATACTCTGACCAAAAAGCCTGCTTTAAACCGCAAGATGGGGCTT/GGGGATGCGCAGGAGGAGCCATCGGGTACTACGACGCAACACTCACAACCTGTCCAGGCTGAGATAAATCCC

X87344	34 C T ---	---	CATCCCAAGGCAC TGGTGTGACTCTGCTTCCCTGTC/ACTGACCCAGAGCCTCTGCCTGTGCACCTGC AAGCTGTGTCTACTAGGCCCAAGGGGACTCTCTGTTTCCATCTCCCCCAGAGCCTGTCAAGAG AAGCATGACAAACAATAATCATTTACCGACTTTAGTGTCTTTT
X87838	179 G T ---	---	GGTGGCTGTATCTAGAAAGTGCCTGACACACTAACCAAGCTGAGTTTCCATGGGAACAATTGA AGTAAACTTTTGTCTGCTCTTTTGTGCGAGGAGTAAACAATACAAATGGATTTTGGGAGTGACTC AAGAAGTGAAGAATGCACAAAGATGGATCACAAGATGGAATTTA/GTCAAACCCCTAGCCTTGCTT GTTAAATTT
Z14138	81 A G ---	---	GTTCGTGCTCTACACAGGGCCCTGTACAGTGAATGGTGCCATTTTCGAAGGAGCAGCAGTGATGA CCTCCTGTGACCC/GTGAATGTGCTCCAGCGGCCCTGTGTGTTGACATGTGAAGCTATTTGAT ATGCACCAAGTCTCAAGGTTCTCATTTCTCAGGTGACGTATTCTAAGGCAGGATTTGAGAGTTTCACA GAAGGAT
Z18859	191 A C ---	---	TAATCCTCACCATTCTCAGGTATAAGTTCTATAAACAGGCTTGGGTAATCTGGGTAATTTAAAAACAGA AAATTATAGTCAATATACCATGACATGAAGAAATGAATCCATTTCTTTGGAGATGGAGTATACATGACT GCAACTGTATTTTCATACGTTCTTTTCAAAGTGGGATAGCTATTGCAGCTTAAAGAGC/A/C/CAGGTTTC CAGTACTGTTTTCACAA
Z23091	159 G A ---	---	AGAACCTGACCAGATGTGGCTCGGAGGGGAATCCAGACCCGCTGCTGTCTGCTCTCCCTCCCTCCCTCC CACTCCTCCTCTCTCTCTCTCTCTCTCACTGCGACGCCCTCCCTTCCCTCCTCCCTCCCTCCTCCG CTCTGTGCTCTTCATTTCTCACTG/A/GGGCCCGCAACCCCTCCTCTCTCTGTCCTCCCGCCCTCTCTGAAAA CTGAGCTTGACGTTTG
11595b	125 A G ---	---	GTTGGCATTGTTAGTAAACCTCATAGGTGAAGAGGAGGATCAGTGAGATTAAAGTATTTTATCAAA GTGTGGTTTCTGCAAGGGCAGGTTTGAACCTGACCCCTAGTTGTGCTCCAGGACCTA/GJGGGTGC TCACTTACCTTGTCTTTGTGTGAAGGAGTGGTTTCCCATGACTGTTTAAAGTGACAAAGTGCCATGG ATATCTACACCCGTCAACAGACTAGATTGTCTCAATGTCTTGGCTTGGAC
11595	125 A G ---	---	GTTGGCATTGTTAGTAAACCTCATAGGTGAAGAGGAGGATCAGTGAGATTAAAGTATTTTATCAAA GTGTGGTTTCTGCAAGGGCAGGTTTGAACCTGACCCCTAGTTGTGCTCCAGGACCTA/GJGGGTGC TCACTTACCTTGTCTTTGTGTGAAGGAGTGGTTTCCCATGACTGTTTAAAGTGACAAAGTGCCATGG ATATCTACACCCGTCAACAGACTAGATTGTCTCAATGTCTTGGCTTGGAC
1241	131 G T ---	---	TATATCACATTAGTATGTCACCTGCCATGGTAAGGACTTTGATCAGTAGGAAATGAAGAACACTTTGAA TGGCTTGTCTCTTCAATAAAAGAGTGACATGATTGAACATGTGTTTGTAGATAAAGGGCAGCTTGT JGCAGGAGTGTTTAGGATGAAGAGAGAGAGATTAAAGGAAGATCAGGAAGAAAAAGTAGCAATGGGA ATGAAATAGGAGGCCCTGAGATCCACTGGATATCTAAAAAACCAAGAGAAAA

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1282	130 C T ---	---	---	GTGGATCACCACACAGTCTAATTTTCAGATGTTTTCAATACCCCTAAAAGAAAATCTTGATACCCATT GCAATTATCCCTCATTCCCTGCCCTCACCCTCAGCCCTACTCTTTATCGCTATAGATTTGCCCTACT TGACATATCATACATGGAGCCATACATATGTGGCCCTTCATGATGGCTTCTTTCACTGAGAAATA ATGTTTTCAAGGT
6810	68 C T ---	---	---	AGTATCACACATACCTAATATATTAGATATACACAATAATAAAATCACTCCCTACCTTGAAAACTTT A/C/JAGAGAGCATTTTTAAATTTACACACAAAGCTCAAAACGACCTACAAATAAGTCTAGTAGCTG TTACGTGCCAAGGGATAAGGCTGAACAATAAATTAACCCCTTTAAAAATGCTATGAACAAGTACAA TTTTCTTTTGAGTCTGCAGAGCAATGACCCTAAGAAATATTTTTAAAGGC
6817	118 A C ---	---	---	CCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTATTTGCTTTTGTATCCAGTTAAGACCA TCAGCATATACAACATCATCACTAACAATGTAGCTGCGGGTAA/C/JGTGGATACCCCTG TGCTCTACTGGCTCCAAAGGCATTGAGGGATCATCAAGATGTGGACACCTTGTTGTTCAATC TTGGTTCAGGTGCGGCTGTGCAGATCGGCTTTTGGTTGGTTGCTTAG
6819b	212 C ---	---	---	CCATTTATTTTCTCTAAATTTTAAATAGAGACTTTAATGGAAAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACCGCAGGAAGCCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTTTCATATACAAAATTTTCTGCTATTTTGTCTTAGCAAA CAGCAATAACTTTTGTGTTCTCTATATGACACCTAATATCCA
6819a	166 G T ---	---	---	CCATTTATTTTCTCTAAATTTTAAATAGAGACTTTAATGGAAAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACCGCAGGAAGCCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTTIG/JCATATACAAAATTTTCTGCTATTTTGTCTTAGC AAACAGCAATAACTTTTGTGTTCTCTATATGACACCTAATATCCA
681xx	39 A G ---	---	---	CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATT[G/JTTATACTATGGCACCATTTGGGACA CAGATTATATATGTCAGACACCCAGCAATGTCCTTTAAGATATGCAGCAAGCACAAATCTGTCTATGGT TTAACAAAAGAAATGAACGCTAGG
6972b	149 G T ---	---	---	AGGATCCCTCTTTTCTATTGATTGGAATAGTTTCAGAGGAATGGTACCAGTTCCCTCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTGGTAAAGTATTGATTGCT CACAAATTCAGA/G/JCCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCTGGTTAGTCTTGGGA GAGTGTATGTCTCGAGGAAT
6972a	122 A G ---	---	---	AGGATCCCTCTTTTCTATTGATTGGAATAGTTTCAGAGGAATGGTACCAGTTCCCTCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTGGTAAAGTATTGATTGATT TTGCCACAATTCAGAGCCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCTGGTTAGTCTTGGGA GAGTGTATGTCTCGAGGAAT

7598k	210 A C ---	---	AAAGGTAATCAAAGTCCCTCTATAAAATATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTAATTTCCCGTATTTTCCT CAATGCAG[A/C]
7598j	208 A T ---	---	AAAGGTAATCAAAGTCCCTCTATAAAATATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTAATTTCCCGTATTTTCCT CAATGC[A/T]GA
7598i	192 G T ---	---	AAAGGTAATCAAAGTCCCTCTATAAAATATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTAATTTCCCGTATTTTCCT CCTCAATGCAGA
7598h	144 C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAAATATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCCTTTTA ATATTTGATCC[C/T]ATATGTGAGAGATTTTCCCTGATATGTTATCTTATTAATTTCCCGTATTTT CCTCAATGCAGA
759Jg	142 C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAAATATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATATTTCTTG[A/G]GGATGCCCTT TTAATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTAATTTCCCGTATTTT CCTCAATGCAGA
7598f	120 A G ---	---	AAAGGTAATCAAAGTCCCTCTATAAAATATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAA[C/]CAGATTTTACCTTGGAGAAATGAAAATATTTCTTG[A/G]GGATGCCCTT TTAATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTAATTTCCCGTATTTT CCTCAATGCAGA
7598e	83 C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAAATATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGC[C/]GCTAACAGATTTTACCTTGGAGAAATGAAAATATTTCTTGAGGA;GCCCTT TTAATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTAATTTCCCGTATTTT CCTCAATGCAGA
7598d	77 C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAAATATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGC[C/]GCTAACAGATTTTACCTTGGAGAAATGAAAATATTTCTTGAGGA;GCCCTT TTAATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTAATTTCCCGTATTTT CCTCAATGCAGA

7598c	56 A G ---	---	AAAGGTAATCAAAGTTCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCA[A/G]AGGAAC TCAATGAAATAAGCCGCTAACCAAGATTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCTT TTAATATTTGATCCCATATGTGAGAGATTTCTCGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
7598b	47 C G ---	---	AAAGGTAATCAAAGTTCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAGGAAC TCAATGAAATAAGCCGCTAACCAAGATTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCTT TTAATATTTGATCCCATATGTGAGAGATTTCTCGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
7598a	30 A G ---	---	AAAGGTAATCAAAGTTCCTCTATAAATT[A/G]TGATTTACAAAAGACACCCAAAGCCAAGGAAC TCAATGAAATAAGCCGCTAACCAAGATTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCTT TTAATATTTGATCCCATATGTGAGAGATTTCTCGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
7598c	116 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTCTCTATTAGACATCTGCCAGCTCTCCTGTA ATACITTAATGAATGGGTAGTCTATCTCTCAAGGTCCCAAT[A/V]CCITGAGGTTCCCT
7598b	94 A C ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTCTCTATTAGACATCTGCCAGCTCTCCTGTA ATACITTAATGAATGGGTAGTCT[A/V]CTCTCAAGGTCCCAATTAACCTTGAGGTTCCCT
7598a	75 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTCTCTATTAGACATCTGCCAGCTCTCCTGTA ATACITTTATGAATGGGTAGTCTCTCTCAAGGTCCCAATTAACCTTGAGGTTCCCT
8071	119 A G ---	---	AAATACAGAAATTTTATTAGAAACTGTTTAAAGTAGAAAAAACCCTGTCAAGAAAGACCAGGTGG AAAAATGGGTTCCCAATAAATGGAAATTTAGGGCAACAAGTCTAAAAGGCC[A/G]CAAAAAGAGA AATAGCACCACTGTCAATTTGAACAATGGCTAGTTACTTGCAATTTTGGCATTGTTAATCACTGAATC TGGGTTTCTCTGAAITCCACACAGAGCATGCACTACACAACATTTTATCAT
8467b	93 C T ---	---	AAGGCTTTCCTCTAAACATCAGTCTACGGAGAACTGGGAAATCCTGGATATTTGGCTTATCATT TGACGCAAAATCCACTTTGCTGTAA[C/T]GGTCACTCCGAACCTCCTTCAGAGAGCAAGCAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAGTATTAGGAAAAATTACTG
8467a	70 A G ---	---	AAGGCTTTCCTCTAAACATCAGTCTACGGAGAACTGGGAAATCCTGGATATTTGGCTTATCATT TG[A/G]CGCAAAATCCACTTTGCTGTAACTGTAACGGTCACTCCGAACCTCCTTCAGAGAGCAAGCAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAGTATTAGGAAAAATTACTG
8498	84 C T ---	---	AGGGTTCAAGGTTTGGTTTAAATCAGGCTGCACACCTTTCAAATCAATCTGACATCTCTATGTCA AACTGGCTTCAGCTAG[C/T]AATCTTCATTAAATCGAAAAAGAAAAATTTGCTTAAAGGAAAAAA AATCCAGTTTAAAGAACAAATTAACATTAGCTTTTAAATAAAAGAGGGCTAATGTTTCATGTTGCT TTATACATCCTTCTCCTCAATACAGAACCCAGGAATGTAATTTTCTTAACCTCAG

WI-18562	29	G A ---			CTAAGGAAAAATTTAATGATGGAATATC[G/A]ACAAATATTCAACATCATTTAAAAACAAGTAG CTTCTCTAATTTACATAGCTTAGTTGGGATAGAAATAGAACTAATGTTTACAATGATTCATTACATTT TAGCATTAATCAGAAACGA
WI-18618	51	A C ---			ATAGCAGACTTTTAAATCAATGCCAGAGACAAAGTGAGCGGAGCTAAGAAC[A/C]CGCTCAGCTTCG TTACAATGAAGAAATGGTTTCCTTTTCGATGCAAGTATAATTGTAACACACAGTGCTCGCACAGTTC AC
WI-18683	22	C T ---			TAAGCTGTTCCAGGACTGGACT[C/T]GGTCCCTTTATTAGAGACTGACAGGCCAGTGGGTCCACCCAAA CAAAAATAAATTTCTCTCCCAAGCCTGCCCTGCAGT
WI-18520	75	G A ---			GACTTTGGTGAATTAATGCTTTTCCCTTAAATATGAGAAATAGGTGTAATTTCTCCTTTTGTCTTTT ACTACA[G/A]CCGGAGTGGTAAATACTACCTACTGCCAACAAACACGGGCATCCACTCTGTCTTCAA TGCCCTCTCCGTGAGAC
WI-18563	94	A G ---			AAATAAAGTTTATTGGCACACAGCCCAAGCCACTGGATGACACATTTGCCACGGGCTCATCTTGCAA TACAATAGCAGGGTTCACTAATGTGAC[A/G]GACATGGTGTGGCTCACAAAGCCAAAGATATT
WI-18582b	69	T A ---			GTCTATTCAATTTAGCTAGACCCCAATTCATCTGTTTAATGGCTACATTTGTTTTCATTGTGAGAC [T/A]GTGCCATAATTTAATCAGTGCCATATTGAAAGACATTTGGATCGTTTCCCGAG
WI-18723f	94	G A ---			AACTTTATTGATCTGACGATCAGCGATTAGTCTCATCCACATTGACTGCTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAACCAA[G/A]TATATAGCTTATTGGTGAATCTTCATCCT
WI-18723e	71	T C ---			AACTTTATTGATCTGACGATCAGCGATTAGTCTCATCCACATTGACTGCTGTAGATTTTGAAG TGGT[C/A]ACAGGTACATAGGTAAACCAAAGTATATAGCTTATTGGTGAATCTTCATCCT
WI-18723c	96	A G ---			AACTTTATTGATCTGACGATCAGCGATTAGTCTCATCCACATTGACTGCTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAACCAAAGTATATAGCTTATTGGTGAATCTTCATCCT
WI-18619	44	G A ---			TTTATTACAAATTTAGGTGGCACAAATAACTAACAAAGCTTCTGA[G/A]ACAGGAGGTAACATTCCTCA TAGACTTTGCCAATCAGCCAGAACTAAACTCGAAATA
WI-18715	76	G A ---			TTATTCAAAAAAGTGATATTGACAGGGTCTGGGGCTGTACATGGCAGGGGCTTGGTGAGCTTTG TACATGGG[G/A]CTGGGAGACAAAGGAGCCTCCAGGTGGAAGGGTATTTTTTAATAAAAAAATAA TGGAGCTACAAACACCCCC
WI-18535	107	G A ---			GTAATAAAGTTTATTGGCACAGCCACGCTCGTTTCATTATATGCCATTGACATCTGCTGTTGCCCT ACACAGCAGGGTGGGACCTGCTCTTCACGGGAGAGCT[A/G]TTGTTTAAAGCAGTGGTCCCCAAAC CTTCTGTGTCCTCCCGTG
D17525	107	C T ---			AGAGTGGTCAGAACACAGGCCGAATCCAGGCTCTATCACTTACTAGTTTTCAGTTCTGGCAGGTGAC TTCATCTCTTCGAACTTCAGTTCTTCATAGATGAA[A/C]TGCTATACCTACCTACCTCGTAAAA GTCTGATGAGGAAAAAGATTAACTAATAGATGCATAGCACCTTAACAGAGTGCATAGCATACACTGTTT TCAATAATGCACCTTAGCAGAGGTCGATGTGCTACCGGACGACGAAAG

-239-

DWU-133c	313	A G	---		TAATTGGCCACTGCCCTATTATTACAAAACAGAAATGCTCATGACTTTTTTATGTGTACCATCCT TTAATAGATCTCATACACAGAAATTCAGATCATGAATGACTGACAGAAATATTTGTGGGCAGTCCT GATTTAAAACTAAGACTGGCTTGTTGTTAAATGAATATGTTGAGTTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236	T C	---		TAATTGGCCACTGCCCTATTATTACAAAACAGAAATGCTCATGACTTTTTTATGTGTACCATCCT TTAATAGATCTCATACACAGAAATTCAGATCATGAATGACTGACAGAAATATTTGTGGGCAGTCCT GATTTAAAACTAAGACTGGCTTGTTGTTAAATGAATATGTTGAGTTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199	C T	---		TAATTGGCCACTGCCCTATTATTACAAAACAGAAATGCTCATGACTTTTTTATGTGTACCATCCT TTAATAGATCTCATACACAGAAATTCAGATCATGAATGACTGACAGAAATATTTGTGGGCAGTCCT GATTTAAAACTAAGACTGGCTTGTTGTTAAATGAATATGTTGAGTTTTGAATTTAATAGTAACCTCC TTCCAAATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102	C T	---		ATGAGATCCTTTAAATCCTCCATGAACGTTTGTGTGGGCACCTCCTACGTCAAACATGAAGTG TGTTTCCTCAGTGCATCTGGGAAGATTTCACQCTTGACCAACAGTTCTCAGCTCCCATTTTCGCC CCTCAATTTATCCCTCAACCCCGCCACAGGTGTTTATACAGCTCAGCTTTTGTCTTTTCTGAGGAG AAACAAATGAAGACCATAAAGGGAAGGATTTCATGTGGAATATAAAGAT
DWU-387	169	G T	---		GTGTATAAATGCAACTGTTGATTTCCTCAACATGGCTCACAAATTTCTATCCCAATCTTTCTGAA GATGAAGAGTTTAGTTTTAAACTGCACCTGCCAACAAGTTCACTTCATATATAAAGCATTATTTTA CTCTTTGAGGTGAATAAATTTATTAACAATG/GT/AAAAGCTTCTTTAATACTAAGTATTTTCA GGTCTCACCAAGTATCAAAAGTAATAACACAAATGAAGTGCAATTATTCAA
DWU-447b	172	---	---		ATTTAGTGTCTTTGCGTTAAAAAATCATTGCAAAAAGTATTCGAAGCTGCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAAATCAGTGTAAATTAATTAGTTTGATTAGAGCACAAGCTTAGCTAATCAA CCATTAATTTTCATTTTGTGTTCTAAGAGGATTGANAATCAGTTTAGTTTAAATGCTTTCTGTAG GCCTTTCTTCTTACAATGAAGAGATGATTCTTCTAGTTTATGGTTA
DWU-447	85	A G	---		ATTTAGTGTCTTTGCGTTAAAAAATCATTGCAAAAAGTATTCGAAGCTGCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAA/GJATCACTGTAAATTAATTAGTTTGATTAGAGCACAAGCTTAGCTAAT CAACCATTATTTTCATTTGTTGTTCTAAGAGGATTGANAATCAGTTTAGTTTAAATGCTTTCTG TTAGGCCCTTCTTCTTACAATGAAGAGATGATTCTTCTAGTTTATGGTTA
DWU-476	63	C G	---		GTAATAATTCAGTTTTTTTCCAGTTCCCTCTTTTGTGCTGCTTCTCAATTAGCGTTTAAAGGTGAG/GJAT AAATCAACTGTCCATCAGGTGAGGTGCTGCTCCATACCCAGCGGTTCTTCATGAGTAGTGGGCTATGCA GGAGCTTCTGGGAGATTTTTT

DWU-505	67	A T ---	---	TCATACTAGGCGAGTATCTCCTCTAGCTAGTGCCTCATACAGAAAATCTATCACCATACAAAATTTA[A] A/TJTGCAGTATTTATGTTTTAAAGCACAGGTGTACCGAAAAGTGTGAAAAGTCTGAATTTATGGGTT CTATGATGCATTTTTCCTAACCTAGAGAAAAGAGTTTGATAAAATTTTACCAGCTTTGAAGATGGAT TAACTTTTGACTTTGAGCTTTAAACTTTTAA
DWU-512	131	A G ---	---	AAAATCCAGGCAATTCGAATCTGTTTTTCATGATTTATAGAGGGTTTACACAAAAGTCCCACTTATTTAA AGAGCTTCCACAGTGAAGATGGAGAAGGTGAATGCTTTTGAATATCCAGATGTTGTTGGTC[A/G] TGCATATGGAGTGAAGATGTTGCTTTTGTCTTGTGCTGCACTGAAAATTTAAATGCTATCAAGAGC AACTATGAACGGTTTTTATCAAGATGCTCCAGAGTGAAGATGCCGAG
DWU-525	97	A C ---	---	AACTGCATATAGATAATTATCCAGGATGTGTGGCTCATCTTTTCAGCTTGTTTCTATACTGTTTGTA ATATACAGTTTTTGTAAACCATATGATTGA[A/C]AAGAAGAAAAGTCTATGCTTAGGCCAGTCAGTACA CCCAATTTTAAAAAATAACATATTTCTTGCTTTACAAAATATAGTTGAACAAGATTTCCCTAAAAAT CCACCAGGATTAATCTCTAAAAATCTAGTCTCTGATTTCG
DWU-59	94	C T ---	---	CATTCTTTGTGAAGTAAATGGACTCACAGGGGAAGAACATGCTGAGAATGGAAGTCTACCGG CCCTTCTTTGTGAAGTCAATGGC[C/T]GAGCCGTGTTTCAGTTCCAGGTGGCAGACTCGTTTTTG GTAGTTGTTTTAACTTCCAAGGTGTTTTACTTCTGATAGCCGGTGATTTTCCCTCTAGCAGACATG CCACACCGGTGAAGAGCTCTGAGCTTTAGTGGTTAAGC
EST11	68	C ---	---	CTTGATCATGGGTGGAATTTTGTGTATCTGGCTTCATGGGATGCATAAAAATTTTCCAGTTGGTAAG CAGCAGGTGCCGAGGCTGGATCAGAAAAAAGGCA
WI-19856b	63	C T ---	---	CACACTGGCATCTAGGCTTCGCTGCATTGCAGAAGGAGAGCCAGTCCCTCTGGAGAA[C/T]G CTGCGTCCCCAGCCCCACACCGGCTTTGCACCACACAGGCTGTTGAGCGAGGAGGTGGGTAAGACGT AGCTGTAGACCCCAAGCAACCCAGCCCTGGGACCCCTGGGGAGAGGAGCACTTTAGAACATGGAA AAGTGTGGTCATCCCATCATTAGACAAGACACATCCTACATAATAAAAAGT
WI-18014	40	A G ---	---	TCCATTTACATTTGGTGGCATTTGTTGAATAGCTACAGAA[A/G]GAATGAAAAGTGCACCATCAGAGT GTAATTAGGCTCTGTGTGACCCAGGAAGTGTCTGTTAAACAGAGATTTCTCAAGGGCAAAAGTGGCTTCT A
WI-18036b	97	T A ---	---	TTCCAATGTAAGAGTCAAGTACCAAGTTAACTTCTAGAAAATACAAAAGAACATGATAAAATCTG ATCACAGTGGAAAAATTTTAACTCTTTCATAA[T/A]CTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18036a	27	T C ---	---	TTCCAATGTAAGAGTCAAGTACCAAGTTTAACTTCTAGAAAATACAAAAGAACATGATAAAAT CTGATCACAGTGGAAAAATTTTAACTCTTTCATAA[T/A]CTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18046	72	C T ---	---	TGTAAGGTGACTTCTATAAGCTTCCCTAAACTGTCAAACTTTTCATTTACTGAGATTATTTACGGCCAAT GTGT[C/T]TGTTGGGCTGAGATTGATTATCAGCTGGGTAAAGTTAACCTGTTCTGTTTCA

WI-18063	105	G A ---	---	---	AGGCTTTAAACTGATAACAAATTTGCCCTTTAATCACAATACAAAACTCTGCACCTTTCATTCCTTCCTTC CCATGTTTCTGATTTGATGTAACCTTAAATTTGTTG[A]TCCCTTTAAACAATATACTGTAGCTGCA
WI-18078	86	A T ---	---	---	AGTTGAAAGATCAGAGAGGTTATGGTTGGTAGCTGAACCTCAGATTCAGATTCAGATTCAGATTCAG TTGTTTTTTCAGCATCAG[A]TGTCCACTAGCCAAAGTTGATCTGTCAGTATCTACATGTGGT
WI-18091	90	T C ---	---	---	CCAAAGCTCACTCAGTATTTAATCATCTGCTAATTTTCATCCTTTTGTAAATCCATCAGACACTGTGGT TTTCATCTCTAGAAGTTTGACTTTCGGGCCCTTTTATACCTTCCATATCTCAACTTGTTAAGC
WI-18119	38	T C ---	---	---	GCAATCTGTAACAGTTTGGTAGTGGTATTACAGAGGATTCJTTGTAATAATGGATTGGAGTACTTTAC CACTAATTCATCTGCTCTGAATAGTTCACTAACCAACTACTGACAACAGTTTAAATTTTGGTCTT
WI-18142	66	T G ---	---	---	TTCAAGATAATTACAATTGGAAGGGGACCAATAATCCACTTTTAAATCGAAAAATATCTATATAC[T/G]CCCAATAAACTCAGTAAATAAGCTTCAAAAAGCCTTAAGACACCACCAAGAGGAAAA
WI-18178	68	T C ---	---	---	GCATAGGTTGAGGGGTGTACAAGAGGAGAACCAAGATTCAGTCCATGCCTGGAGGTTAGTCTGGGG GT/C]CGGCGGGATGGACACACAGACAGACATAGATCTGGCATCTGATAGCAGGGGCATACAG
WI-18244	35	G T ---	---	---	TCAATCTGAAACTTGTCTAAGCCAGCATGGGTG[GTGGGAGGTGATTATGGCTGGGGAAGATG GGCACTCACCCGACAGCAGCATCTAGCACACAGTGACAGGACGTTGAGGTGGCAGAGGGCTTT
WI-18245	115	G A ---	---	---	ACAGATGTCAGTTGTTGAAATGGGCCATTAAAGTATGGGGCTTTCTTGTAAAAAGTCATTCCAAA AGGCTTGGCAAGAGTTTGTCTATACACGGAGGACAGAGAAACATGA[G/A]CTGGGGAGTAGGCTCT GACAGAAGGTGGGCTGTC
WI 18261	26	G A ---	---	---	GATTTGAAGGGATTGCTTTATTAACTG[A]TGAAGGCGTGATAGAGGAACTGTTTAAGATAAACAA CTTATAAATACCTCCCAATTTGTAGAAAGTGAAGATTG
WI-18268	88	C T ---	---	---	TAGAGGGAAGAGGAGGTGGGTGCTGGGCCCTCAAGACATGAGAAACGGGIGGTGGCTTCCAAGC TTCCCTACTTCCCCCATAGATCTTCTGACAAATGTCGTCAGAGCCCTCCAACTGGAAC
WI-18299f	107	C A ---	---	---	TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACCTGGTTGGCCAATTTTT ATCTATTTGGGTCTGAGAAATCCACAAATTTGA[G]GAATTTCTTTGGCCAATTTATGACATATTCTG CAG
WI-18299e	101	A G ---	---	---	TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACCTGGTTGGCCAATTTTT ATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAATTTCTTTGGCCAATTTATGACATATTCTG CAG
WI-18299d	77	G A ---	---	---	TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACCTGGTTGGCCAATTTTT T/G]ATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAATTTCTTTGGCCAATTTATGACATATTCTG CAG
WI-18299c	67	T G ---	---	---	TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACCTGGTTGGCCAATTTTT T/G]ATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAATTTCTTTGGCCAATTTATGACATATTCTG CAG

-242-

WI-18299b	52 G A ---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCATTAACTTG[A/J]TTGCCAAATTTT TTATCTATTTGGGCTGAGAAATCCACAATTTTGAAGAATCTTTTGCCAAATTTATGACATATCTG CAG
WI-18299a	48 C T ---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCATTAA[C/J]TTGGTTGCCAAATTT TTATCTATTTGGGCTGAGAAATCCACAATTTTGAAGAATCTTTTGCCAAATTTATGACATATCTG CAG
WI-18307	76 G A ---	---	TCAACTGTACCAAGTTTAGCAGCAAGAGGATACTTCCTTAGAGACTTTCAGTGGACTTAAACTCAG TTCCCGCTG[G/A]TGCTATGTAAAGCATCCACGATGGTTTATTGACTCTGCAATCTGCTTGGTCAC
WI-18324	72 C T ---	---	TTTGGTATGAAATCTTCTCTGACATTTACCAATCATCATCTTAAACTCCGGGGGTGGGTACTGATT TATC[C/T]TAGATCCAAATAAAGCATGCAGAAAGTG
WI-18350	48 T C ---	---	ATGAAAGTCACITTCATCAATAGGGTCAAGAGAGAAAGAAATGTTTCAGAT[C/J]TAAATCTATGAAAA GGTGTATCTGCTTGAATTTAAGAAACACACAAGTCA
WI-18395	77 G C ---	---	TCCTGACATGATCTGTGAATAACGTGATTGTGGTTGAATTCCTCGGAAAAATTTGAAGAAATAAATTG ATTATTCAAG[G/C]TGTGCATGGTTTATACATATCTCTCTTCTTAAATGCAAAAGCTATG
WI-18398	62 G T ---	---	TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAGAAAAAGAAACAACTCAAGGGT[G/T] GATAACATTGCCAGTATAACCATTAATTCAAAACAGCAGAGAAATTTGGAGGATAATTTGTT
WI-18396	21 C A ---	---	CTCGTTGGTATCTCTCATCC[C/A]TTCCTTTTCGCTCTTTCTAAATTTAAAGAAAAAGCAATGGAATT TTAAAGATCATCTAAGAAATAAGAACTTACATATGTAACTTATCAACTTGTACAAAGTC AATGAAAA
WI-18409a	20 C A ---	---	AAGTGGGAAAGAGGAAATC[C/A]TTTTCTTACTAGAGATTTTTTCCCTTTAATCCTTTTCAAAT TCAAAGGATCATCAAAGGAGCAGGTGCAGAGCTCTGGGGCCAGAGGCCCCCAAGTGCTA
WI-18442	62 C T ---	---	AAAAAGGAAAAAGAAAGGATGGAGTAAGAGAGAGAGACAGAGAGAAACAAAATAAGTTTCTGG[C/T] JTTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCAGAAAGGAAACACAAAGAAAAAAGG TTTATAGGTGGGAGAGAGGA
WI-18452	38 G A ---	---	TTGATGTTAATACTGTCTATTCTGGAGATCGGCTAAAAT[G/A]AAAGCATAGTTATTATTAGCTTTGG TATATTCTGCGACAGATTTAAACAAGTAAGACATATATCAACCCCTCATATTTTCCAAACCA
WI-18489	102 A C ---	---	ATATAAGCTGGAGACTGTGGAGGTGAGAGGCAGTGGGACTAGCTGTTGAAGAGAGAAATGTAGC AGTAGTAAAGATGAAAGACTGCAAGGATTCAAACA[A/C]GGTTATGGCAATAGAGGTGAAAAAGAAA AGGCCATATAAA
EST5b	93 A ---	---	CTGGTGGGAGGAAACAAATTTGTGGTATATTCATACAAATGGAAAACTTTCAGAAATAAGAAAGGAA CAACCCACTGAATCACACAACATGGACAAATCTCAATCATTTATGCTGATGGGAAAGAAACCATTTCA TAAGAATACACAGTACAT

EST5	93 A ---	---	---	CTGGTGGGAGGAACAAATTTGGGTATATTCATACATGGAATACTCTCAGAAATAAGAAAGGAA CAACCACTGAATCACACAACATGGACAAATCTCAAATCATTTATGCTGATGGAAAGAAACCAATTC TAAGATACACAGTACAT
EST6	48 C ---	---	---	TTAGCTACTTTTTCAGAAATTGAAGGAGAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGCTCT GAACAAAGCTTTTCTTCTTTTGAACAAGACAAAGCAAGCCACATTTTGCAATTAGACAGAT
EST8	158 A ---	---	---	GGACAGGACCTCTATTCOCGCTGTCAGCAGCGGCTGATGGACTGAGGCCCGCAGGATACCTGGGCG CTCTCTCAGGGGCTCCAGGACCCAGAGCTGTTCCCTGCTTTGAGTTTCCCTAGAGCTGTGCGGCCA GATAGCTGTTCCAGTTGCAAGCAGATGGAGATTTGGACACTGIGTGCTTTGGTGGGT
WI-18740c	104 G T ---	---	---	TCCTCATTTGTTGGGATGATGAGAAGAAATGATTTGGGAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAATCTCATTTACCATCATGTATCCAGTAGTG[G/T]ATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI-18740b	96 C G ---	---	---	TCCTCATTTGTTGGGATGATGAGAAGAAATGATTTGGGAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAATCTCATTTACCATCATGTATCCAGTAGTG[G/T]ATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI-18985a	105 C T ---	---	---	CCAAAGTCTCCTGTCGCTATAAAGAAATTTTGGATGGGAGAGAATCCAGACCATCTTTGGGGCA GCCAGGCCCTTGCCTTCAATTTACAGAGGTAGCACA[G/C]TGTATCCAAACACAAACCCCTTCCCC TTTTAAATGATTTCTGTTCTAATGCCATAGATCAAGGCCCTCAGAAACCATTTGTGTTTCCCTCTT TGAAGCAATGACAAGCACTTACITTCACGGTGTTTGTGTTTCTTAT
WI-18746	114 G A ---	---	---	GCCAGCAGCTGAAGTCTCTTTTCTCCTCTCGGCTGGAAGAACATCAAGATACCTTTGCGTGGATCA AGCTTGTTACTTTGACCGTTTTTATATTACTTTTGTAATATTCTT[G/A]TCCACATCTACTTACGCT TTGGATGTGGTTACCG
WI-19112j	212 G A ---	---	---	CCGTGTTACACACACACAATGGCAAGCATAGTCGCTGGTTACGGCCAGGGGGAATATGCCAAGG GACCCCTTAATGGAAACACAGATCAGTAGTGCTATCTCATGACACCAACCAAGAAACCGACGACAAA TCITTTGCGAGATTTCTTCTAGTGGCTTAGAACATGGCTTTAAGAAACACGGTGATATCTTTGAG GGTGACAAGGC[G/A]TCTCTTCAACAGTTCATACCAACTGCTTTGCTCTAG
WI-19092	232 A C ---	---	---	TGGTGGCTGGCTAGCTAGTTTCTACAGAACATAATTTGCCTCTATAGAAGGCTATTCTTAGATCATGT CTCAATGGAAACACTCTCTTCTTAGCCTTACTTGAATCTTGCCCTATAATAAGTAGAGCAACACAC ATTGAAAGCTTCTGATCAACGGTCCCTGAAATTTTCATCTTGAATGCTTTTGTATTAAACTGAATTTTC TTTTAAGCTAACAAAGATCATAATTTTC[A/C]ATGATTAGCCGTGTAAC
WI-19057i	175 G A ---	---	---	CCCATTTATTATAGGCCAGTGATGTCTCAAAGAGTAGAGGAGCGTCTACTGGTCTTCAACTCCTTCA GTCTTCTGACGGCGGACTTTACCGTGACAGCGGAAGTGGTATTGTACGTCCAGGCACCGCAGCCACTG TCTTCATGCAAGGAACACAGTGCCAGATCCCCACAGCTC[G/A]TCTCTTCTATCTTGGTTTGGCCACA

WI-20103	168	C T	---			TGGGACTTCCAACTCAGAGGATGTGGGAATCCCAGCTCAAATGATACAGGATAAACTGGGATGGGCT AGGATGGACAGGCTGTGGATATGGGAGTCATGGGTCAAAGTCTTATCCCAGATGGTCCAGGTACAG TGGGCTTCTGGGCTGGAAGCTGGGTCTCCCA[C/T]TTCATCTCTGCTCAAAGCTTCTTGAAGGAGC TGGTTGACTTCAACTTGCTAGAGCCTAGCCCTCATCTTTCAGTCAACTGGGA
WI-20441	111	G A	---			GCCTTACCCATTTTGCACATATATACATATGCACCACCTTTGCAGTGGCAACATATATATCCACACTA TAAACATACCACATTTATAATCTGTAGGACAAGAAATGG[A/G]TTGAATAGTACCCCCCAA CATATACAAGAAAGTTAGCATACCTACCCCGTTTTTCACTACATCAGAGGCCAAATAAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGG
WI-19911b	116	A G	---			TGGTTACAAACCTAAGCCCATATACAAAATTAGGAACACATTTAGATGCCCTTTTGAAGAAGCGT TTTAGTCTTTTAAACTGAGTTTAAAAAAAATAACAATGCAATTTT[A/G]ACACTGTTTTTGAAA ACTTAAAGTGCAGCAATA
WI-20613c	165	A G	---			GTCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGCAGTTAGAAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAAGTTGGAA[A/G]AAAGGGAGTTTCCAGCGCCAGTGGTGAGC TGC
WI-20613b	156	A C	---			GTCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGCAGTTAGAAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATA[A/C]AGTTGGAAAAAAGGGAGTTTCCAGCGCCAGTGGTGAGC TGC
WI-19984	47	A G	---			CAGTAAAAGAGTGATTCAGATTGCAGTAATACACTGACAGGTAAATA[A/G]TATAACATTAGAAAA GCAAAATCTTTTAACTTAAAGACAGACTGAACCATCAGGTATGGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGTTTTTCCACACTGGAAAAATGAAGGCAGTTTCCAAATCTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135	T C	---			GCCAGTTGGAATATGCCCTATACGAACCAAGAGTGTATACAAAATGGAAGTGGTCATCAGGCAATA ATTGTTTCCTTGGAACTCTGCACCGACTGTCCATGCTGTGGGGACTTACACATTCAGTTTGACAG T/C]TGAAAAACCAACTGGAGCTGCTTTTCCAAAGAAATGTTCTGTGTCCTTCAATAGGAATCCATG TTATTTCTTTCTTGCTTAAGCTCTTATATCTTTCAAAATGACCTAAGCTGA
WI-18846a	49	G A	---			GAGTGCCATACCTTCTCCAGGCTCTGCCCAAGAGCAGGAGGTGCCT[G/A]AAAGCTGGGAGCGT GGGCTCAGCAGGGCTGGTCACTCCCATCCCGTAAGACCTCCTTCCCTCCTCAGCAGGCCAAACATG GCCAGACTCCTT
WI-18959	123	G A	---			AGCAGTGGCCTTATTCATCCCAACCAACCGCTCTTGACAGGCTGCCCTCTTGTGGCAGCAACGGC ACAGCTAATTTCTACTACAGTGTCTTTAAGTAAAAATGGTCGAGAAAGAGGCAC[C/G/A]GGAAAGCCG TCCTGGCGCTGGCAGTCCGTGGGACGGGATGGTTCTGGCTGTTGAGATTCCTCAAGGAGCGAGCAT GTCTGGGACACACAGACTATTTTAGATTTTCTTTTGCCCTTTTGCAACC

WI-20146	31	T C ---				TGAGTCTTCTGTAAATTCATTGAGCAGTTAGCT[C]/C]CATTTGAGATAAAAGTCAAAATGCCAAACACTAG CTCTGTATTAATCCCATCACTACTGTAAAGCCTCATTTGAATGTGTGAATTCATCAATACAGGC
WI-18922	74	G A ---				TAGGAATTGGTTTACGCCCTGAGGCAATTAGACACTTTGGAAGATGGCATAACCTGTCTCCTGACCTGGAC TTAAGC[G/A]TCTGGCTCTAATTCACAGTCTCTTTTCTCCTCACTGATCCAGGTTCCCTCCAGAG GAGCCACCAGTTCTC
WI-18763b	53	A G ---				TTTCTGTGTTGGGGTCAACCGTACAATGGTGTGGGA/G]TGACGATGATGTGA/G]TATTTAGAATG TACCATAATTTTGTAAATTAATTTATGTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA TGTTGTTTGCCAA
WI-18763a	38	A G ---				TTTCTGTGTTGGGGTCAACCGTACAATGGTGTGGGA/G]TGACGATGATGTGAATATTTAGAATG TACCATAATTTTGTAAATTAATTTATGTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA TGTTGTTTGCCAA
WI-18771b	75	G A ---				CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAGAAGATGTTGGG AACAGAA[G/A]AAATAAATGAGTTTAAGGGGACTTAACTGCTGAATTCACCTGTGGA
WI-18771a	57	A G ---				CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAGI/G]GAGATGTT GGGAACAGAGAATAAATGAGTTTAAGGGGACTTAACTGCTGAATTCACCTGTGGA
WI-18820	70	T C ---				GGGAAAAATTTGAGACGCAATACCAATACTAGGATTTGGTCTGGTGTGTTGATGAAAAATCTGAG GCC[T/C]TGATTTAAATCTTTTCAATGATGATTTCTTTTAGGATATTTGCGCTAAGTGAAACTT GTCA
WI-18742b	51	C T ---				ACAAAGTCCTGTAGCCCCCTCACCTTTCTGTTTCACTTTTGCCAATGTA[C/T]ATCGGGTTTGGTTT TCTTGATTTATTAACGGTTGTGGTTCTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCAGGAGA GTTTTACC
WI-18882	94	C T ---				GTGTGTCCAAAAATGGGGTCTGCTCCTGCTACCTTGACCCCTTCCCTTCTGCTCTCTCTCTCATCA TCAATCCCAACAACATCCTCTGCCA[C/T]ACACAACAAAACGTAAGTTTCATTTGGGCAAAAATTTGA GC
WI-19970b	167	G A ---				TATAAGCCCGAGTACCAGGACGGCCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCCTGCCCCACC GGCCCCGGCAGTGCAGTCCAGCGGGGAGGAGGCTGCCCGTTCTGCCAGTTCCCTCACTGCGGGGACC AGCAAGGCCCTTCTCACTGGGTTGTCAAAG[G/A]TAGTCACCTTGGCCTGGTGCATCCACAGAGGA TGTTGTTCAAACCAGAAATCTTTAAACGACTGACCTTCCCTTAAAAACAGA
WI-19970a	126	T C ---				TATAAGCCCGAGTACCAGGACGGCCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCCTGCCCCACC GGCCCCGGCAGTGCAGTCCAGCGGGGAGGAGGCTGCCCGTTCTGCCAGTTCCCTCACTGCGGGG ACCAGCAAGGCCCTTCTCACTGGGTTGGTCAAGGTAAGTACCTTGGCCTGGTGCATCCACAGAGGAT GTTGTTCAAACCAGAAATCTTTAAACGACTGACCTTCCCTTAAAAACAGA

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WI-19042	193 A C ---	---	---	TTTGTCAAGTGGCTCGCAATGCCCTCAGTAGCATCTCAGTGGTGGTGAAGTTGGAGATAGATG GATAAGGGAATAATAGCCACAGAGGTGAACCTTTGTGCTCAAGGACATTTGGTGAAGTCCACACAG ACACAATTTATCTGACAGAACTTCAGCATTTGTAATTTATGTAATAACTCTAACCA[A/C]GGCTG TGTTAGATTGTAATACTATCTCTTTGGACTTCTGAAGAGACCACCTCAAT
WI-18984	208 A C ---	---	---	ATTGGCCCTGTACAGTTTGCTTATTTATAAATTCATTAATAACACTACAGGTGTGAATGGTTAAAA TGAGGCCCTCCAGTTTCATTTTCAGTTATTTTCAGTGTGCAGACAGCTATTTTCGCACTGTATTAAT GTAACCTATTTAATGAAATCAGAAAGCAGTAGACAGATTTGGTGAATAACAATAATTTGTGATGCATT TATCTT[A/C]ATAAAATGCTAAATGTCAATTTATCACTGCGCATGTTTGACT
WI-18851	90 T A ---	---	---	GCITCAATTGGCGATTGATTCAGTGCCCAATGTAACAGGGTTGGTAGTTGTACTCATTTTGAAT ATACCTTTTCCCTTATTGTATTCT[A/G]ATAATAGGATCCTGGAAATGAGACCTGGTGGAA
WI-18821b	76 T C ---	---	---	TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC ACAGAGGCT[C/G]GGGGTAGCCATTGTGCAGTCATGCCCCGGGGGAACTTGCCAACTTCGTGTGTCAG GTGCTGTGT
WI-18821a	69 C T ---	---	---	TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC A[C/T]AGAGGCTGGGGTAGCCATTGTGCAGTCATGCCCCGGGGGAACTTGCCAACTTCGTGTGTCAG GTGCTGTGT
WI-19021a	20 C G ---	---	---	ACTCCTCTGCTGCTGCCAT[C/G]ACTGCTCTTTGAACCAGGAAAAGTCACAGAGTTTAAAGAGAA GCAAAATTAACATCCTGAATCGGGAACAAAGGTTTATCTAATAAAGTGTCTTCCATCACGTTG CTACCTTACCCACACTTCCCTCTGATTTGCGTAGGACGTGGCATCTCTACTTACGTACGTGGCATAAC ACATCGTGTGAGCCCATGTATGCTGGGTAGAGCAAGTAGCCCTCCCTGTC
WI-18908	70 G C ---	---	---	TGGAATTTCCCTTCATCTGGAACCATCAGAAACACCCTCACACTGGGACTTGCAAAAAGGGTCAGTA TGG[C/C]TAGGGAAAACATTCATCTTGTGATCAAAAATCTCAATTTCTCCCTATCTTTGCCACCC TCATGCTGTGTGACT
WI-19037b	155 A G ---	---	---	CACGGTTCTCTGCATCGTTACAGAGCGCTTCTGGTCTAGCCAGCCCTGTATGACCGGCAATA TCCCCAAAGCTTTTGGTCTCAAGTCATGCCGAATTTAGATGCTGTGCTATTTCTGGAGAGGGTC CCCTCCCTTACGAACACA[A/G]AAACCCAGCCACATGACTAGCAGCTGAGCTCTGCAGGGACCA GTGCCAGGCACTGGGGGTGGAAGTGTGTGACACAGTGAATGGAGGTGG
WI-19037a	47 C A ---	---	---	CACGGTTCTCTGCATCGTTACAGAGCGCTTCTGGTCTAGCCAGC[C/A]CCTGTATGACCGGCAAA ATATCCCCAAGCTTTTGGTCTCAAGTCATGCCGAATTTAGATGCTGTGCTATTTCTGGAGAGGG GTCCCTCCCTTACGAACACA[A/G]AAACCCAGCCACATGACTAGCAGCTGAGCTCTGCAGGGACCA GTGOCAGGCACTGGGGGTGGAAGTGTGTGACACAGTGAATGGAGGTGG
WI-19064	66 T C ---	---	---	TTGAGGAGGTGGGTGAACCTGCTCTTGGCAGGATTTGTACACTGCATTCGCTGGGCTGTGTTCC[T/ C]GGGCTCTCTGGACCTTGACCGTGGATACAGGCCATGTGCCATGTTGGTCTCTGGAGGG TGGGTGAATAAAGGC

WI-18972a	112 A G ---			AGGCCTGTGGCTTATGTACCCCAACAGAGGGGCTCTGAGAAGTCTGGCTGCCTGGGATGCCCCCTGC CCCTCTGGAAGGCTCTGCAGAGATGACTGGGCTGGGGAAGCAG/AGTGCCTGCTGGCCATGGAGCC TCATTGCAAGTTGTTCTGAACACCTGAGGCTCTCCTGTGGCCACCAGGCACCTACGGCTTCCTCTCC AGATGTGCTTTGCCTGAGCACAGACAGTCAGCATGGAATGCTCTTGGCCA
WI-19016b	184 C A ---			GTTTGAACCAACATGTGCTCTTTTTCAGTCATTCACTGTTTTAATATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGTTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAAACCTTAGATACATAGCCGACGTATACAGAGGTTTCATCTCAACCTCAACACTATTGAC TTTTGGGGCTGGATAGTTCTCTGTTGTGGGGGTTTGTCTTGTGCACTGTAG
WI-19016a	161 C T ---			GTTTGAACCAACATGTGCTCTTTTTCAGTCATTCACTGTTTTAATATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGTTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAAACCTTAGATACATAGCCGAC/CTTGTATACAGAGGTTTCATCTCAACCTCAACACTATTGAC TTTTGGGGCTGGATAGTTCTCTGTTGTGGGGGTTTGTCTTGTGCACTGTAG
WI-20096	21 T C ---			GGTTTGGGGGCAATTTATTC/CTGATAGAGACTGGCACAAGCTTTGGGCTAAGGACACCCGCCCC ACCCTCATCTAGAAACAATCTCTCGCCAGACTTG
WI-19591b	156 C A ---			TGGGGCAATTTTAAACAAACCCAGGCAAAATATACATATACCTGAATATAAGGTAACCTCAAGCCATG AGTAAAGATTAAAGGCAGTTACTTTTAAACAAAGGAAGTGGCATAAGCAACTCAGTGTGCCCC CTTAGGTGGGAGCTCTTCCC/C/ACTACCACTCCCCACCCCAAGGCATCATTTTGGGAGAAAAA GTGCTCTATCTGGCTAGCTGTGTATCTAGGGATTGCACCTTCTTACACGG
WI-19591a	45 T A ---			TGGGGCAATTTTAAACAAACCCAGGCAAAATATACATATACCTGAATATAAGGTAACCTCAAGC CATGAGTAAAGATTAAAGCAGTTACTTTTAAACAAAGGAAGTGGCATAAGCAACTCAGTGTGT GCCCTTAGGTGGGAGCTCTCCCCCTACCACTCCCCACCCCAAGGCATCATTTTGGGAGAAAAA GTGCTCTATCTGGCTAGCTGTGTATCTAGGGATTGCACCTTCTTACACGG
WI-20310	125 G A ---			TCCTCCAGCTCTGTCATCCTTGCTTGAGGGTTCTGTTACGGCCCTCCAGGCATGGTTTCTTCAT TTAGGTAGGAACAAAGGCCAAAGAACATACAAGCCCACTCTCTAGAGGCTCCA/G/ATCAGAA CTGGACCTTTAACTACAAAGGAATCTTGGATGAATTTTATAGCGGGCTTCAGGAGCAGGTAGC AGGCCAAAGTGCACACTCAGGCCATCTTCTCCCAATGCTCTCCCGGGG
WI-20860	224 G A ---			CTCTCCCTAAGGAGCCTTGGCCTTGCAGCCCCATTACGAGGGATGGAAGTCAAGACAATGAGT GGAGCCTCATGCCCTCCCATGAGGAAGCCCTTAGTATTGCTGACATCTGCCCTTATCCTGCTCTCCT CCCCAGTGTGTCACACTTGGCAAGCAGAGTGGTGGCAGACCCAGCCTTGAGAGCTCTTGAGACC GGAAGGAAGGGCGGTCAT/G/AGGTGATGGCTCTGCTCTCTGGCTT
WI-19359a	39 T C ---			GACGTGGACAAAGGAGGTTTAAATGAATACTTTGTTTG/CTCATGTTCAAAAAAGAGATTAAAT ATTTTGTGACTGCTGTGAATGAAGACACTCAAAAAGCCATGTTTCCAACCTTAGGTTAATAATAA GGCTATTGTCCACCCACTCTCGGGCATTTGCTGCAATATTCCTGGGCCCTCAAGTGGGAGGCCACGTG GGAACAAGGCCTCAGAAAAACAAAGGACATGACGCTCCCTGAGCCAGTTCT

-249-

WI-19766b	93 A G ---			TGGCCTCAATGACTGGTACATTGGAGAAGCTGTGCAGCAGCATCCTTTCTGTGGTGGCAGGGCAGG AGATGAACCATAGGAGGCCAAAGTC[A/G]GACAAACAGAAAGGACACACCAAGCCTGAACCCCTC CGGACAAACAGCAGAGTTACCAAGCTGAGGGATGTCCCTGGAGGTTTCTGACCCATGAGAGGCCCCCTC ACCTCCTTCAACCCCTCCTCTACCAACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-19766a	31 G A ---			TGGCCTCAATGACTGGTACATTGGAGAAGCT[GA/G]GAGCAGCATCCTTTCTGTGGTGGCAGGGC AGGAGATGAACCATAGGAGGCCAAAGTCAGACAAACAGAAAGGACACCAAGCCTGAACCCCTC CGGACAAACAGCAGAGTTACCAAGCTGAGGGATGTCCCTGGAGGTTTCTGACCCATGAGAGGCCCCCTC ACCTCCTTCAACCCCTCCTCTACCAACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-20512d	126 C G ---			CTTCTCTGTTTGGCTTTCATTTGCGATTGTCGATTGGAAAAACCACTTGGAAAGGAGACTTCTCTGCAA AACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGAAGTGA[G/G]AAAGC TTAGAAAGGAAGTGAATTCCTTTGAATATGATTTAGGGCGGGCGTGGTGGGCTCACGCT TATTAATCCAGGCACGTTGGGAGGGCCCAACGCGGGTGGGATCACCTGA
WI-20t:12c	59 T G ---			CTTCTCTGTTTGGCTTTCATTTGCGATTGTCGATTGGAAAAACCACTTGGAAAGGAGACTT[GT/G]CTCTG CAAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGAAGTGAAGCAAGC TTAGAAAGGAAGTGAATTCCTTTGAATATGATTTAGGGCGGGCGTGGTGGGCTCACGCT TATTAATCCAGGCACGTTGGGAGGGCCCAACGCGGGTGGGATCACCTGA
WI-19599	230 C G ---			GGGCTTAAATCCCTCTGTTGGGACTGGTCTCCAGTTTACAGCAAGGATCGCACCCCTTTTCC ATAACCCCTTCTACATTGGAAGAGCACACCTTGTATACAGAAATGGCTCCGTGAAGTCTTTTAAACG GACAAAGGTAATACAGCTAACAAACGTCATGTTGGCTCACACGTAACCAACACCTCTTTTCA GAACAGAGAGCGTTAAAGTAAAGGGCA[C/G]TTCCCAAGAGTAACACTGCTA
WI-20679	82 T C ---			TGTTTGAATAAAAAATTCATGGTCTTAATTGAACGTATGTTACTTTCTTTTGAATATCCTTTT TTCAATTAATAAT[AT/C]TCTAAACCACTCTATGTGTTCAACCTTCTGTTTAAACACTAAGATATGGGT TTTTGGAAAGGCCACAAAGTCACCAAGCTCCATGAAGTGGCGAATTGGTCTTGTTTTGGAAAGCTCTC CAGGGTGTCTCCAGAAA
WI-19909a	29 T C ---			CCAGAAATAAAGCCTGAATATTCCTTTCT[C/T]TAAAAATAAATTTTCTTTCTTTGCTCTTCCAA GTAAATCTTAAATGAACCTGTTCTAGTCTATTTTAAATCTAGGCAATTATAACACTACCTAGGCGG TTTTTCTTTTATACCTTGTCTGTACGTGGGAATCAACTAA
WI-20341	221 G C ---			TTGAGAGGCTGAGAGAAGGCTGTTGAGACATTGTAATAGTGTCTTAGGGCATGAGACATTAGGAAG GCCACAAATTATGAGTAATGAATGTGGAGGCTGATGAGAAGTACTGCTCCCATTTGTTTAGCAGGA GGCAGGAAAGTATCTGGGGTCTCTGGCAGCAAAAGCGTGTGTAATAATTTGGGTGACGTATGC ATCCCCCATGCATTGGTTT[GT/C]ATGTCCTCAGTGAGCTGTGGCAAGTCT

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WI-20113	60	T C ---			TTC TGG TAC ATG GTA AGT GCT CAG TAT TAC T GAG TGA ATG AGC AAG ACG CCG T GAA ATA C T G T T C J GGA AAC AGT AAA AAG CAA AAT ACC A C A C A A T T A G G A G G A A T T A T T T C A G A C A T A G G A T A T T T A A A A C A T C A C T C A A A T A C T G G A G C A T G A T T C A G C A A T A A A T T C T A T T C C A T A A A C C A G G T A G A T A A A T G T C A C A G C T T T A A A T A T A G T T A A G T A C A G T T G A T C C T C G T T A T T C A T G G A T T C C G T A T T
WI-20895	107	G C ---			TGATGGCAAAGTACAAAGGCTCTGAAAGACAGAGTAACAAGAGAGCGCAGTGCGAGCGTGTGGC CACTCCCAAGGAGGAGCAACACTTGACTTCATTAAAGGCAAA[G/C]CTTTACTCTGTACTTTTTCCTC CCACATAGTTTAAACCCAAATAGAAAGGCAATCTATTCTCACACTACTGCTCTCTCTAAGGTCCTAGGAA TATAACTGGTACTATAGGCAAAACAGATGCA
WI-20721	72	T C ---			CCTGCAATCACAAAAGTGAAGTGTGATATTTTGAATCATACTTTGATTTAACCACCTTCAGAAA TTC T A T T C J A A A A C A C T A G C A A C T T C C T T T A T C A G A
WI-19415c	161	A G ---			CTGGATTTTAATATTTCTGGCTTAATAACCAATGTATCAATAAATTTGGTCAATATCTCCACCTC ATTCTGCTAACATGTTTTCAGAGATTCCCTAAGTAAGGTATTGACGACTGAGACTAGTCCGGCAAA GTCATGAGACCCCTTAGCTGATCTCATJAGJAGTCCACCTCATGAAGGAGATGATTCAACATCTCAA GCTAAGGTATAAAGTGTGGACATACAAAGGCTTACAAGTTTACACTTCCTG
WI-19348c	103	C T ---			GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTTCTG GCGGTGCGATGAAGAGACTGTGGTGCATGCGCGTGA[C/T]GTCCCTTCTCCAGGCTCATATGGATGTCTT CGAGGTGCACAGGGAACCTGCTCTGCTTGTAGAAGCTTCTCC
WI-19348b	98	G A ---			GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTTCTG GCGGTGCGATGAAGAGACTGTGGTGCATGGCJAGJGTGACGCTCTTCTCCAGGCTCATATGGATGTCTT CGAGGTGCACAGGGAACCTGCTCTGCTTGTAGAAGCTTCTCC
WI-19635	98	A T ---			ATTAGTTCGTGTGGCCACATTCAAAGCCATCCACACAAGCTTCTGTAGGCCATTGTAAACAATG TTAAAAGGTACAGTAAAAATACAGTATTATJATCTTATTGTGTAGCAGCGCTGTGAGGCTCATT GTTGAATGAAGCATCCTTAGGCAGCAGCTGACTGCATGCAGATATGTGTGCTGAAAGAACTTTGCGCTT T
WI-19641a	46	A G ---			TCCAATTTTCAGAAACATGTTCCATGTTTATTGTGATAAGCACTAGJAGJATTATAGTCTCATGTTT TTAATTTATGAATAACGCTGATTCATTTTGATTTTGATTTTACAGAAAGATGTCAGGGCTATCTCATTC AGTTATTAAATAAATGGATCAGAGTAGTAAGTCAAGAAATAGTGCATAATGTGGTTTAAATTTTAAAA AATACTCAGATGAGGTAGTATTTTAAATTTTAAATTCATCCACCCACCTTG
WI-19642b	52	C A ---			ATATAGAGTACCATCCATGGTTTCAAGCATGGCTGGACACATTATCCCCCTJCAJGGGTAAACCAG GACTATTGCATGAGCATCTTTAATACGTATTTTGATGGACACAAGTTTTTCATGCTATTAT
WI-19673b	180	C T ---			TCTGCCATGATCACATTGTGATGAAGAACATGATGGTCACTAGTAGGTAACCTTCTGTGTCATTGCCT TACTCTCAGTGAGGTGCTAGTGGATTTACCTACCCCTGCTTTTGGATCACCACCTGTAATCTAATAGT GAAAAGGCAATGATGTCTCAGTATCACTGTGAAACAATTTTTCJCTCTGTTGGACCACTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGCTCAAAAAAACACAGCCC

WI-19673a	35 G A ---			TCTGCCATGATCACATTGTGATGAAGAACAATGATG[G/A]TCACTAGTAGTAACITTTCTGTGTCATTG CCTTACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTTGATCACTCACTGTAATCTAAAT AGTGAAGAAGGCAAAATGATGCTCAGTATCACGTGTAAGAACATTTTCCCTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCACACGCTCAAAAAACACAGCCC
WI-19724	35 A G ---			TTATTGGGAACAAGGATTGTAATTTGGGTAA[G/C]TGAGTACGGTGGCCCTGAGTAGTGTC CTAGAAAGCAACACGAGAGTTTTGGTTTTCTCTT
WI-19307	196 T C ---			TCCTCTCCCCAACTAGATGGTATTGATCACTCTGCCCAAAATGGTACCCCCCTTCAGCAAGAAGCTG CAAGCCCTTCTTGGATTGCCCTTCATGAGAAATGGTGGCTGGGATGGAGGTGACATTCCTTGGCTGT GGTGAAC'TGCAAGAAGGAACCCAGGCAATGTATTCCATAGAGGCCCTTAAAGAGACCCG[T/C]TGG AAATGGGCCATGGTCTAAITTTGGTGTGAAATAAACTAACCTCTTTGGCTG
WI-19269	85 A T ---			CTTCCCTATCCCTCTTCCACCACACCATCCCGGAACAAGTGTCCAGGATTCCTGCCCCACTGGC CATTTGGAGTGTCC[A/T]TTGGGTAGCAATGTGGAAACCACAGGGCCTTTGTGGAGAAATGG AGGGGTTGAGGAGTCCAGGAGGGCTATTGAGGGCCTTGCCACTTGCTCATAGGCGAGCTCG ATCTCTCATCATCTGGACAGGTGGAAGCGAATCTTCCCGGGCGTAGGCA
WI-19946	122 C T ---			CAATGGACTGAATGAGTGCCTGGGTGGGTGGGCACACACACTTCAATACACGTCAAGTCTG CTTCCAGTTTTAGAAAAACAGAAATCTGCATCTCAGCCTGAGACGCACAGAGAGGT[C/T]TCTTCCCTG ACCCAGACGCACCTCACGAGCCAGGTCCTGGTTTCAAAACTGCAATTAACCTGCGCCAGAGAGTTCAAC CGTAGGCATCTTTAATAAACTAACTCCAGCAAAATGTGGGTACGGTTACTAA
WI-19956	141 G A ---			CACAGCATGGTGAATAGCATCAGATTGAATGAAAAGTTTGAATGCAACCATAAATAATTATA ATAATATACATCAAGTAACTTTACAGCACACATTTTATAGGCCCAAGTTTGGATCTGTCTGGACCT CAATGT[G/A]CTCTCGGAGAAGCAGCCACGTTAGCAGCAGATACCTTACAGCTTGTCATCTACTCAA GTGATGGCCAACAGAAAGCTTCTGAACCTCCTCCTGGGGAGGTAGTGACAAAG
WI-19076	40 G A ---			TTGGTTGGATACTTGTGGAIAAAAAAAGCAGTTTTAA[T/G/A]GTATTCAAAAATACCTTTTAAAAA GTATTCTAGCACAAAGATTTTCTGTAAACTAGATTATGTGTGAAACTTTTTCTAAATCTGTAGGAG TGTCGGTTGTTAAGAACTAGAGCTTATTCCTATTCCAAATCTATCTTGGCTCTGAAAAACTGCAGA AAGGCACTTGAAAGCTGTCTTCTTTAAGATATGGGATTCCTTTTATCTTT
WI-20218	26 T C ---			CCACACACTCTGGTTTTATAAGCTAT[T/C]AGGACAGAGCAGAGATGGAACTGAAAAACAGGGTAG AAAAACATAAAATGGAGGGGAACAGTGGGATGCAGAAAGAATGACAACAGCCACATGTGCCCCCA GTCAAATACTTTTAGTCCCTGCAGCAGAAGATGCCAACCAAGTCTCTATACTGGCTGGGGATCCTGCC ATGGATGCAGGAGAAAAA
WI-20295g	154 T G ---			CAACCTTTTGCAGAGGGGACGTGAATTTCTGATGAAGTTATCTTACCAAGTTTAAATTCATAATTG GGAATTCCTCTTTTAAATATCTCCAGGCTTGATTGGGGAGGGGCTGGGCTCTACCCCTTCTCTTCCCA TCCAGTCTATTGCCAGAT[G/C]CAGAGAAAGCGCGGAAGCCAGCTCTCCAGCATAGCCACTGTGG GTCCGGCTTCACTTCTGTCCACTCCTCATGCTGGGACTTGCTTTTCGGGG

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WI-20361a	192 GA ---			CTGGGAGTGCTGACCTAAGTGACATTTTAAATGCCAAATACAGTAATCTCCAAAGCTTTTAATGGCTTATGCAAGATGACAGAAATATGTGAATCTGATTGTCCAGAGATTACACTCTGCACCTCCAAAGCTACAACAGTGCACAGCTGAGAGGTTCCCTATACCTTCTACTACTGTGACAATTTAGC[G/A]ATCCTTCAAATGGGAAATTCCTAACTACACGAGACAATGGGTCTCTACAGTAGGCCCG
WI-20572	75 A G ---			GAGCCAAACCCAAACAAATAAAACAGAACTCTTTTGTAACTAAGTCATACCTACTTTCTCTCTCAGAAAT[G/G]TCATAAAACATCATCTTTACAACATGGAGAAGCGAGGTAGGCCATAATTTGTTCAATTCATCTTCTCAAAATTTAAATTTGTTTAAATCCCAAAGGTGCTTATGAATTTCTTCAAAAATAAATGCCTATCAGGTATCATACCTGCAATGCTTCTAATATCTCTTGATTAT
WI-20588	133 GA ---			CATGACAAAGACAAAGATCAAGGAGTAACATAAAATTAAGTTGAATAAATAGTATACAGCAATCTTACATTTTAAAGAAATGTGAGATCCTTTGTTGGTTTTTATTTCCTTAAGTACAAAATGCTAAAC[G/A]GGAGCCGAGCTCTCCGCATTCAGG
WI-20593	79 A G ---			TGACCTCATACTGGTCTGGTTAGAACACAGCCACTAGAACAACTCCAGTCTTTTTCAGTCTGTTGCTGACTTCAG[G/G]TTTAAATCTGGGAATGAGCATGCAGCAATGCTCCACCAGATGAGGAAGAAAGCTGTTAAAGGAACTCAGGATGTTGTTAGGAAGGGGAGTGATGCCAGGCCCTTCCACCAGACTATCCAGAAGCCATTCATGGGGTATTGGTCTGCATCTGTGAGACACTGAGCT
WI-19765	57 T C ---			TTCTTTGCCAAGCCTGTTCTCAAGTTATTCAGAACTGGGTGTATACCTTGCTCTCAT[C/A]TGATATCTTGTCCTGCTGCTTTAGGTAGCAAGGTGATGAATCTTTAAGTTTGTGTTCTTTCCCTCGTGGTATCAGTGAATACTGATCTATTCTGGCTAGGGTCAATTTACAAAATTGCCATGGAACTGAGCAAAAGCCCACGTGGGATAAAATCACTCACCATCGAGGCCACCAGTATT
WI-19066f	239 A G ---			TGACAAGGGGAGAGAAGGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCACAAAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACTGGCATATGTTCTTGCGTTGGTGCACCCCTGAGCTGAATTAATCTCTCCATATCCGGATGCTCAATTACAGTACCATTCAGGGCAAACTTTTCTTAAACGCCCTTCACT[G/G]TTTCTTTTAA
WI-19066g	184 C T ---			TGACAAGGGGAGAGAAGGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCCAAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACTGGCATATGTTCTTGCGTTGGTCAACCCCTGAGCTGAATTAATCTCTCCATATTC[G/TTGGATGCTCAATTACAGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTAA
WI-19066f	148 T C ---			TGACAAGGGGAGAGAAGGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCCAAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACTGGCATATGTTCTTGCGT[G/G]TGGTCACCCCTGAGCTGAATTAATCTCTCCATATCCGGATGCTCAATTACAGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTAA

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WI-19066e	147	G C ---				TGACAGGGAGAGAGGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAGTGG CATATGTTCTTGCGJTTGGTCACCCCTGTAGCTGAATTAATCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCAGTAGTTCTTTTAA
WI-19066c	100	G A ---				TGACAGGGAGAGAGGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAG TGGCATAATGTTCTTGCGTTGGTCACCCCTGTAGCTGAATTAATCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCAGTAGTTCTTTTAA
WI-19066b	87	C T ---				TGACAGGGAGAGAGGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAG TGGCATAATGTTCTTGCGTTGGTCACCCCTGTAGCTGAATTAATCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCAGTAGTTCTTTTAA
WI-19066a	72	C T ---				TGACAGGGAGAGAGGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAG TGGCATAATGTTCTTGCGTTGGTCACCCCTGTAGCTGAATTAATCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCAGTAGTTCTTTTAA
WI-20660	105	G C ---				TTTACAGCGAGTTTTCCCGTCTCAATAAGTATGAATCTAAATAGATTAGGGTGAAGAAATGTG TGCTAAATAAATCTCCCTTTTGAATGTATATTGTCGTTAAATAAGGGAAGCAATTAATATTA CAGACATAATTACAAGGTTCTGAACATGAGTGATTCATTAATCTGTTCTGTACAAGATAGAACAAA AAGCTATCCACCCGCCCCCAAAAATACTGTTTAAACAACACTATGTTTAAAGA
WI-18768	120	C T ---				CTGCTGCCAGCTTCTCTTGGCCCTGCTCCAGATGGGGTCTCCTGGCAGCCTCCCTCAGTCTTCC TCCACCCGCCCTTCTCTCCAGCCTGCCCTGCATGCATGTGCACCCCTGGTCGTTCTCGCTCCATCGCC TTGAAAGCTCTGAA
WI-19087	37	A G ---				TTCCCCAGGGTTCTGTATTGCAGCTAAGCTCAAATGTAGJATTATTAACCTCTAGTTGCTCTTGCTTTG GTCCTTCCCAATGATGCTTACTACAGAAAGCAAAATCAGACACAATAGAGAAGCCTTTTCCATAAA GTGTAATTTAATGGCTGCAAAACCGGCAACCTGTAACCTGCCCCTTTTAAATGGCATGACAAGGTGTGC AGTGGCCCCATCCAGCATGTGTGCTCTATCTTGCACTACCTGCTCC
WI-18790	49	A T ---				GAAAGCCAGAGATTAGCCCCGATTCGGCATCTGTCAACCAGGACAGAAJATJGTCATGGACAAGGGA TGAGCTTTACAAAGATGATGCATTTGGAGATCAGAAAAATTCATATTAAGCAAAGTGATACAAACA CAGTGATTTGGGAATGCT
WI-18987	35	G A ---				AGGAGGCTGTTCCAGGAGTCTGCCAGCAGCCTCQGAJGTGGCCAGCCAGACACTCACCCACCTT CCCCAGTGGCCCCGTGGATCCTGGTCTAGGCTGGACACAGGATTCAGAAAGACACAGGCTGCACA GAAAGAGCCAGATGGACCTGAGTGTGGTGCACAGCCCCCTACACTCAAGGCTGAGAGGCCCTCAGGAA AGTCA

WI-18919	26 C T ---			TGGATGAAACACAGGGATTCCGGA/C/TGCCAGACCCCAATTTTATACCTTCTACAGTG TTGTTTGTTGTTGGTTTATTTTATACCTTTGGCCATACCACAGAGCTAGATTGCCAGGTCT GGGCTGAATAAA
WI- 18741c	64 G A ---			CTTCTGGTCAAGGCTTTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTC[G/A] CTGGAGTTCAAGCTTGAATTAATGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI- 18741b	38 G C ---			CTTCTGGTCAAGGCTTTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTAATGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI- 18741a	23 T G ---			CTTCTGGTCAAGGCTTTGGACAT/G/C/TCTTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTAATGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI- 19179a	170 G A ---			TCAGAACGACATGGCATCTGTTCTGCTGCTTGGTTGGTTGTACCTTTCAGGACCTGAATT TTAGAAITGCCAGTGTGCCAGAGTGAGTGAGTAAATTCCTTTTCAGGTAAGATAGGCTATCTC AACACTGCTGAGTGATTCATAACATATCAACCA/G/A/TAGCATTAACCCATTTTATTTCTGTCCTT AGTGTCTGAAGATGCTCACCAGTTTCTGTGTACAGTAAGGCAGCATGCT
WI-19212	46 T A ---			CCAAAGTGCATCCATGTTGATTTCTGTGATGAGACTAGAGTGACAG/T/A/GTTTCAGAACCCAAATGT CCTCAGGTAGTTTGGAGCATCTCTATGAGATGGGATTTATGCAGATGCCCTATGGAAATGCGAGCTGC ATAATTAACACATTATCAAGTCTCTTACAATTTATTTCCGCAGCATGTACAGCTAAGTAGACCCA ATGGGAGAGAAATGCCTGCTTCTTCCCTCTTCTGCACTGCCATAT
WI-19183	210 G C ---			CTGTTGAAGGCTTCTCAGGCCAACTCCAGCTTAAAGCCCTAGACAGTAAAGACACACATTGGATG GCAGCATGGTTTCTCCCATTTATGGCATGAATATGTGTTTGAATAGGAACAAGCATTATT CCTTGCCAAACAGCCCTCACTTAAGAGGCTTTTGTGCTGAGTCAAGCAACACACTTGCTGCTCTGCC CTTGGAG/G/C/TGCAATTTGACCTGCTCTCACTGGTAAGGIGACTTGGTGGC
WI- 20014b	214 T C ---			TTGAAATCCAGTCTCCTGGCCCCCAGGCAGGGTCTGTCAACATAGATGTCTCTACTGGGGTC GTTCTGGCTTTTGTAGAACTTGGTCTGAGATGTTCTCCCTGTCCATTACCATTCGATGTTCTTT TGTTCAAGAGCAATGTTCTGTATTCTGAACTGGAACTGAACCAAGTTTGCCTTTCTCCTAGTCACC AAGCATACTT/C/TCTGGCTCCCCAAGTACTTAAATGTTCTCATCTGT
WI-19041	198 T C ---			GTCTCCCCAGAGTGTCTTGACCCCCAGCCCTGTCTGCTGTAAAGGGGATACAGAGAAGCTCCCCG TCTCTGATCCCTTCCCAGGGGGTGGCTTAGTTGGACATGCTGGTAGCAGGACTCCAGGGCGTG CAGGTGAGCAGATGAGGCCCAAGCTCATCACACCGGGGCCATCCTTCTCAATACAGCC/T/C/G CCCTTGCAGTCCCTATTCAAATAAAATAGTGTGCTTGCCTGTCTGT
WI-19135	20 G A ---			CAGTTACCTTGTCTTGCCTC/G/A/JAAAGTGTCAATCAATTTTGTAAATTTAGTAACTCTGTAAAGT GTCTGTAGGTACGTTTATATATATAGGACAGACCAAAATCAACCTATCAAGGCTTCAAAAAC TTGGGAAAGGTGGGATTAGTACAAGCACATTTGGCTTACAGTAAATGAACCTGATTTTATTAAC GCTTTGCCCATATAAATGCTGATATTACTGGAAACCTAGCCAGCTTCAC

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WI-19236	54	G A ---	---	TACACAGAGGGTGGCACTTGGACTCTGAGGGTGGGTGTGGAAGGGGGAAAGG[G/A]GATGGAGAC CTGCTCCCCAGCTCTCTGTGAGCCGGTTACATGGGAACAGGGTTAACATCTGTGTAGGGGAGGT CACCTTACCCTTTTCATAGGGGAAGAGTGTACACTCCTGGCTATCTCAGGGGAATGGGAAAG AATCTTTCAAGGGCAAGAACTCGTGGGAGGATGCTGTGTATGTAATACT
WI-19144	222	G C ---	---	GTCCAGTCTTCCAGAAAGCAAGGACTGCCCTTCATTGAGCTGTGAGCTCCAGCTCCAGCCTTTCTAAGG CTCAGCCCCACGGGACTCTGTGGCTGCCAGCTGTGAGCTATCTATCTATATTCATTTCATAGCCAA ACAGGAGACCCCTTTGCAGGACTTGCACACAGGGAGGCTGTAGCCAGGAACCCCTCTTCTCCCTGGT CTGGCTGTGAGGGG[G/C]TGGGAACCAACACCTTCAGTGTGGTG
WI-19139b	110	C A ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGAC GGCAGATGCCCTGACAGAGAGTGGGTGGCAGACAACACACTAG[C/A]ATTTACAGGGGTGGGCAC ATGGGTGGCACTGGACGTGTGCAGCATGTGGCGTCTCTGTGAAGCCACCGTGTCTCTTTGG GGGGCCGCGAGATCTAGCATCTCTGAATCCTGGCTGTGGAGGCTTTGAAG
WI-19139a	66	C T ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGA C/TJGGCAGATGCCCTGACAGAGAGTGGGTGGCAGACAACACACTAGCATTTTCACGGGTGGGCAC ATGGGTGGCACTGGACGTGTGCAGCATGTGGCGTCTCTGTGAAGCCACCGTGTCTCTTTGG GGGGCCGCGAGATCTAGCATCTCTGAATCCTGGCTGTGGAGGCTTTGAAG
WI-18910	112	T C ---	---	GGCTGGGACCTTTAGGAAAGTGAATGCAGGTGAGAAGAACCTTAACATGAAGGAAAGGGTGCCCT CATCCCAGCAACCTGTCCCTTGTGGGTGATGATCACTGTGCTTG[T/C]GGCTCATGGCAGAGCAATT CAGTGCCACGGTTTAGG
WI-19235	173	A G ---	---	TTCAGGAGGTGGAGTTGCTGTCAGCTCTCTGCTGTGATGTGGAAGCTTCTGATATTTGAAGAAACA CGAATGTCTGTAGCTTCTCTTCACTGCCCCAGATTGCTCTGTATTTATCAGCGATGCCCCCTGT CACTCATGCCCTTGCCTAATTGTTCACAATGGTGGAA[G/G]GCTTCATGTAATGATCAGGACCCACC TCCAGTCTTCTGAAAGTGTGACAGTGTCCAGCCGGTCTGCAGCACTA
WI-19222	179	C T ---	---	CGTTTTCCTTAACCTACCCAGTTTAGTTTGGGATGATTTGATTTCTGTGTTGATGCCATTCTAA CTTGGAAITGTGAGCCTCTATGTTTCTGTAGGTGAGTGTGGGTTTTCCTCCACCAGGAAGT GGCAGCATCCCTCCTTCTCCCTAAAGGGACTCTCGGGAAC[C/T]TTTCACACCTCTTTCTCAGGGAC GGGGCAGGTGTGTGTGTGTACACTGACGTGTCCAGAAAGCAGCACTT
WI-19117	134	A G ---	---	AAATAATGCAACGAGGAGGAGAAAGAAATGCACCTAAGACAAGAACTTCTCTCATAGAACAATTG ATCTGTTTACAGGAACAACCTTGCCTTGAAATTTACACAGTGAGACTGTACATAATTGCATGAA A/GJTAGCTATTTTTCCTAAGACATTTTTCATTTCATGAATATTTCAAGTTTTCATACTGTACA CATTCTTAAACACATGATACCAGCAGCAACTGAAATGAATGCCGAATTG

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WI-19134c	263 C T ---	---	CTCCTGTTGTCGACCTGACAGGGTGACACAGCCCTTTTACACACTCTGTCTCCTCTATCTTCTCGGGTAGA TGCCCTGGTGTTAGGGCTAGTACTGAATGGTCTTCCATCCCAAGAGGGGTGAGCCAGGGTCTAG GCCCTTCAGAGCCAGGGCTAGAGGATGACAGGTGGCTAGAGCCAGCTGCACATATCTTTTCAGAGCAC TTCATCCACTTGTCTCCTCCTACCTCGGCACCCCTGGGTGGGAAAGGG
WI-19134a	162 T C ---	---	CTCCTGTTGTCGACCTGACAGGGTGACACAGCCCTTTTACACACTCTGTCTCCTCTATCTTCTCGGGTAGA TGCCCTGGTGTTAGGGCTAGTACTGAATGGTCTTCCATCCCAAGAGGGGTGAGCCAGGGTCTAG GCCCTTCAGAGCCAGGGCTAGAGGATGACAGGTGGCTAGAGCCAGCTGCACATATCTTTTCAGAG CACTTCATCCACTTGTCTCCTCCTACCTCGGCACCCCTGGGTGGGAA
WI-19224	112 C T ---	---	GGTTTACCAGTCTTTTCCAGGGAACTCCGATGAAGTGTCCAAACAAATGAGCGAGTGAAACCAAGA AGAGGATGACATTAGATCCAGGAGATACAAACAGAGGAGATAATCTCTTCAGGATGCCTGTGAAGA AAGATCCCTGGATCCAGGATGATTATAGGACAAGTTGTTCATAATCCAGCGCCAGAGAACTTCC AGGGAACTCATTCAGGAGGTGAAAATGATGGATGACTCTCCCAAGATGAAAA
WI-19201	179 T C ---	---	GCAGCTCCTAAGGACCACTGGCCATTAGCTCTTGTCTTTGATGGCATCTCTTCCACCTTGTCTCTC CTTTGCTCCTCTGTGTAGTGGCAGGTATGACAACTATCCAGTGGAAACACAGCCCTCACACTGCC CTTCCGCCCCCACACTTTCCTGCAGGTGCACCGAAAGGACCTCTGGGGGATAAAATTCAAAAA GTGTGATGCTGCTCAGAAAGTCCAGCTCCATGTCTGCTTGGCTTCA
WI-19034	45 T C ---	---	GAAATGGCTCCACTCAGAGCTACCCGGTGATGAGGATAGGGAAATTCACCTTCTATTACATTAAAG GCAACAGCAGTTAGTAAAGGTTTACAGTGTCTGCTGTTGAAAGTGCAATATAAATTTTGG CTAGCCCATGATCAATCGACTTCTATTGTTGATATACACTCAGCATTTAAGTTCTGTGCGAATTGAC ATTTGCTACTTATAAACTAGTCCCTAAGCTCTTCTTATGCTGTCTATATA
WI-19102	25 C G ---	---	TGTTCTGAGTCACGCTGAGGAGAGCTGCTTCACTCAGGAGTTTCATGCTGAGATGATCATGAGTTCA TGCGACGTATATTTCCCTTTGGAAACAGAAATGAAGCAGAGGAACTCTTAATACCTTAAATCGTTCT TGATTAGTATCGTGAGTTTGAAGGCTAGAACTCCTGTAAGTTTGAACCTCAAGGGAGAGGATAT AGTGGAAATGAGTGTGAGCATCGGGCTTTGCAAGTCCCATAGAACAGAAATGGG
WI-18548b	65 A G ---	---	AAAGGAGGGAGAAATCTTTTACATAAATGCCTTGATCATCCTCCAGTCCCTCCTGAGGAA(A/ GJAAAAGCATCTNTCAAGCTTTTGICCAACTTTGGCTGC
WI-18548a	62 G A ---	---	AAAGGAGGGAGAAATCTTTTACATAAATGCCTTGATCATCCTCCAGTCCCTCCTGAGGAA(G/A/ AAAAAAGCATCTNTCAAGCTTTTGICCAACTTTGGCTGC
WI-18700	97 T C ---	---	GGCAGCAGCTTTTAAATTTGAACACTTCTCTTGGAGGACACACCTTTCAGTACAGTTAACAAATGGT TACACCTGAAATCTGCTGAGAGCAGAGCTTTCJAAAGATCCACAATTGCAAGGCCACTGCTGGCTCA CTTCTCACA
WI-18501	121 C T ---	---	CAGAGGGAAAGTTTATTGATCAGCCACAGAGGAAACAGAGAAACAGACACAGAGGGTTCTGTGT GCATGGAGGAAATCAGGGCGCCGNACAGCTGAACCTCGCGCAGGACAGAGGGGCGCTGGACAGCA GCGCATGCCACAACATTCA

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WI-18017	87 C A ---	---	ACAAAGAAAATGGAATAGGTTTGGAAAACCTTATCTGCAATGACAAAAGTAATCCCGGTAGATAA GGAGAGGCAACCCNGGAACA[C/A]ACTGCTGGATAAATCGTTCAATTAATAATATATCTCTTTGCAT CAGAGCTGGTGGAAAATCAT
WI-18148b	101 A G ---	---	TTATTGGTTCTCTCGATAACCTCTCTTTGGGACTATGAGATCATCACCAGATGTGAAAACGAAAGCA GTGATTTAGAAAACNTCGATTCTGAATATCCC[A/G]TGGGGCATATGCAAAAGGAAGATGA
WI-18254	64 T C ---	---	TATACGGATCATGTATTTGTGTGACCACCACCTACCACAGTCAATTTGTAGAGCAGTTAAATCAC[T/C] JGCCAAAATCCCTCTTCTTCTTGTAGTCAGTCTCTCCCAACCCAGGNACTTGGCAACCTGTTT TCCGTTCTTAGACATTT
WI-18265b	117 C A ---	---	CAATGGGTGGAGTGAATAAACCGCATATTGAGAACAAAGACGGCCTTCTGGCCNCTCTGCGTCC AAGCTGTAAAGGICTCAGGATTGCTGCTAAGTGAGCCATGAACCTGGCTG[C/A]GTTTTCAACCTTTTC CTTGGGTGGTTCTTCAG
WI-18295	40 C T ---	---	ACCACATTTTGTGAGAGCCTATTGTGGAGAACAAACAG[C/T]TTGGGAAGTAAAGTTGATTACT TCCTCTCCAAGGATGATGTTTAATGAATCCCTTTNCCTTAGCTTCATTCTCATAATGCCAAA
WI-18459b	64 T C ---	---	GGGCAAGAGACAGAGATTTAATTGAATAAAACCTCCAGGCTGTGACACGGTGGGAGACACAAAT/ C]GAGTAATTAAACAACATAATATTTANATGACAGTGCAATTAATTAACGTCCTGGTAAAGCCAGAG GGGAGAGGGGGCTTTCA
WI-22585	56 A G ---	---	TTATTTTAAATTTGCATCCTGAGATAATAAAATTTATCTGACAAGTGAACAATG[A/G]CAGAAGC AGCAGTGAAAGTTTCGGAGAGGCGAGTATCCTTCATTTGGCACAGCTGTATATAGATTGA
WI-21155	36 A G ---	---	GGGCTGTGGAGTAACAGAACTTGATGGAAAATTTGGC[A/G]TCTGTGTAGAAATGATTTCTAAAGCTTTC AGACAAATGGCAGA
STS- F02766b	88 G A ---	---	GCCTTTGCTCTTTGCTCTCAGAGGCCCTCAGATGGATACGACGAACTTCCCTTTGAACCTTTTAT TTTCCTGGCAGGAAGAAG[A/G]GGATCCAGGAGTGAGATCAGGAGGTTCTGTGTGCACAGACAG GGAAACAGGC
WI-19888a	98 C T ---	---	GGCAGGATTCACCCATAACAGAGAAAATAACTCCTTATTGGAAAACAAGGTTTATTTTGATATGATG AAAATATTTGGAACTAGAAAGTAGCAGTG[A/C]TTGGACAACGTTGTAAGATATTAATGCCACT GAACTGTTCATTTAAATGGTAATTTTCATGTTATGTGTATTTACACCTCAATTAAGAATGGAACATGT CTTATAATTGTAATACATGAGANCATATTTATGTTGGAAGTGAACACAAG
WI-21485	82 C T ---	---	TGAGACCATCCTCCTCAACAAGAATCAGTCAGTTCAGCACCCTAATTTTCCACACTGAAGTCTACG CAATTTTCATGCAG[A/C]TTGTGGACACAGTACAGTGACAAATCCAGAGGGCAACACATTTGTAATT CATATCATCCGTTTCCAAA
WI-20601a	125 T C ---	---	TCAGAAATGCTTTCCTCCACTGCCCAACCAAAAGAAATTTAATGAATGONCTTACAATGAGATGACTT GAAGTAAAGAAAGGTACCTTCCTTGGAGGTTGCATGACAGGATAGTCTTCTGT[T/C]CTTGGT GCAAGTTGAACCAAGTATGATGACCATTCATCAGAGCATCTGTTTCCCTGTCAGATCCCCACTAG

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WI-20561b	94 T C ---			CGTTGCTTATTAAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTATG TACTTCAGATGAAAAATCCTTACATGTC/GGGAATCAATGTCTTTTAAAAATTCAGATAAAGAAATTT NCATTTGAGGAGACATACAAATTGTAA
WI-20561a	25 A G ---			CGTTGCTTATTAAAGATGGCTGTTT/A/GJTAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTA TTGTACTTCAGATGAAAAATCCTTACATGTGGAATCAATGTCTTTTAAAAATTCAGATAAAGAAATTT NCATTTGAGGAGACATACAAATTGTAA
WI-20116e	69 T A ---			GCCTTCATTTTCTGTCAACCCCTGTCCACCAGTTATGTTGGCTTCAATATATATGGCGTTAGAACAT A/T/AJATAAATCTATATCATATATTTATACACACAAACACATTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGGAGATAA
WI-20116c	59 T A ---			GCCTTCATTTTCTGTCAACCCCTGTCCACCAGTTATGTTGGCTTCAATATATATGGCGTT/AJTAGAA CATATAAATCTATATCATATATTTATACACACAAACACATTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGGAGATAA
WI-20116a	22 C G ---			GCCTTCATTTTCTGTCAACCCCTGTCCACCAGTTATGTTGGCTTCAATATATATGGCGTTAGAA CATATAAATCTATATCATATATTTATACACACAAACACATTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGGAGATAA
WI-20466b	133 G A ---			AAAGATTTCAGTCTGGGACACAGTTTGGAAACACATATTTATAAGTTGCACATATTACAAACAG NTCCAAATGGTGAACTGGTATTTCTAAGATGAAAGCTTAATGAACATAATGAAGTGAATAACGGC G/AJTGGAACATAATGTTTAAAAAGTTAGAGCTTGTCACAGTCAGTCTTAAAGATAATAAAT ACAGTAACACTACTTTTATTTCTTGGCTCTTATCCCTTICAGGTTTCGATT
WI-21444	39 A G ---			CTGGCAGCAAGTAACCATTTTAAAGAAATACTCTCAAC/A/GJAGTCTTTTTTATGGGTATTTCA GTTGTTAAACAAAGTTAAATACTTATTGGAACTAATCTTTGTATTTTATTCGAGGAAGAAGATCT ATAAGATTGACTTACTCATTTGTTGACTGGTTTTTTGAAGCCTTACTGGGG
WI-21034b	148 T C ---			AGAATGGACAATGATGCAGATGATTGTGAGCATTTTGTAGCAATTTTGTAGAAAGTGGTGATTAGAAGGATACAG CATAAATTTAATTGTAAACATGCTTATCTAGCTAACCTAATCTGTTTCTGTAGAATTACTGGTCATGG GAGATTGGATAGAT/CJGCTTAACCTATCTCAATTTTAAAGTAATGTGAGCAA
WI-22091c	205 G A ---			GGCGTGATTTTGATGCAATGTCCCAACCAAGTCAAGCTATCATTTGAAATCCAAATATTTCCAGTAGAG ACATGCAGAGCAATGTCAATGTAAACATACAAAGCATATTACCTCCCGCTTAAGTGACTCATAATTTTC ATTACTTGTGCTGTAGCTTTTAAAGGTTTAAAGATGTAGCATTAAGTGGTATTTACTTTGAGGGCA ACA/G/AJAATTACGGCTTAAACAACACACTAAATCATGAGGCTCAGGGATTG

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WI-21609a	42 C T ---		TCATGAATATGCAGCCTCCATAATCTCTCCCTTGTAAACAA[C/]/GTGCAGTCCGTTTCAACAGCTGT AAAAACAAGCCCAACCAAGACATCACAAAGAGGCAAGAGCAGTGGCAGTGAGAGGGGAGCCTGTGA AAGGATGTTTCAAAGGAGGGTCCCGGCTATGTGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG
WI-22512a	104 T G ---		ACATTCGGAGCCAGTTTTTCCATAATTGCTCCACTGGCTAAATCCCTTGGTGCCTCCCTAGGGCTTCA GGGTAAAGCCCTGACATCATGGTCTTTGTGATCTGT/GIACCTCACCCATGTCTCCACCTNAGTTCC CACATTTCCCCACGCTAAGGGCAGGCAGCTACACTTGACTGCA
WI-21028b	139 A G ---		ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGTCCCTTTTAAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTCTGTGATTGATTGAGCAATCTAGGGGATATGTGACAGGGG TTTC[A/G]TGCACTGGTACAGAACACACAGGGAGTTTCACAAATTTTTTATACAAATGCTTGGGAAT CTACGG
WI-21028a	121 A C --		ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGTCCCTTTTAAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTCTGTGATTGATTGAGCAATCTAGGGG[A/C]TATGTGACAG GGTTTCATGCACTGGTACAGAACACACAGGGAGTTTCACAAATTTTTTATACAAATGCTTGGGAATC TACGG
WI-18829d	58 A G ---		ACAACATGCCTGTTACAGGGGGAAAAATCCTAGGNAATAACTTATGTGACTTCTTG[A/G]TTTCA TCATACAAGACAAGCACAAAAGCACCACCCATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI-18829b	35 T A ---		ACAACATGCCTGTTACAGGGGGAAAAATCCTAGGTT[A/AA]TAACATTATGTGACTTCTTGATTTC TCATACAAGACAAGCACAAAAGCAACCCCATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI-20964	87 G A ---		AGCCAACTCAAGGCCCAAAAAAATTTCTTAATATAGTTATTATGCGAGGGGAGGGGAAGCAAGGA GCACAGGTAGTCCACAGAAAT[A/G]GACACAAGAAACCTCAAGCTGTGAGGTCAATTTGTAAATTAA AAGAATACTAAGATTAGATGAACACACACACTCAGAAATACTCTAGGAGAGCTGAAAAAAGGAAGC AGATGTTAACAAAAACAATTAAGGCTGCTGGGGAACCTGAGTCCATGTTAAGCTTG
WI-20059a	59 T A ---		CTCTGAATAAGGGCCGTGAAGGCATGATTGGTTTGGCACACAGAGTGGATAACCAIT[A/JACAT TGGCTGGAATGAGGTGTCAGGAAAAATAAANTGCACAAATCTAACACCATGTTGAAATCATGTCTGA GTTCTGGAGAAAGTTAAAGTGTAAATAATTACAAAGACTGACATGCAACTCTTTACCTTACATTATT CATCTACAGACTATTTTCTCCCTTAGGAGATGAGGAGTATGGGCCCTTAGGT
WI-22130b	165 C T ---		TGTTTTGAGGGCTGTAGCAGACTACATAATGAGCGGTGAAGGGCTGCCCTTCCCTCTCCTGACAC CAGCAAGGGGGAGGCCACCATCACCAGCCCTGCCCATCATGCATCCATGATTACTAGCACTAGGAA GCCAACGGAANAGGACCCCGCGCTTGCT[C/G]TGTTTAACTCCAGGTTAAGCTATACAGGTTAA ATACATGTCGGAGGTTACATGGTCTCATGCAGTCCCTGTGATGGGAATGAC

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WI-21661	117 GC ---	---	GCTTAGTCTCCACCCCTTTTAAATGTACTCTAGGTACAAAAATAAACATTATACACATATAAGATCAGTCTTTCCCAACTTTAGAAATGTATAAATAAGAAATGACATTTTAAATAAAATAG/GCTTTAGTCACAGTCACACAAAACACTACCTTCTAAGGAAAACGTGCCAGTGAAGCCGTTAAATTTGCTTTTCAGCTATGAAGGA
WI-21980a	25 TC ---	---	TCAGTTTAAACACATTCATCAAGGAT/CJAGATTAAATTAATGTCAGGTGAGCATAAAGGGAGATTATAACCAGAAATGTGTTTTCTGGGAACCAAGTTTCAAGTCACTCAGGATAAGTTTTATTAAATTTTCATGGTGAAGCCCTGGGATAAAG
WI-21636	71 AG ---	---	TGCTTGATTAAATGTGGTGTTCACATTATCCTATTTTACAGATGGAACAGAAAAATACCAGCTTTTTTAAA[G/G]TAGCAATATCTATTATAATAATATTGAATAACACCATAATAATATCACTAAGGAAGTAATCTAATTGTGTTGATTTGCAGAGGGAGAAAACATTACCTCTAGAGCTGAGGCTATTGTGCTCATGCAAACTCCAATCTGAAGGTGGTAGAACTAGGAAGGACACAGGGATTTC
WI-22457a	112 GA ---	---	TTGCTATAATTTCTTAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAAATCACTCATTAGAACACAGTAAACATACTGGACACGGTTTTCAGGCATGAAGGATACA[G/A]CAGTTAATTAACTAAAGGAACAGAGTCCCTGCATTCTGAAGCATAGGATGGGAAACAGTAATGCAGATTAAATACCTGGGGCCAAAACCCACTGAATCAACCCAGCTGAAAACACTGAAGGATACTGGGTAAAGGA
WI-21524b	97 CT ---	---	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATAGCCGTGATGACGACCTTCGCGTCATCTTATAATGGTTAATAACAGCATCTCTGCTACCCGATGATGCTTCTCTGCAATGGACTATTTGCCCAGTTGCAACAGGGCTAAGATTGTCGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTCCTGTCAGAAAAGATTCTTGACTTTCTCCAAGTTACTTCTTCCAGGGGATG
WI-21524a	35 AC ---	---	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAAT[AV]GCCTGATGTACGACCTTCGCGTCATACTATAATGGTTAATAACAGCATCTCTGCTACCCGATGATGCTTCTCTGCAATGGACTATTTGCCCAGTTGCAACAGGGCTAAGATTGTCGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTCCTGTCAGAAAAGATTCTTGACTTTCTCCAAGTTACTTCTTCCAGGGGATG
WI-22652a	32 GT ---	---	TTACCTTCCAAAACCCAGGCCACTTTGGAGAAAG[G/T]AAGAGAAATGCTATTATCAATAAGCCAAGACAATAGGGACTACCTGGGGTAGACCAAGATGGGCAGTCACCATACACCATCATCTCTGCCACAGAACCTTTTGGACATGCTGCOCTCCCTACTCCGCACTCACCTGTCTAATTGGGACCTGAAGCTTCAGCATCCCTTTCITTAGGG
WI-21703d	197 AG ---	---	CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGCAGGGGCTCTGCATCCCTTCTCTCAGCACAGCACCATCTTCAACCCTCTCTGGGAAAGCAGCATTTGGAGCCTACACCACTTGCTGCTTTTCTCACCAGGGTAAGAAATGCAGGTATTTGCAGAGGGGAGTGAGTCTGGGAA[G/G]GTGGGCAGAGCACAGCTAGGGGCAAGGACTTAAGGGAACTTGTGGGGGAAGAG

WI-21703c	134	A G ---	---	CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTCTGGCAGGGCTCTGGATCCCTTTCTCAGCAGCAGCACCATTTCACCCCTCCTGGGAAAGCAGCATTTGGAGCCCTACACQAG/CJTGTGCTTTTCTCACCAGGGTAAGAAATGCAGGTATTTGCAGAGGGGAGTGAGTCTGGGAAAGTGGCAGAGCAGCAGCTAGGGCAAGGACTTAAGGGAACCTGTGGGGGAAGAG
WI-22663c	139	G A ---	---	CCCTTGTCAGTCTGTGCTCGCTTCTCACTGCACCTGGCAGGTGAGCCGGCTCGCTAATCTTATTCACAGTCTCGGTGAACATGGGCTCAGTCTCTCCCGGCTCAGTGTGGGTTTGCACCTGGTGCACCTTACAGGC/GA/GAAGAGCTTCTCATTTGCTGAGGGCTTTTCTGAATCCCGTGTGAATGTGGGT
WI-22663b	55	C T ---	---	CCCTTGTCAGTCTGTGCTCGCTTCTCACTGCACCTGGCAGGTGAGCCGGCTCTGCTAATCTTATTCACAGTCTCGGTGAACATGGGCTCAGTCTCTCCCGGCTCAGTGTGGGTTTGCACCTGGTGCACCTTACAGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTTCTGAATCCCGTGTGAATGTGGGT
WI-22663a	38	C T ---	---	CCCTTGTCAGTCTGTGCTCGCTTCTCACTGCACCTGGCTGAGGTGAGCCGGCTCGCTAATCTTATTCACAGTCTCGGTGAACATGGGCTCAGTCTCTCCCGGCTCAGTGTGGGTTTGCACCTGGTGCACCTTACAGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTTCTGAATCCCGTGTGAATGTGGGT
WI-22668	99	A G ---	---	TCTTTTATCTGCTGCTGCCTGAGTATTCTGGGAATCCTACAAGGATTTGAGGGAGCCCTTGGGATTCCAACTTAACAAATAGTTTCTGTAATATT[A/G]TCTAGTCCATTAGATTGTGTAATGATCTAAATGGNGTAACCATTTAATATCAAAAGTATAACAGCATTTAAGTCAGCTTTTTCGAAGAAACCTTTATT
WI-22631a	52	T C ---	---	AAGATATAGTGGCAGGACAAGATTGGTCACGAAATCCTGGCTCAGTCTGAT/CJAGCACCATTTTCAAGTTTTAGGCAAGGTATTTAACCTCTCAGGGCTCATTTCTCTTTTGTAAATGTGAT/AJGGACC
WI-20258	157	G T ---	---	TATGTACCATCATAGGGTACTTGGACAAATCAACIGAAATTTTAAATCCACACTTTCACGGAGGGGACAGCTGCCATGTCTCCACAGGCTCACAGCAGCGGGCTACTCTGCTGGTGGTTGGTGGCAGGTGGAGATGGTGACGGGCGCATTTGAAACCGTAAGGCATGACAACGGAGGCCCGCGGGGTGTTTCAAG/GTJCGCGTTGACGCAGGTGCATGGCTGGCAGCGGGCTCTACAGAAGGAGGAGCGCAATTCACAGCCTCTTGACGTAGTTTCCGGGGAAGTACC
WI-22714	212	C A ---	---	ACTACACATATGCTGATTTTCAACAGTAAAAATTAACATTTTACATTTGTAGAGAAATCTAGGGTCTACTAAATAATCTAGTACTTGTTCACCTCTCTGCTAATCTGACAGGAGTGTGTGGGAAACGAAGTCTGAAAGGATTCAAGGGGGTCTAGGATTTGCCACAGATCCTGTAAAGGAAGGATGAGGTGAGCTTTACCAACCCCA/CJATGAGTAGGGGGCCAAACATCCTTAACAAGCTAGTTGCT
WI-22734a	44	G A ---	---	TGGGGTACTTTAGATGGGATGGCGTCAGGGTCTGGGAAGGCC/TG/AJCTTAGAAGACATTACCCAATGATGAGAGGCAGCCAGTCGTGAAGCCATAGTTTGGATGGCGAGACTTTTCCGGCAGAGGAAATAGCAAGTGCAAAAGGGCTGAGGGAGAAATGAACCTTGGGCTTGCTCCTACAGGGTGAAGGGCGCCGGTNTGGCTGAGGTTTAGTGGATG

WI-22724	117 A G ---	---	---	TGATATGATGCTGAGATTGCTTCCAAATATGCTAGGAAGGGAAGAGTGTAGAGATATAGGA CAAAATCAAGATTGTCAAAATGTATAGTAACCTGTAAAGCTTGCTAAAGGT[A/G]GTTATTCTATTTT TGGGATATGTTGGGAATT
WI-22750	48 G A ---	---	---	TGTAACCTGTGTTTCTGAAAGTTGAGGGAAAGCTGAGGCAGCTAA[TG/A]GGCTCATACAAAGGT TTGGAAGACCCATTCTGACTACCTAAAGGAGAGTCAGCATTTCTGACCATTTCTGACTGTGCT
WI-22775a	60 A G ---	---	---	TGCTGTTCTTTAGTTTATGACGTTTATCACAATGTGCTACTGTTCCTTCCATTGTTTACATC[A/G]TAGTA GGAAAGGGAATAAATCCCTAAGGGCAGCAATAATTTCTGCTTTGAATCCTTCAATCAGGCCAAA TATTTGTTGAGCACCAAGGGCCAGATGGGAACCTGAGGTATGTAGGTGTTGGGAGCCAGGAAAGGAAG GGT
WI-22808	143 C T ---	---	---	CTTTAGCTAATGAAACTGGCTATGIGGACTATGATAGACCAAGAAAGCTACCCAAAGTCCTGAGGGAG CCTAGTCTCTCTAAATGCAGACAATGTACCCATGACAAGGCTACAGCTTGGCTTAGCAACACAGGA GGATGAAGA[C/T]AGCAAACTGATTAAGAGAGTAGGTATAAGAAACCCAGGGAGAGTGGGGTCCAAAT ATC
WI-21016	207 G A ---	---	---	TCTCTGCTGCTTGAGCCCTCATCCACACCCCTCCAAGCCCTCATGCCACACACCCGTGCCACAAT CCCCATCTCCCTGCTGCTCCCATCTCAAGTCCAATTCOAAGGCCAGAGCCCTGGCAGCTTTCTG GGAGACAGCATGAAAAGGAGGGAGTGGAGATGGCAGAGATGGGTGGAGCCAGTGCGCTGTGGGTC CT[G/A]TTGGCGTGGTATGTGGGGCCCAATCCTGAGGCCAGAGTTCA
WI-21031	31 C T ---	---	---	TGAACACCTGACCTGACCTCTGACATGG[C/T]CTCTGGTCCCATTTGTCTCCAAACGGTGGCACA TCTTCATCTTTGTTATATCTGCAGGAACACTCAGTCTCTTCAGCAGCCGAGAAACACACACA
WI-21314	122 A T ---	---	---	CCATATCCAGTCTTCTTTGAAGCTTTCTATTGACTTTTAGGGTTCAGTTATTATATCCTTTATCACTAT GACTTCATTGATTTTTTATTGTTTCTCCATTTCTCTGCAAACTTTCT[A/T]TTTGTATTATAA ACTGTTTCTAAACTTCACTTAATTTCTCTATCTGTATTNCTTGTAGTTCCTGAACTTCTTTTAGAGG AGCGAGCATCAGAATCACCTAGAGGGTTGACTAAACACAGACTTCTGGACCCCAACCCAGAGCTTCT GATTCAGTAGGCCTGAGGTGGGCTTAC[G/A]AATTAGTATTTCGAAGACCTTCCCTAAGTGTGCAG ATGCTGCTTGTCCCGGGGAACACACTTTGAGAACTATTGTTCTAAATGTTCTCTCTCTTTCTTTAAA GGAGAGACAGGAATTCAGAGAACTGCTAAATTTAAGCATAATGATTGAAT
WI-21186	95 G A ---	---	---	CCACGATAACTATAAAAGCAGAAAATTAGCTTTGAAAATCAAAATCAATATTAGTAACACACATT CATTTTATAAACACACATAAAGACACC[A/G]GGNTCTCAGTAATGCTCTAGTCCAGGGTCTCAA AGTATGGCTTCAGACAAGCCCAATTTGCATCACCTAGGGAAATGCTAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAAACTCTGAGGGTGAGACCAAGCAACCTGT
WI-21187a	94 A G ---	---	---	

WI-21190	39 T C ---	---	TTTTCCACATACCAATGCACCTGTTGTATAAACTATTCGTGGGTAGCCCTCTTTGGAGAC CAGTGACATAGACATGATCCCATTTATATTAACAAATAATTAATAATCTGTACTATTACTGC TTTAGTTATCTAGTGTATTGAGAAAGGAGAAGTCAGCATAGTTATTTCCATGTAATAAAGCTT AACACA
WI-19937d	186 G A ---	---	ACCATGTGCATTTATGGCATAGGAATAGTGACCAAGAAATGCAGCANCTAAACTTGAAGGAAA GAACTATTGCACAAACCAACATTTACATATCTGATTAGACAAGCAAAAGCAGCTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATGGTGTGTTCCCTCAGCAAGTCGATCCAAACCTTC CAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCAATTCGCCTCAGGAAGAA
WI-19937c	185 C T ---	---	ACCATGTGCATTTATGGCATAGGAATAGTGACCAAGAAATGCAGCANCTAAACTTGAAGGAAA GAACTATTGCACAAACCAACATTTACATATCTGATTAGACAAGCAAAAGCAGCTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATGGTGTGTTCCCTCAGCAAGTCGATCCAAACCTTC CAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCAATTCGCCTCAGGAAGAA
WI-21117b	227 C T ---	---	GAAACGGGTGCTAAACAAAGAAAGTCTCAGATCCCACTGAAATCTGTTCAAGTTTCACAGGCTC TCTCCAGAAAAATGCATATGTACCAATTTGCATGTACAAATTCAGAGCCTTCAATACATCTGGGG TCCAATCACATCTCAGGTTCCAGACTCCTAGCTCCCAATATTCCTACAGTTCTGAAGANTTAGCAGT CCTCTCATTTCTACAGTCTGATTTCTTCTACTGAATCTGGGTGGAG
WI-21122a	42 C T ---	---	TCACTTTGTATCAATAATCCCTGTAAAGCTAAAGTTATTCATC/TTTAACAGGAACCTGTTTTTCC TTATTCAAATGTACAAAGCCTGACGCTTACTGTACATATTTCTAGCAGGAGACAACCTGGAAATACT AAACAAATACTGGAATTCACATTACAGACAGACGAAACCAACATGGGATGCCACACACATAACTTCTT TTGTAGGTTTCACAGAGAGCCTATTTGTGGGTGCT
WI-21254	53 A G ---	---	CAGTTTGTGTACAGGAAGGGCCCATGAATGTGGGCGGAACATTCACAGGAGAG/G]CAAGGAGAAG CTGTCTCTGG
WI-21054	23 G T ---	---	AAGGAAACTGCATGGGTACAAATG/TTCCTCAATTCATACIAACAAGGTGGGAAACGGGTCAATCT TGGCTGCTCCAGAACAGGGCGAGTCTATGCACCTCTG
WI-21059b	181 T C ---	---	GGGACCAAGGTAAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGGCTGAA CTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCAGCTTCGTACATCTTAATTTCAAGCTGAAA AATCCTGGGAAGAGACATACCTCACTGAAGTCAATTTCTCTATTC/TCTATTGATAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCTCTGCCTAAT
WI-21059a	63 C T ---	---	GGGACCAAGGTAAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGG/C/T GAACTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCAGCTTCGTACATCTTAATTTCAAGCTG AAAAATCCTGGGAAGAGACATACCTCACTGAAGTCAATTTCTCTATTCATTTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCTCTGCCTAAT

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WI-20442	37	T C	---			TCCACGTGAAGGAAGAAAAAANGGGGGGGGCTT/CJTAAGGTGGCACAATTTAAGAAAT ACCATCCATTTTCTCAGTCTAATCTGAATCCATACATTAACAAACAAAAGTCAAGTGATGAGACGAA CA
WI-21235	43	T C	---			GTGACAAGAGGTGAAGCAAGGGACAAAGGGCAGCAGGGCAGTCT/CJCTCGGGCCGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57	T C	---			ATCAGAACTGCAATCTGCACATGAAAAGACCTGGGGGGAATGCCCTACATCTGGAATTT/CJCATTAAC ATCAACGTTAAATTTTGCCGACCAGTTCTTCATGCTGATCAGTCTTTTGATAATGACAGATCCCAACAT GAACTCCTGAAGCAATGAATATTTACCTTGCTTTTCATGCAAAATTTAGGGACCAAACTCAAAGG TTTCATCCATGCTGGGACACCAGATCTAAGGAATTTGACAGGGATCTTCT
WI-21149a	167	G A	---			AGGACCTGCTCTCACACGTTCCCTCACCCACCAGCTTTTGCAAGATAGTTGACTAAATACCACT AAATAGTGGCTTTTCTTTTAAACAATGACCTTATTTATCTTTTAACTTTAACTGAGTCTTATATA CAGACCTGCCCAACTGGAAGCTTTTACACG/AJTGCTTCAGAATGCGGCGATTTGCACAAATGGTT TGGGCGAGGTTCTGTGGTTAAACATGGGATGGAACCCAGGCTCTACCTG
WI-213,db	188	A G	---			GGTGCAACTTGGAAATATGGTTTAAACACAGGATAAGCATTAAAGGAAAAACACTTTCAATGTGTC TTCCATTTGATGAATTTTCTCTCTTTATCCCGCAAGTGGAGTTTCATGCTCGGTGAAACCA GACAGTGAATCTGTTCCAGCCCAATCTGCAGCATTAGGGATGAGTTCTC/A/GJGAAGTGATTCT GAACTGAGCACGCATCTGCTGATGGGGAACCTCTGGGGAAGAGCCT
WI-21382d	125	C G	---			CCATTGCAGTCCAGAGATGAGAACTGGACCAGAGGCAATCATGAACAGACGGGAGTCAAGAGA AGGGGTTTCTAAGATGGAGAAGTGGGGCGGGTTGGATCCAGTGGAATGGCTTCCQ/CJGAGGTT GCAACCCCAAGGAAGTCTCTGGAAGC-A/GCACCAGTCTGATGGGGGAGCAGAGCTGCCATCCTC AGTCAGGGTCCGAGTCCGAGGAGAGCTGCTGCTCCATAGTCTCGCAC
WI-21437a	201	G A	---			TCCCTGAGGTTGGAGTCTAGCATAGCTCCCCCTCCCTCAAAGAGGGACAGGGGTGAGGGCAGAGC AAAAATCCAGTCTGCTCAACCACGGAGACTGCCCTTTGGGATGGAAGTTTCTGGAGCTCCCTCCATT CTATTCCTGTGGGCGAGGAACATGCCAGGGCTGCTGTTAAATGGCAGGGGTACCTTTACCAGGGC[G /A/CAGGCATAGTGTGGCCCTGCTGCCCTGGGGGCCACCCCTGGGAACAGT
WI-21202b	156	A C	---			CAAAATAGAAATCTTTGTGAGTGGATTGACTTAAATTTTATTTCTGTATAGCTAAATATGTTGATCT GTTTTATGAACATGTATTTTATAAAAATGGTCACAATATATTTTAAAGTTAACTGATTTATTGAGGG AGGAGGAGAGAGTTGACCAA/A/CJGTCTACATGCATAGACAGTCTCTAAAGCGTATCTCAAAACATG A
WI-21202a	61	T C	---			CAAAATAGAAATCTTTGTGAGTGGATTGACTTAAATTTTATTTCTGTATAGCTAAATATGTT/CJGA TCTGTTTTATGAACATGTATTTTATAAAAATGGTCACAATATATTTTAAAGTTAACTGATTTATTGA GGGAGGAGGAGAGTTGACCAAAGTCTACATGCATAGACAGTCTCTAAAGCGTATCTCAAAACATG A

WI-21627b	153 A G ---	---	---	GCATGAAAGAACTCCAATCAGACTTTATTCATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTCATTATGGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAAA/GJTCCAAAGTCATCTAATATTAAACCATATTTTACATAAATTTGTAGG GACAGTACTAATACTCTACAATAAATAAGGGTTTAAANAATGTGTGCTTA
WI-21627a	106 A G ---	---	---	GCATGAAAGAACTCCAATCAGACTTTATTCATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTC/GJTATGGATATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAAATCCAAAGTCATCTAATATTAAACCATATTTTACATAAATTTGTAGG GACAGTACTAATACTCTACAATAAATAAGGGTTTAAANAATGTGTGCTTA
WI-21399a	75 C T ---	---	---	GGATTTGAGTCCCACTTGATCTCAAAATTCACCTCTTGCAATGTAACAAGCTCATTCCTCTAAAAGTT TCAGTTTC/JTTCACCAGTAAGGAAAGGTTGGACCAGACATGTTGGCCGTAATGCTTGGTAA CTGCCCTCTGCATTTGCTCTGAGGTTGTGTCCCTAGGACTAGGTAGGATCTCTCTTGCTTTCTGCC TTACCTAGGCATAGTGCCTGATAGCAGGCTGAAGCCCAATTCATCTGT
WI-20329a	68 G A ---	---	---	CGATGCTCTGAAGATAGGAGGTTAATCTTTACATGGTGGTGCACAGACAGACATCAAT C/GAJTCTGTTAGCAGCGAGAGACACTTTAAGTTGCCCAAGAGTACAAATCCCATCTATGAGAC AGCAGTGTGGCTTCTTAAACAGATAAACCAATCAAAAGAAAGATTAGAGGTTTCAGACATT AGGAACAANTGTGGCCAGATACCAAGAGCCCTGAAGGGAAAGGCCCTCACT
WI-21249	155 T C ---	---	---	TTCTGGCATTCAAATGTACATGTAAATCCAATTTAACAGATCAAAATGTTACACTAAGTTTCACCT TAGTATCTAAGTATCCAATCACAATGTATCTAAGTTTCACTTTAAAGAAACATTATAAAGGTAATT AAAACCTAGGTGTACTTAT/CJATGGAAC TAGTTTATTTCCNATTTAAGTACTGTTTCATTGCGTA AAGTATGTTGTCCCAATTTTCAGCTGTTTAAAGGAATTATAAACAATTGAGA
WI-21504	147 C T ---	---	---	TGACACAGCATCAATTTTCATGAATACCTTTGAAAGGGCCATTAGAAAAAATAAGAGCCAAATTTGGGTC ATTTGAGAAACATTTTCAGCACAAATTACAGTGGGGGACGGCGCTTCGGCTCCAGCTGGGTTTCCC AGATGCAACAATTC/JGCGGTTCTGGCTTCTCCACTGGTGGGGATGGGGATCGCGCCCTTCGGAGCTCT CAGGG
WI-21242	115 G A ---	---	---	CTGCACCAGGAGGACAGCTGCTGGCAGGGACTAATAAACCTTCCACCTGGCCATGGTGGTGGTGT CTCTATGGACCGAGGCGCTGAACCGCGGGCAGGGAGGGGAGAGAAC(G/A)CCTAGCTTGGGGGTG GGCACCAGCTTCAGACCCCTT
WI-21475c	181 A G ---	---	---	TAGCCCTTCTGCCAACATCTGCCAANTGAGGCTGGGGTGGACGTTGGCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGCTCCAAACCCAGGCTTCTCACTTGTCTACTAAGCACAG CAGTCTGAAGCTTGGGACCTGGGCAAGTGGCTCTTTGGAGAAGGCA/GJAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTCCCGTTCTCCACCCTATTTCCCTCCCTGAAG

WI-21475b	117	A T ---	---	TAGCCCTTCTGCCAACATCTGGCAATNTGAGGCTGGGGTGGACGTTGGCCTGATGTTGCCAGAGTAG GATGCTGATGCTGCCAGAGTAGTGGGCTCCAAACCCAGGCTTCTC/TATCTTGTCTTACTAAGCA CAGCAGTCTGAAGCTTGGACCTGGCAGTGGCTCTTGGAGAAGGCAAAAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTCCCGTTCTCCACCCTATTTCCTCCCTGAAG
WI-20893d	207	A G ---	---	TGTTTGTGTTCCAGCCACATCTTCTCCAAAGGAACCCACCCAGCCCGTGTGCAGGCTTGTGCAGGG CTGTCTTCGGCGTTAAAGTGTCTACTGAGGAATACAATCATTTGTACGTAAAGTTATCATCCGCACTCC AGCGTCAGGCCAAACCTTTCGGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGCAGT TTC/A/GIACATAACATTTGGTAGAGTAACAAACAAACCCACAAAGCCTAAATG
WI-20893c	179	T C ---	---	TGTTTGTGTTCCAGCCACATCTTCTCCAAAGGAACCCACCCAGCCCGTGTGCAGGCTTGTGCAGGG CTGTCTTCGGCGTTAAAGTGTCTACTGAGGAATACAATCATTTGTACGTAAAGTTATCATCCGCACTCC AGCGTCAGGCCAAACCTTTCGGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGC AGTTTCAACATAACATTTGGTAGAGTAACAAACAAACCCACAAAGCCTAAATG
WI-19941c	71	C G ---	---	GAGCTCAAGGGAAGACCCCTTACCAGATAGGGACTAACTGGAGGGGTGGAAGGAACAAAGGTGAAA GGTATC/G/GGTCTGTGAGACAAAGCAGGGGGGCTGAGAACACAGAGCAAGGTGGTGTGGAG GGAGCACAGCAGGGTGCAGGAAGGAGATGGGGGACATTTCTTATTCAGTGCAATGCCCTTAAAT AACTGGGTACAGGAGCATTTGGAAGGAGAACCAAGGACAGAGCAAGGCG
WI-21552b	166	C A ---	---	TGGGTACATGGACAGATGTATATGTTTATGGGTATATGAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAATGCGATCTCCTCACCTCAAGCATTTATCCATAGTGTACAAAGAA TCCAAGTATACCTTGTATTTAAATGTA/C/AJAATTAATTTATTTGAATTTAGTTACCCCA ATTGTCTATCAAATATTCATCTTATTCATCTTTGTAACTATTTTGTGTA
WI-21552a	66	G A ---	---	TGGGTACATGGACAGATGTATATGTTTATGGGTATATGAGATATTTGATACAGATACACAATGTG /AJTAATAATTACTTCAGAGTAATGCGATCTCCTCACCTCAAGCATTTATCCATAGTGTACAAAG AATCCAAGTATACCTTGTATTTAAATGTAACAATTAATTTATTTGAATTTAGTTACCCCA TTGTGCTATCAAATATTCATCTTATTCATCTTTGTAACTATTTTGTGTA
WI-21512	54	C G ---	---	TCCTCGTACTTCATGCTCCCTCCCTGCCCCAGAACCTTACAAAATATTTCTGT/C/GTAGAGAGGGA AAGAGCTGGTGGCTGCTCTGGAGGCAACGTCAGGTCCGGGAAAGGCACTCGTGGTCTGTGATCTGTC TCAGTGATGGGAGGTCTCCACTCGCCCCACAGGAGCCTCGGGGCCAGAGATGAGAAATATGCTGTAA TCCAGTACAGGGGTGCGTGTGGGGTCCCAACAGCTCCTTCTTTGGGG
WI-21513b	192	G A ---	---	CACATAGTTTCTCAAGAAGAGGATGAACGTGAACCTCTAAGGCAGGACAAAGCAACTTTCATT ATTCTAGTTTAGACCAGATCTTTAATTTTATATTTCTCTTTAATACTGICAAAATACACCAATA CTTAGAGGAAAATATTCACAGTATACCAAAACATTTAAGATAAAGAGGCGAGTGTAA/G/JAGTAG TATTCTCTACATACCACAGTATACAATGATGCTTCTCTGCAGGTTTAGGAAC

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WI- 21514b	133 C T ---			TTGAACCTCTGAAGGTGGCTTATGTCTGACTCCTCTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGATATCTCAACATTACAAACCCCAATCTTCAAGAAAGGAGCACATTACCATGGAGC[C /T]ACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCTTATGCAGGAAATAAATGAGG ANITTAAGGCTCAGATGGGTTAAGGTGATTTGTCAAGGGTCATAAGGAACT
WI- 21514a	100 A G ---			TTGAACCTCTGAAGGTGGCTTATGTCTGACTCCTCTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGATATCTCAACATTACAAACCCCA[A/G]TCTCAAGAAAGGAGCACATTACCATGGGA GCCACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCTTATGCAGGAAATAAATGAGG ANITTAAGGCTCAGATGGGTTAAGGTGATTTGTCAAGGGTCATAAGGAACT
WI-22020	27 C G ---			ATGAACATGTTGCAAGTGGGATGAAT[C/G]TTATCATGATGCTAAGTGAATAAGCCAGACACAAAA AATCCAAATGTATCATCTACCTGTATGAGGGTACTT
WI- 19576a	113 A G ---			TTCATCGGTTCTTAATACAGTACAATCCTTTTGTGAACAAAAGTCACACTGGCAATGATTATTACA GATCCAAAATAGACTCAGGCTTCAGACATAAAAAATTTAACATT[C/A/G]TCTAGTTCAAGTATTAGT CACAGAAATTAACATCTGCCAGATGTACACAATTTGGTAAAAACTACAGCTTCTCTCCACGGGGA G
WI- 21695a	141 A C ---			ATACAGGCCACAATTGCAGGATGGAAGGAGTGGGCACTTGAAGTGACTACACATACATGGCAATA AGCAGCCTATCTTTACCACCAAGATTTCTTGGGGCATGTGATGGCCAGACCCCTTTCCAA GGGAATA/C]TACTACACTAAGCTACACTGTACTGTGAGAGTCATGGTGAACAAGGCCACAGGC AGTGGAGGAAATGTGATGACTTCACTGTTCAGANTTCTAAGGCCAGCAT
WI- 21574a	235 C T ---			AAACCCAGAAATTTAGGTACTTTTGATTATGAGGAACCTACTATAGGAAGCAACTTATGAGTG TGTAATATTGATCTAGCAGCAACTTCCACTGATCCTGGCAGGTGACAGCTCTCAGTGAACAGCGC TCATCACCTAAAGTGAGAGGCTGTCTATTCTCATTTGTAATGTCCTCAGAGTCACTAGGAGGCCATT GGGCAGGCCAGGGAACCTTACTGCCTACTTCC[T/C]/T]GTCTGTGAGGTGGGA
WI- 21644c	151 T A ---			TGACTGCCAAGATTTAGGCCCCAAGTGGGCAAGGGTCACCTTAACCTTTTCAGGAAGTCTTGGGT GTGACCCACTGCATAAATGGATTTTACCATANTATTAAACAGACTCAAGGTACATACAAGCTTG TTTCATAAATAAGGGA[T/A]TTCAATCAAGATCCATGGAATGATGCAGTTAACATGTGTTCTCAGC TTGCCTACTGACCACCTTCTCTTTCTAAATATGGCAACAGCACAGCAAGTC
WI- 21614b	55 G A ---			TGCTTTAACCTCAAAAGTCCAAATAAACATATAGACATTTTGANTATAGCTATC[G/A]TTTTAACA AACCTCATTATGATCACTGTTCGAATTTCACTCACCTAAATACGGAACCATGACTATTAAATAACA TTTACTGTCTGTGGGTTTGTGGGACTGAACATTAACCATACGTGATTTCTAAGGTACTAGGGAGTT GGAACAGCTACTACGGGTCATGGTATTTTGGGCAGTTGGCTGTGIGTGGG
WI- 21615b	151 C T ---			GACCGAGAAAAAAGTCAAGGCATATGATGTTTGTGCAAGTATACATGACTATTTCAGCTTATAGA GAAACTTGCAAAAAAGTACAAAGATGGCTATTTTAAATTTACATACATATTAAAGATAAGGATGGACT CTTTCAGTGATATTAT[C/T]JAGGACACAAATCGACGGATGTAATCTATTTGANTTATACCATAGGCC TATTCTATATGGCCAAAGGGAAGGTAGGATGGGTACTGTGGAAACGGA

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WI-21981	61 T A ---	---	TGTCATCTCATTCTGGAGAAATCATAGATGTGGCAGAAAATACATATTCCTTGAAGAAAAAAAT[A]GTCTCCCTTATGGGTACTGTGATTTCAATAGGGTGTGGGATAGTACATGACAACATGCATGGGATAGACACTCTGTCTCTACAGATCCGTGCTTTGGGAATTACAGGAACATAAAGGATATAATGGATGGGTTATTACTTTTACATGTGGACAATCTAGTTGTAGGCGTTTAAAGTTAAATTGG
WI-21660	120 C T ---	---	TCCCAACTAGCCTCTCAGTATTTAGATGAGGATAGAACAGATACGGGTGAACACGCCTCTCCACTGCTTACTGTGTGTACCAAGAGGCAGAAAGCAGCTCACCCAAAGCCTAAACCTGGCC[C/T]TGTCTTTTTCAGGCTTCTCAGGATGCCACAGCACATACTGGGAACCTGGGATGCAGGGAGAACCCAGGGTCTGTCTTCAGGAGGGTCAACAGC
WI-19105c	211 C T ---	---	TGGAAAGTAGCCCTTCTGGACAGAAAAGAAATATTTGTGGTCCATGTGGTTGAGTCTGTTAAGAAGGACACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGGAACTCCTCCTTGTCTGTAGGTTTCCAGGGCTGGGCACAGAGGTGAGGGCAGAAATNTGGGGTCCCAGTGGATCTCCCCACAACCTC[C/T]TCCAGGGGCAAGGATTCCACCCAGGGGCCAGGGTGCCTCG
WI-19105a	33 T C ---	---	TGAAAGTAGCCCTTCTGGACAGAAAAGAAATATTT[C]GTGGTCCATGTGGTTGAGTCTGTTAAGAAAGGACACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGGAACTCCTCCTTGTCTGTAGGTTTCCAGGGCTGGGCACAGAGGTGAGGGCAGAAATNTGGGGTCCCAGTGGATCTCCCACCAACTCTCCAGGGGAGGATTCCACCCAGGGGCCAGGGTGCCTCG
WI-21760c	81 C A ---	---	CAAACTAGTCACTCTACTGATGCAAAATGATTTGGAGGTGCTTCTAGCTTTACAATAAGNGGAGGACCTTGACTGCA[C/A]CCTCTGTCTCAGTTTCAGGGCA
WI-21760a	35 A G ---	---	CAAACTAGTCACTCTACTGATGCAAAATGATTTGG[A/G]GGTGTCTTCTAGCTTTACAATAAGNGGAGGGACCTTGACTGCACTGCACTCTGCTCAGTTTCAGGGCA
WI-21569b	198 T C ---	---	TCTGCCATATTGTTCCAGCACCACCTATTACTGTTATTTCTCTTTGAGGAAAAACAGGNATTAAAGAAATCTGGTTTGAATTTCCATGATGCCCTAACTCTATGGTTAAAAATCCTTTTCTTACCAAAAAAGGAACTTCTTAATCACCAGAGAAACAGAGGGAGAGACTGAGATATGTTGCAGAAAATTTATCTCTAC[T/C]AGAGACAATTCATAGTTCATAATCTTTCAGGGTTGTGCTTACITGGGGGGC
WI-20934a	72 T G ---	---	CCAACATGCAACATAGTCTTTCATTCTTAAAAAGTACATAGTAAAGGTATGAAAAACATTTGTATTCAAGAA[T/G]TCTAAGACAAAATGGTCAAAATATTCAAATGGCCTGGCAGTGGTAATTCAGCAGACAAACAGCATAGAAAAAGGCCGGGAGACAGTAATAAATACGTGCCCATTTGCAATGAGTTACCCAATCAAGCCCTTTTACCTCCTTAAGATGGCAGATTAGAAGACCCCTTTCCTCCAGGAGA
WI-21561	55 T G ---	---	TTTCCATTTTATCAGCCGGGCCATCAGAACAAATAGCATCTATACCTTCGAAACCTT/GJCCTCTTAACCTCTCCAGGCAAGAAAGGAAAGTATGATATTTGAATTCCTCAGAAATGGTGGGATCTCAAGACTTTTAGAAAAGTGCTTATTAAGTATAAGAGGCTTGAATATAATGATGATAAATGGTAGCCTTTCTGGAATAATTTTGTGTAATCTGTTTAAAAAGATTTTTTGGATGCATTGTCCCCA

[illegible]

WI-22082L	67 C T ---			CAGGACTTGGTTGCTGCCAACTGCACATAAATGTCCTTTTGTGAGTTATGGTTGTGIG[C /T]GTTTCCCTTTTGCATAAGAAATATGTCATTAGTCCAGAGGCTCTTGCTTTATCCGGATGACGG AGGGTACACGGGGCTCCGCTCAGTCCCGCCGGAAGGACGTATTCGCTGAACCTGGGACGAGTCTACTC CTCCCCACAGGAGGCCACGATTTCAAATCCTCTTTGCTGCAACCTCT
WI-20993	139 A G ---			AACACAACTCCATGCTTTCAAGATTCCACACCCAGATACTAAGACATATTAAAAATTTACAGCAAT TAAACAGTGTAGTTTGGTACAAATACACATATAGCAATGATACAAATTAGGGGAAAAAACCTGG GCTTCT[AG]TAAACAGTGTAGTATACATTAAAGACAGTATTGCAGAAATGGCTTCAGGATTAATTTGA TTAATTTAGAGAGAGCCTATTTCAAGGTCTTCTAGCTCATCCACACATCACC
WI-21723b	125 A G ---			AAGCGATTTTATTAAATTGATTTGGACATACCTGTAGGTCAATAATATTTCTGAAGATAACAATTA TGGACITTTAAAGCTCGACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTTCCCA[AG]CAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-21723a	82 G A ---			AAGCGATTTTATTAAATTGATTTGGACATACCTGTAGGTCAATAATATTTCTGAAGATAACAATTA TGGACITTTAAAGCTC[AG]ACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTTCCCAACAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-22132	99 T G ---			CAACAGATGCTTGAGCCAAAAAGCAACATAGGCAGAAATACAAATTGAGAAATATCTTCATGTTTC AACCTTTAATCTGACTTGCCTTTTACTATCCTT[AG]GCCCCATTTCTTAATCTCTTTGCTTACAA TATATTACCTTCTAGGTATCACCTCATCCTATAGGAATGCCCTTCTAGTTTAAATGTCCTGCCCAAAACA ATACTAACCCATTGAAGGATAACTATGGAAACCTTTAAATGGGACAGTGGG
WI-21006a	106 A G ---			TGACAGATCACACCCACATTTGTTTGTAACTTTTCTCCTTCAAGAGTCACCCTTAGCTTAAGCCAGAA GATTCTCTTAAAGAACACATACACATGTGCACACAC[AG]AGAGGCAAGTACAAAAATGTAAACC CCACCAAAGTGCATGTGAATGAAAGTGCAAAAAAGGCTTCATTTCGAAACTCTGAGGATCATTTCTCT CTGCTTCAGGAAAAATAACAGAAAGGTCCTAACTGCOCTAGGCT
WI-21761b	138 C G ---			CTGAGGCCTGCTCTAACTTCATNTGACGGAGCGAGTTTCTGCTTGGAAATAACTGAAAAAGATTTCAT TTTCTCTTTGTGTACAAAGGATTCAAAATATTTACATCTTCTCTGCCAGTTAACGTGCCGTGG CTC[AG]CAATACACACCAAGCAAGCGTAACCTTGGCTGCCTCAGGAAGGCTGGGAGGAAGTGCCAG ATGGTA
WI-21079c	166 G A ---			AATGAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCACTGTGTGCGCAAAATCAAGTTGT TTTAATACCAGTGTGCAGCTTGATTCCTCCATGAATTAAGCTGTGTGCTCACTTGTTTACATAA CTCAGGCCACCCCTGAAATATCTGCTAGTGG[AG]AATTTACAACCCACTGACCATCTCAGCTCAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAAATAGGCATGGGCAAT

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WI-21079a	50 G A ---			AATGAAATGCCACCCAGAGGTTAACAGCTGCCATGCATGCAACTGTGTG G CGCAAAATCAAGT TGTTTAAATACCAAGTGCAGCTTTGATTCCTCCATGAATTAAGCTGTGTTGCTCACTTGTTTACA TAACTCAGGOCACOCCTGAAATATCTGCTAGTGGGAAATTTACAACCCACTGACCATCTCAGCTCAA GCCAGATGACTATCACTTACACATCTGCCAGGGTAATAGGCATGGCAAT
WI-22129a	45 T G ---			TCTGTAGATTTAGCCATGCCATATATTTAACTTTAAGGAAAGT G JTATATAACAGTCATTGCT TGGTAGAATCCAGTCTGTCAATAAGTTAGCTTAACAGTTAACATTGAAGCTTATACCTTATATTTA AATGTTAGCAATCTCTACTACATTTTCAATATAAATAATTTGGTGCAAATCCAGNAAAGGGCA TTAACAAACATGGGACTGATCCTGGGGCTTCCACCTGACTAAGTTTITA
WI-21941	79 A G ---			TGGAGTTAAGTGGGGCTCTGCTATTTCCCCCAAGAGGACTCGGAAGATGTTGATTCAGGGCAGAGT GAGGGGCAGAC A G GGATGAGGCTCTTCTGTAAAGTCCACAGACGCTCACAGATGCTGGGAGGCT GGGACTGCCAGTTGGAGCCTCACCCAGAGAGCCTCACTGCAATGACCCACACOCACCACTCACG CAGCACAGGCACACGAGGACACGACACACACGNTGCACTCACACGC
WI-18916b	42 C T ---			AATGGCATCCCTGTCGATACCAACATCTTCAGCAGCTCAGC C TGGCTCCCACCTTCTTGGTACCC GGTTAACTGCCAGGNGGTGACAGTGATGCCAGGGCTGCCCACTACTGCACTGGACACAGCCTCACCC AATGCCACCTTCATA
WI-18916a	35 G C ---			AATGGCATCCCTGTCGATACCAACATCTTCAGCA G C TCAGCCGGCTTCCCACCTCTTGGTACCC GGTTAACTGCCAGGNGGTGACAGTGATGCCAGGGCTGCCCACTACTGCACTGGACACAGCCTCACCC AATGCCACCTTCATA
WI-19828c	200 A G ---			TTCCCTTCTCCCCAAGAGTGGGCAGAAAAGCTTTGTTAACCTCCTTTTACAGATGAAGAAAAACAA GATCAGAGGTGCTAAGTGTAGCTAGCTAGTCCAGGNC T CTGGCCCCAATCTGGTTCTCCCAAG CCCATGCTTCTCCACTTCTCACAATCTTTACTTCTTCTCTGACCTCACCACCACCAAAAT A G C TTTAAATCTGGAAAAGAACCCAGCTGCACACTGGGCACACTTGACCT
WI-21863b	47 C T ---			CACAAGAGTCTGTACAACCTTAGGGACACAGCCCTGGCCCTGCCC T C T GCTGCATGCCACCCTC ATATCCCACCCCATCCCCAGCCTCTGCCCCGACACCCCGAGGCTCCCTGCTCTGGTTGAAGTATTT CTCCAAGGCAGGAATGAGTCTTGATCCAAACACAGCATCT
WI-19860	51 C G ---			TTGACCTAAAGCCTAGCATAAAATAGCTAAGTAGAATGTTTCCAAAGATG C G CTGCATCAGTAT CTCCCATCCACATAATTTCTGTTGATTTTGCCATTACCCCATAAATGGTGGGATCTACCTCCCT CCTTGCAATTTGAGCTGGNCTCTGATCCTGCTCTAAGGATCTGAAGCC
WI-19899b	80 C T ---			ACCCAGCTCCTCTTACCCTCTGGCTTTCAGTAGGCTTTGGCTAATGGCCANTGAACTGCAGGGCAAG AGGAGTGAGGGG C T TACAGCATTTATTTCCCTCTTTCACTCCCTGTTAGCTTTGGTAGTGGCTGTAT TTCTCTACTGATAGTTCTTGGCCACAGTCGTAACCTATTCG

WI-19891c	172 C G ---	---	TGTTGGTCTGAGATTACAGCTTACTACAAAGGAAGCTGAGAAITGCTTGGTGGCCCTCCCCCCCCG ACTCCTCTGCTGGGAAACGTGGCTTTGNCTCCAGACACGTGTGAGATGCCAGCTCTCCTCAGCGG AGTCCCGATCCCTCAATTTGCCATCTGTCTGACTC/GCGTCTCCCGGGCGTGGGGCGTGTCTGT CAGGCAGGGGGGGAGGAAGGAAGGAGATCCAGGGTCTGCTG
WI-20155a	81 C T ---	---	GCACCTGTAGGGGTAGCTTCCATGGTTCTCCAAAGCAGGGCTGTACATTACCTTAGGCTGACCAT TCCCTTGGGGGGC/TGCAAAACGTCTTTGAGGAAATNTCCAGGAGGAATAAAC TAGAAGACGC ACCTGCTATTTCCACCATACTATGGAGAAATACAGCTAATGAAGTGTGGCAGAGCTTGGCCGTGTGA GTGCCCCAGGGTAAAGTCTCTCTCTCCAGTCCAGAGCAGAGACTTCTC
WI-20270b	91 T G ---	---	AGCCATACAATGCATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGACGCGTCAGTGTACAAT ACATTCATGTCCAGGATAAGGAGCA/T/GJACACCAGGATTTATACCGGTGGCAGCGGTATAGGCA CGATGATACAAATATAAGTATATTTCCATCTATATAAATACACAGCTGGGGTGGGAAGGATGCT GGGTGATCTGTTTCCCGCAGAGGGCTGGGAGGCGGNGGGTGGTGGAA
WI-20270a	53 G A ---	---	AGCCATACAATGCATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGACGC/GA/TTCAGTGTAC AATACATTCATGTCCAGGATAAGGAGCATACACCAGGATTTATACCGGTGGCAGCGGTATAGGCA CGATGATACAAATATAAGTATATTTCCATCTATATAAATACACAGCTGGGGTGGGAAGGATGCT GGGTGATCTGTTTCCCGCAGAGGGCTGGGAGGCGGNGGGTGGTGGAA
WI-20622	130 T C ---	---	CCACTTCAATATTTACAAATGCTCAGCAGCAATATGAAAGCTTCAACACTTCCCTTTGTA ACTTGCTGCAATAAATGCAACTTAAACAAACATACAAATTTCTCTGTATCTTAAAGTTGAA/T/C TACTAATTTTATGATGTTACTCATATTTTATTCATATACITTTAATGACATCATTTGCCAATACATA CATATTTCTNTAACTTTATTTTACAATAAGCCAAACATCTGTCATGCAG
WI-20768b	190 C T ---	---	TTCCCACTCAAAACTCCCAACCTTCTTGGAGGCGAGGCTAACAGGACCTCTGCTGCTGCTGC TCACGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATTCGTATATCACCACTCTA CAGGAGAGGTCTATTTCTGGGGCACCCAGAGNITCAGCACACATACTGCTGGGAC/T/CAGGGACTC GTAATTCGCTTGGTCCAACTCTTCTATGGGGTTTAGCTGCCCTCATTC
WI-20768a	71 C T ---	---	TTCCCACTCAAAACTCCCAACCTTCTTGGAGGCGAGGCTAACAGGACCTCTGCTGCTGCTGC TCA/C/T/GACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTATTCTGTATATCACCACT CTACAGGAGAGGTCTATTTCTGGGGACCCAGAGNITCAGCACACATACTGCTGGGACCAAGGACTC GTAATTCGCTTGGTCCAACTCTTCTATGGGGTTTAGCTGCCCTCATTC
WI-21909	153 A T ---	---	TGTTTGTCTTGTGCCAGGTACTTACTGCTTTACATAAATTAICTCATTTCTGTACATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGCACCTAAAATAGGATATTTGGTGCATCTTTAAAGAAA TGCTTTAATACATACCAAG/A/TJAGTGGAAATCAATAGATAAATATTTAAGTCTTACAAAGCGTAC GACACTAAAGTAATATAGGATACCCTAAATTTATATTTCTATGTATGGAAAG

WI-22202	128 A G ---	---	TGTTGCTTTGGTTGTTGCTTCTGGAAACATATTGGAACACCTTGTTTTCATAAGCTGTCTCCTGACAGT GGACAATCCCATCCATCTTCAGGCCCTTTTAAATAGGTCATTATGAAATCTGAAATTTCTTGA/GJTAAAT ACTCTGGTGCAATTCATCTGCAAAAGCAACTGGCACAAACCACCTCTGCGGGTGACGCTCTCGG AGAACATCTAATATTGAGTCTAGTCTGTGCGGGAACCTTCTCCAGCTCAC
WI-22189	70 C T ---	---	CCAAAGGATGAAATTTCCACATTTATTTTNCCTTTATGTGAATAGAAAATGGCAGTGAAGTGTCTCTATG AACTGTGAGGCGAGGAATGGCATGGCGCTGCGGTACCAAGCTGGACGTTGTGCTTCCAAAGTACAC TATGTGTGGTGAGACAAAGGGT
WI-22283	109 T C ---	---	GGGAGGCATCATAGAAAAAAACCCCTCAGCCAGAAAGTTAGGACATTGTGATCTCAGCCCACTAACGA GCTGTATGACCTTGGTCACTAGGCCCTCGCAGGCTCTGGTTGTC/TTCATTGCAAAATAAAACCCA GACCGGTCACTCTTTCAGTTCCCTCCAGCTCTATTAATTTATGATTTGCTCTTAGTCTTTATGAGCCA TGTATGATTTATCAGTCTCCCTGATGCACCTCACTCCCAATGATGCAAAAG
WI-22290a	136 C T ---	---	GACGTCATCTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGGTTTATGGGCCCTCTAAGCACCG GCCAGTAGTGGGAATGCCACATGCAATGGTGAGTGGGATCTGGGGGGGTCAAGGACCTTGCTTTT C/TJTTCCAATCTCTCTCTTACCCAGAACTTTGCGAGAGCCCCCTTNNATTTCTCTCCCTCTATTCC CCCTCTTCCCCAAATGTCTAAGTCCCAATTCACAGACCCCTCCACG
WI-22292	53 A G ---	---	CCAGTGAAGGGTTACAGCCATAGTGAGGTTCCCCCATTTGCTCAGTACCAGA/A/GJTTTGAGTAC GGTCGTTAAAAAATACTTATCTGACCACAGTGGAAA
WI-22387	186 C T ---	---	ACCTTGACACACCTGCCATCCGGTGCCATCTCCTGGTGGCACATCTATACCCACTCTGGCTCTGAAAG GCTTGTCAACCAAAAATGGCAGCTGGGGCTAAGGCATATTTAAACAAAGCTCCAAAGGACCCCTT TCACCTGGGTCTAGCATCCAGCCTCTCTCTCAGCAAGGCAGGATTGGGTCT/TJCTTTGTGTTTCTG AACAGGGCCAGGCGAGCAAGGCATGCCATCACTGCAGCACTCAACCCCT
WI-22395b	127 A G ---	---	GCCGTTCCAGTATTGATAATAATTTGTGTTTAAATTTCTATACAGAAATGGTCTTCTTGAATATTTT GTAGGGATGGATGAATTGAAAGTGAATTAAGTCAAGATAAAGGGGGCAACTCTTTAAT/A/GJAAG GAAATGTTACCAATCCATAGTGAAGAGTAGAATATGTTCTTTTAGAGTAGNTAGAAAAGTCCCCAGG CTCCT
WI-22405	90 A C ---	---	TTTATGGCTCCTGAGTGCCCTTACCCAGCTACACTTTACCTTGATCTATATAAAAGTGAATTTAGAGT AAATACATTGGCTGTAAAGTCG/A/CJGATCAGGTGCTCTCCACCAAAAGCAAAACAAACTGCTGA AATGTGCAAGGTTTCTCAGTG
WI-22419b	67 T C ---	---	CCCTTCTGGACAGTTGCTTTATGTGTTCCAGACATCAAGGNTGCCCTTCCAGGCACAGCCCCAGTGCTT /CJCTGGATGGCATCAGCACAGGCTCCCTGCCCGGCCCTTGAAGCATGGCTGTGTGCACGAT
WI-21342d	59 T C ---	---	ATTTTCCCCTTCTGTGTTTCGTATTTCCCCCTTTTGTGCAGTAAATNAGCAATACACTGAT/TJCTGGAA ATCTGCATGATTAATAACATTAACAAGTTCAATAAACACACCCCCATATCAGAGTATAAAGCAAGAG GTTGAAAAATATCCCCTAACCGAATGCAAAATTAGGTATCCCTCAAAATTCACATAATCTCCTCTAGTT T

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WI-21763b	154 A G ---	---	CATACCCCTTTAGGTGCCACATTGATCTTAGTTAACAGTCTTGAGTTCCCTCTTTAGGCTTCAAGA TAATTGGAATTCATCGCACCCAGATACITCCAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT GCTCTCCACAGCTGATTAGCAGACATTGCCTGTGCTTCTACCCAGCAGCTGTCTAGTGCACCTT GA
WI-21763a	135 T C ---	---	CATACCCCTTTAGGTGCCACATTGATCTTAGTTAACAGTCTTGAGTTCCCTCTTTAGGCTTCAAGA TAATTGGAATTCATCGCACCCAGATACITCCAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT T/CJGCTCTCCACAGCTGATTACAGACATTGCCTGTGCTTCTACCCAGCAGCTGTCTAGTGCACCTT GA
WI-22440	64 A C ---	---	CAGTCCATTTGAGTCCCCAGTCGAGGGTGCATTCCTCTTATCTTGCTTAAGCCACTTGGGTAC/CJ TCCATTCAGCTCTGCACCTTCTCCAGTTTCTCATGTGAGAAGTCCCTGGAGGGAGGCTTTCTGG AAAT
WI-22449	74 T C ---	---	CAATGAATGTTGTGGCATATGATTNCCATTGTGTGACAATTATTAGCTGGCATCCGAATACAGTAC TTCTTTT/CJGAAAAAATACAAATGGGAACGTGACA
WI-21965a	112 A G ---	---	CAGGTTCCACACAGAGGCTTTATTTACGCCACTCAGGACCCCTGGCTTCTGCTCCAAAGGCACCTGAACA CAGTCAGGCTCTTAAACACTGGCAGGGACCTCCCCACAGCC/CJCCCCACAGGGTCTCTGTT TCCCAAGTCTCTGATGGATTAGGCAAGACCTTCACACATTACCCCACTACCTGCTGGAGAGGGGTC ATGAGGCAGCCTGTGGTGCCAGCTCAGTGTGACACACTGCCAATGTGC
WI-21687c	115 C G ---	---	CACCTGGCAGTTGAGTCAGATTGTAGGAAAATTAAACCAGATGGGTCTACATTTTNTTCAAGTTCA AACACATGTTTCTAGTCAGAAAGTCTCATGGACTTCTTCCCTAAG/CJGTGTTCTATGATCAGAC CACCTCCTAAATGTGGCTTTTACCATTACAGGCTACAGTTGAATCAGGCAGGAGCAGCTGCTGGAG AG
WI-22374a	149 T C ---	---	AGCTTTTACAACAAAGCGAGGGTTTAAAGGAGCCTGAGAAGAAATTTTACAACTATTGACTATACAGAG TCTTCAATTCCAAAAACAGTTAATAGTAACCTGGTGGCACATACAACATGCATTGAATACTCTGTAT TATTGAGTAACTAAAT/CJAGGNTCCTGCATCATCTCTTACACA
WI-22250b	132 C T ---	---	ACTTGTCTCAGGCAGGCACTTCTGGGATCTAAACTAGAAATCCTTGAAAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACCTGAGTGGGTATTATGGGGTCTCTGCCCTCCTGGCTGTGTTATG/CJ GGANCCAGGAGTGAGGAGAGCCGTGGAAATAGACAGGGGAG
WI-22250a	89 G A ---	---	ACTTGTCTCAGGCAGGCACTTCTGGGATCTAAACTAGAAATCCTTGAAAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACCTGAGTGGGTATTATGGGGTCTCTGCCCTCCTGGCTGTGTTATG GGANCCAGGAGTGAGGAGAGCCGTGGAAATAGACAGGGGAG
UTR-04932-2b	192 G C ---	---	GCAGCCATCTCCTCTCCAGACCTCCAGGCCACCCCTGGGGCCAGAGCACTCATGCCAGCAGCAC CTAGTGGCCCGAGTACGGACCCCGCTGGCCAGGTCTCTGGCTCTCAGGACGTOCCAGCAAGTGGA GCCAGAGGTTTGTGGGACTCCAGCCAGGGGATAGGCCAGCCCAAGAACCTG/CJGJAGTGCTTC TTTGACGGGGCCCGCTGCTCAGCTGCTCTCTGGGAGGTGAGGAAGGAGGT

UTR-						GCAGCCATCCTCTCCAAACCTCCAGGCCACCCCTGGGCCAGAGCACTCATGCCAGCAGCAC CTACGTGGCCGAGTACGGACCCGCTGGCCAGGTTCTGGCTCTCAGGACGTCCAGCAAGTGA GCCAGAGGTTG/C/TTJGGGACTCCAGCCAGGGGATAGGCCAGCCAGCAACCTGGAGTGCTTC TTTGACGGGGCCCGCTGCTCAGCTGCTCTGGGAGGTGAGGAAGGAGGT
04932-2a	149	C T	---			GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACAGGCCCTTGCACCTGTCTCTGCTGCCCTCTCTGTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAGATGCAGCCAGGAGCCTCTCTGA AGGACAGTCTGGTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
stFIBBb	412	G C	---			GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACAGGCCCTTGCACCTGTCTCTGCTGCCCTCTCTGTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAGATGCAGCCAGGAGCCTCTCTGA AGGACAGTCTGGTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
stFIBBa	341	T C	---			GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACAGGCCCTTGCACCTGTCTCTGCTGCCCTCTCTGTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAGATGCAGCCAGGAGCCTCTCTGA AGGACAGTCTGGTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
stIGLV2	61	T C	---			GTCACAGAGGAGCGCTCTCGGGACGTCTCCACCATGGCTGGGCTCTGCTGCTCCTCAGT/C/C/CTC CTCAGTACAGGACACAGGTGACGCCCTCCAGGGAAGGGTCTTGGGGAACCTCTGGGCTGATCCTTGGTCTC TCTGCTCCTCAGGCTACCGGGGCCAGCACTGACTCACTGGCATGT
stSG1001	70	T C	---			GTTCAAGGCTCATCTTGAACCTCTGGTGTCAAGCGATCCTCCACCTCGACCTCCAGGGTGTGGGAT TA/T/C/JAGGCATGAGCCCCACACCTGGACACAAAATACATTATATACCTCAAAGTATAGGATTACT TTAAGAGAGGAACTAAAGTATGATGGCTTACTTTCTAATCC
7a	33	G A	---			GTTCAAGGCTCATCTTGAACCTCTGGTGTCAAGC/G/A/TCTCCACCTCGACCTCCAGGGTGTGGG GATTATAGGCATGAGCCCCACACCTGGACACAAAATACATTATATACCTCAAAGTATAGGATTACT TTAAGAGAGGAACTAAAGTATGATGGCTTACTTTCTAATCC
stSG1002	63	A T	---			TAATGATAATTAGGCACTTCTCCACACGAAAGATGACACAATTGACCCAATATCATTGAGGC/A/T AACAGTTTGGGCTGTTTCCAGTAGTATGACAGTGA
stSG1009	36	G C	---			GTGAGAAAGATCGTCTTCTCCCTCCCATGACG/C/G/GGCTTCCCGGGCACCTGTGCGTTTCC ACCCCGAGACGGCCTTGTAGGAGCCACTGCCACTCCGCTGCTGTGCGCTGGTTCGCGCTCCTAG GGCTCGAGTGTTTAAAG
stSG1011	107	C A	---			TAGGCTTAAACCTGGAATCTACAAGCCAAAAGTCCCTCCCTGCTGAGGGGAGTACCTCCATTGGGC ACAGTCCAGACCCCAAGTCAAAGATGCCCCATCTTGGG/C/A/CTCAGCCCTCAGTTCCCTCATTTCC ACCAGGCGGTGCTTGTGAGTTTCTCCAGTGAG
stSG1012	89	T C	---			TAGTAGGTAAAGAAAGCAAGGAGGATGCTTATGCGATGACTGTTTACAGTGGTGTGACACTATGC CGTGTTCACGAACACTTTAATA/T/C/GTGTGTGTAATCTGATTATCTCTCGTCTTACAAATG
stSG1017	42	C T	---			TTGAAGCAATATTGCTAGCACTCTGCTGGACATTAAAGTCCG/C/TJGGGAGGAGAAGTGAACAGGAA TCGATTCTTGTCTTTAACTGCCCTTAGTAGGAGATGTTAAATACTTGGC

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stSG1019 3	136	G A ---	---	GGAAACAATACTACCTAAGGACAAAATACTATTATAAAAAAAGCTCTTCTAGTGTATATTGTGTAA CACATTTCTGGAGCTGGTAGGAATAACCAATTTTATTTTCTGTAGTGCCATCTATACAAAACCTTTTAC T(G/A)TTTGAAACCTGAGATTTAAGTTGCAAACT
stSG1020 2c	143	G T ---	---	AAGTAACTTAGGTGAATGGTGCCACTCAAGGTCTTTCCGAGGGAAGCTCAGTCCCTGGCTTGGCAG AGTCAGCCTTGGTCACTCATAAGGGGCTCAGCTAAGCGTCAAGGCTCAAGGAAGCAGTCCCACTGCTTCT CGCTGTCA(G/T)CAAGACCACAAGGCAGATGCCACTGCTGTCTCTTCTTCTGTCTACTTCT
stSG1020 9b	75	A G ---	---	TCCTTTCTCTTTTCACTCTCAGTCACCATGATTCAAAATAAACTAATTCCTCTTAAGATCCCACTTTAT TTTTA(G)CTCCAATAAATGTAATATCAGCTGCTGAAT
stSG1020 9a	34	C T ---	---	TCCTTTCTCTTTTCACTCTCAGTCACCATGATT(C/T)AAATAAACTAATTCCTCTTAAGATCCCACT TTATTTTTAACTCCAATAAATGTAATATCAGCTGCTGAAT
stSG1021 8	29	T C ---	---	TACTAGACATGCAAAATGAGAAGATTACA(T/C)GTGAATATTTAAAGAAATTATATTTGTTTGACAT AATATGCATTGTACCCGGGCATAATAAAGTTAAAGCCAGTTATTCTGA
stSG1025 2	108	A C ---	---	ATAGGTTTCAGGAACAAAATCATTAAATGGAAAAATGAGAAGAATTCCTTTATTTTGGACCAATTTT AGGCACCTAAGAGTTTCTTTCTCTCTTCCCTTTGATCA(A/C)AGTGAAGATATGATAGGGAATTC AGAAATTTCTCTCTTG
EST10915 0	123	A C ---	---	CTGTATTAAATGAAGAGGCATTAATGAGGGGACGGAAAAATCTACCTGTACACAAAAATTCGTGAC TTTAAACAGCATCTTCAATAAACCTTTAAAGGATAATGGTTTACGATCATTTTAAAG(A/C)ATTTTAA GAACTGAGTTATTGGAC
EST11023 1	166	T A ---	---	TTTTTTGTTAAACCAACCCTGAAAGTTTCCACATGTGAAATATAGATACAAACAGTGAACAAAAT ATGTGGCCTCCCATGTACATTTGGTTACCTATGTACAAGTATCTATACACAGTAAACAGCAGGGC AATTAGTCAATTAATAAAAAAATAGTACATGTTA(T/A)GTGTAATAAAATTAATTTACAAAGGCTTT TCCACTCGTGGATTGTATTCCTTTTGGAGGGGAGTAACTCCTGG
EST14096 8	71	G C ---	---	GGGATGTATATTACAGATAACACAACTCACAATAATACCATCAGACATTGAAAACTAAGGCCATTCT GTGA(G/C)TTATTTTAAACCTTGGTGTTCACACATAATGATCTTAAAAAAAATGAATTACCAAA ACCAAGATTCTCTTCTAAATGAAAAATTAATGCAGGTACAGGATAAATTTAGGGCTATATCTAATC TGAAG
EST22113 6c	125	C A ---	---	TGCAATTTGTGAAGGCAGCAGGGGCCAACCCCTGGGACCTCATCTCTGTCTAGAATGTGAGGTGCG CAGGGATGCTTAAGTCTTCTCTGGCAGAGACCCGAGGTGCAGAGATGATTCCTCA(C/A)CCCTTC TCTCAGGGTCTGGAG
EST22555 7	60	G A ---	---	TCAAGCATGTGTAAAGGCACCTGCCCCGCCAGACCCCTTCTAATCTCTGCACACTGGAAGGT(G/A)AAA CCTGGGAGAGAGACACTCCCTCCCTAGCTTCTACCTGGGACCCCTCCAAAGATGAGCATTCATC TTGGAGACCAAAATAAAAAAGGACAAAAGACCAGGGCTCAGAG

EST22917 6	74 C T ---	---	---	GTAAACCTTGCAAAGCCATGCTAAATGGAAGCCTGACTGACCAGGGGCTCTGGGCTCTCAATGCA ATAGAAAC/TTGACATGGGCGCAAAAGACTTCCAGACAAAAGCACGCGAAGGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458 6	65 A G ---	---	---	CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGTAACTTAACCCTCAGGCTGCTCCTACTCA/AV GTTGGTTTGTAGCTCCTCACTCGCACACAGGAAGCTTGAATTTGGAGGCTCCAGTCACTCTCCA GAGGGGAACCTTCAAAGAGGATCCAAACAGTGAAGCAGATCATGGGGCAAAAGTC/AVG/CTATGG GGCAGACTGAGGTTGAACACACACAAAGCACTCCAAGCTGGGCCAATCCCAACCGCTGGTGAAGCCGC ACAGACGGAGTAGCCAT
EST36745 3	56 A G ---	---	---	TGTGACCATACCAAACCTATGCAATAAAAGAAAAAATCCTCACTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAGTTCATAGCATTTTGGGA ATTTATGGTTTGAATAAATAACAAAATGTGTATCTCCTGAGACACATTTATAAACATTTCTGGTATG T/ATTTATGTGAGTGGTCTCTAGTGGCCAAT
STS- R37410c	201 A T ---	---	---	TGTGACCATACCAAACCTATGCAATAAAAGAAAAAATCCTCACTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAGTTCATAGCATTTTGGGA ATTTATGTGTGAATAAATAACAAAATGTGTATCTCCTGAGACACATTTATAAACATTTCTGGT ATGTATATTGTGAGTGGTCTCTAGTGGCCAAT
STS- R37410b	139 G T ---	---	---	TGTGACCATACCAAACCTATGCAATAAAAGAAAAAATCCTCA/CTTTAAAAAACAACAA AAAAACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAGTTCATAGCATTTT GGAAATTTATGGTTTGAATAAATAACAAAATGTGTATCTCCTGAGACACATTTATAAACATTTCTGGT ATGTATATTGTGAGTGGTCTCTAGTGGCCAAT
STS- R37410a	48 C T ---	---	---	TATCGTGGGAAGTTCCAACTCATCTATGCTGCTTTTCTACTTGCTAATATTGGATGCTTCTTGCCA GGCTC/CTTTAAATTGTGCTGAACCTGGGAAGAAACCTTCTACTCTCCACAAACCTGAA
STS- R42778	74 C T ---	---	---	CAATCTGAAGAGATGCATAGCGGATTGGTGGCTTTCAGCAGCTGTGGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTATGGGTTTCTCCCGGGATGGTGAATAATGTTCCGGACCTAGATA/CTGTTGACGA AGGTAGCACGACACTGTGAGTGCACTAA
UTR- 04350	125 C G ---	---	---	GAAATAAACTAAACTGCAAGCAAAATCACTGTTTAATAAGAAATGTTCTTCTGTTT/CJGACAGTTG AAGTGGGTGTGAGATGGGCATAGCAATGAACAGTGGGAGCCAATGAGGTCTCAGAATGCGGGCAAA CTCCTCTGIGAAAATGTAT
sISG1026 6	55 T C ---	---	---	GTATAATTCAGCATAAGCCAAAGCCCTTTTAAATAACCAATACTATCATTTTATGAAATCTTTTACA AGA/TG/AAGCACAGTAGTACAATAATTAAGCACTCAAGTCTCCATTTAAGAGTTGACTATC
sISG1028 2	70 T G ---	---	---	CACTTTAGATATGAGGAAAATGGTTTAAATGGACACAAAAGAGTCAAGCCAGTTGGAAACCAACATAG TTTCATACCACGTTGAAACCATGTGTTTGTATGCAAAATAACAGCAAAATAATTTTTCACCTC/ATTTG TCAATGCCAATGCATTGAAAGGCCAGAAAATGAGAAAAGGATAACAACTTTTGTATAAAAAGGTA AGAATTCCTGTGTG
sISG1031 0	128 C A ---	---	---	

[illegible]

stSG1847 b	95 G A ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACCCCTAAATGAAAGAAATTT AGAGGTTAAATAAACAAGTGAGAGACC[G/A]TTTACTTACATCAGTTCGGTTTATAGACATTTGAA TCATATCTGAATGACTGACTTGTTCCAAATGTGAAACCAAAATTAATAAATTAACCTGATCACTGTGCT TCAAACACAACCTG
stSG1847 a	49 C A ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTAC[C/A]CTAAATGAAAGA ATTTAGAGGTTAAATAAACAAGTGAGAGACCCTTTACTTACATCAGTTCGGTTTATAGACATTTGA ATCATATCTGAATGACTGACTTGTTCCAAATGTGAAACCAAAATTAATAAATTAACCTGATCACTGTGC TTCAAACACAACCTG
stSG1897 a	83 A G ---	---	CTTAATGCCCTTCTCTCTCTCTGCACAGGAGACACAGATGGGTAACATAGAGGCATGGGAAGTGG AGGAGGACACAGGACTT[A/G]GCCCAACCACTTCTCTCCCGGTCICCCCAAGATGACT
stSG2022 a	86 T C ---	---	TGCTTGAGGTTTCAAAATCTGAGATATCTATGGCAAGTTTATAAAAAGTACATTTGATCAAGGTACAA TTTTTAACATTAAATACAT[C/A]TTCCATAATCTCATCTATTTAACATTAAACACAGGCCCTTTGTGT TGTTATTTTCTCCCTACAATATTCCTGACTCTGTAGGACAGTGGGCTCAGTTGGGGGTTGAC T
stSG2076	104 C G ---	---	AAACGTTGTCCTCCAAATTTGTTTCAGTTTCAACAAGTATAAAATAAGACTTCTGAAAAAAGTTTACA ATTAGTTATAAACACTTAAGAAATATTTTGACATT[C/G]ACATCAGTGGGGCATTTT
stSG2108 c	71 A G ---	---	TTGAGCAACAATGATTGCGGAATTGGGCAGCTCCAAACCAAAATGATTGAGGGCTCCACAGAGA GAGC[A/G]TAAGGGGAAGACTTTTATAGGACAACCTGTAGAAGTAAAGCAAGCAGCGTTTGATTG GTTACAGTTACACAGTTGTCTTATTGTTGCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2108 a	49 T C ---	---	TTGAGCAACAATGATTGCGGAATTGGGCAGCTCCAAACCAAAATGATT[C/G]GAGGGGCTCCACAG AGAGAGCATAAGGGGAAGACTTTTATAGGACAACCTGTAGAAGTAAAGCAAGCAGCGTTTGATTG GTTACAGTTACACAGTTGTCTTATTGTTGCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2141 b	173 A G ---	---	TTATTCAGGGGACAAGCTGCACAAAGGAATGTTCTCTCTATTTATTTAAACAAATGACTGCGTGTAC TGAATCTGACTGTGTGAAATAATCTCAGAATGGCAGCACCCTGCGCATGGCGATGGTGCAGGTGGGT GCAGTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAG[A/G]AAGTCCCTATTATTATTTAAGGC AGTTTCAGAGCACTGGCATCTTGTTGCTCTG
stSG2141 a	113 C T ---	---	TTATTCAGGGGACAAGCTGCACAAAGGAATGTTCTCTCTATTTATTTAAACAAATGACTGCGTGTAC TGAATCTGACTGTGTGAAATAATCTCAGAATGGCAGCACCCTGCGCATGGCGATGGTGCAGGTGGT GGTGCAGTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAGTCCCTATTATTATTTAAGGC AGTTTCAGAGCACTGGCATCTTGTTGCTCTG

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stSG2148	50	A G ---				TGGAAACAACCGGCTATAGTCTGAGTCATATTTTATAGACCGTGATTTTC[AG]JAAAGAAACAATAA ATGTGGATTAGAAAGGAAACATCCATTACTGTATTTTCGATACCTTGTGATGTTCCACAGACGAGCTC ATCAC
stSG2175	68	C T ---				CTCAATGAGGACTCCATCAGCCAAAGCGGTTTATATGGCAGATGAGCTGCTACAAATCTGTTGTGCT [C/]GCCGCGTACTAGCTAATGCTACCGGGTTGGAGCGCACACCGAGCCAGCCACCTTTTCCAT ACCTGGCAGAGGGAAGGAGTGGAAGGAACA
stSG2189	41	C T ---				CAAGTGGTGAAGCTGGGATTGAGCCTGATATTCACACTA[C/]TCTACATTCCCTCCAGTATAATA GGAACATCATCGCTAACTTTGAGCACTTAGTGTTCTGAGTACTTCGTATAGGTTATCTCAATCCTACTC CAGCTTTGCCAAC
stSG2200	49	T C ---				TGTTGATGACCATAGAGGATGCAAAGCTCCGGGCTGGTTCTGTATGATG[T/]CJTATATTTATGTAT AATGCTTAACCTGATGATACCCAAACATATTACTAGCCTTATAGATGAGGATGGATGGCAGCTTGGCTG GTCAAT
stSG2243	85	G T ---				CATTTCTGCCTCCTGCTTCCAGTACTACCCCGTCCAGCAACTGCCTCTCGTATAAATAAGTATCAA GATGGTCAGTAGAAAG[G/]TAGAGCATCTCTCAGCCCTGGAAGACAGTGTGGGAGCTTCAGCT
stSG2257	65	A C ---				TCAGTGATTGTAGGAGCTGGCTAAGTCATGCTAAACTCTGTGAGGCAAGGCTATCAGAAGGGCAG[A/ C/]GTGCAGGAACCTCGCCAAAGCACTGGGCTGCTCTCAGGCAGAAATTTCTTCCT
stSG2306	67	A G ---				GTCATCAGCGTAGAGGTCACTGGTATAAACAACACAGTACTATATGATTTTGGGAACATATTTTACA [A/G]TATGCTCCCATTTGGGTTTCCAAACTGATACACCATGAGGTGAACACTTTTCACTGTTTCACAG TTCTCCAGAGA
stSG2334	70	T G ---				GAAACTACCCACAGCATGTTAAAGAAGAGAGATGAAAGAAAAAATCCCCGCAAAAAACA AAAA[T/]GTGCAGTGGAGGGGCTGTGGGAGGGGTGAATG
stSG2339	63	T C ---				AGAGCAGAATGGTGAATCAACAAGACCTCAAATTTGCTTGAAGTGCAGAAAGTAACTGCTGTCAC[T/]C] GTTCTCAGAGTCACCATTAACGGTGACTG[T/]GCTATTTCTGGCTGTGCTTCTCTATTCATCA
stSG2465	76	C T ---				CAAGACTAAGAAGCCGACCCGAGTGGTCCCACTCAAAAAAGAGATTTCTGATTCTACCTCAAAATG CAGAAACCA[C/]T]TACAGATTAAAGAGAAACACACACACACTTTGAGAAACTCGCCCTTCCTC ATCTTCAAAGTGTGGGTATGCA
stSG2549	140	T C ---				TTGCAGGCTTGTATTCACAAATAACAAAGTCATGTATAGAGAATGTGAAATGATCTTGAAAAACCAA GATATATAAAATATTGAAGTCATTTATGCCCTTTTGATGACTGGGTTAAATATGCAAAAGCAGCTAAAG GAATAT[T/]C]TACACCACCCACCCCTTTTAACT
stSG2577						AATTGCCAAATGGAAAATTTCCAGAGGATTTTATAGACCAACTTTGCCCTGTGCTATCCCAAGTTGGT CCCAATATAGGCCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAGCA[T/]G]GAACAATC CCGGCCCCAGATTAAATTAT
b	123	T G ---				

stSG2577 a	121	C T	---			AATTGCCAAATGGAAAATCCAGAGGATTTTAGACCAACTTTGCCCTGTGTCATCCAGTTGGT CCCAATATAGGCCTCTGCAAGAAAGAGATCAATGCCGAACCGAAGCTGTGAAGAG[C/T]ATGAACAATC CCGGCCAGATTAAATTAT
stSG2700	58	G A	---			ATCTCTGACTGCTTTAGTGGGAAAGGAATCAATTAATTAAGAACTGTCCGGCCCG[G/A]AGTCAC TCAGCGTTGGGGAAATAAACCACTGTCCAGAGAGAGGAAGGCTACTTGAGCCGGACACCA
stSG2724 b	101	T G	---			AAACAAGCTTTGTCAATTTCCACTACATTTTGTGTGCTTTATTAATATTGCAAAATGCTATAAT TTAATACTTATATCCAAATGCTTGCAATAATCA[T/G]TTTTTTTAAATCCTGGGGTGTGAAAGAAC
stSG2776 a	65	G A	---			GTGCCGATCTTTACTTTCCAGAAAAGGGGTAATAAACCCTGTAGAAAGTCTCGAATATGC[G/ AJATTTGGCCCTTTGGAGTTAGGCCAGGAACCTCAACAAGGGACACTGCTGGCCCAACCACAAAA ATATCCACTAATCCCGAATATAGTAACCCGTCTTGTCGAATG
stSG2791 b	109	G T	---			AAGGAAAGGTGGAGGGAAGAAAGGGAAGAAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTTC TATTATACCTCTGAACGTAACCTAGCAATTTTAATAAATAT[T/G]GGGTCCACTTAAATCTATTA AAGCAGAAAGGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAACCAATCAG
stSG2791 a	100	A G	---			AAGGAAAGGTGGAGGGAAGAAAGGGAAGAAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTTC TATTATACCTCTGAACGTAACCTAGCAATTTTAATAAATAT[T/G]GGGTCCACTTAAATCTATTA AAGCAGAAAGGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAACCAATCAG
stSG2826	85	C T	---			CCGCAATTTCAACACACATCTATGAAAACCTAAGGGTGGATCATGTACAAACACAAAAACAAGC TCCCTCCCTCCAAAACAA[C/T]GAACAAAATAAAGAAAGAAACCCATGAAATGCCCAGGTTTA ATTTTTTTCC
stSG2850	88	G A	---			ATGGGTGCATTGTAAAAGGCAAAATTAATACITTTTCAGGCAGGGGCTGGCAATTTAATGAGCTGA TGTGTCCTCAAGGGAGACGGCC[G/A]GGCTCACACATCCCATCAATACTCTCTCCCAT
stSG3031	71	T C	---			ATACTACGGGGGCTGAAGGGCAATGTGAAGAGTGAAGTCAAGTCCCTGGCATTTTCTGTGGTGTGAGC AA[T/G]GCCCCCTTATTTTAAATGATCCAGACATCTGGGCAGCATAGCT
stSG3058	81	G A	---			GTCCCAACTCTCTCTCTTAGAGAAAACCTGTGATTACCTCAACTTGAATAIGAAAACGTGATTG AAAAAGTCAAAAC[G/A]TGAAGAAGCATCAAGCCAAAAGGCAAAACTGGCTGAGGC
stSG3092	94	T G	---			CAGCATCTCCAGAACATTCCTAGAACTGAACCATTCCTGTCACTATTGAAAAACAAGCCAAAGTTC CAAAATCCAAAATAATAATGAACGTGC[T/G]GATAAACATTCCTTCTTATGGTCCAGCCCCCTACTTT AGTT
stSG3230	95	A G	---			AAGAAGTACTTTGGTAGCTATTTAAATAAGAGGGGGGTGGGAATGAATGCGAGATACGAGCACCTG CATCTTTTAGTCAATTGTCAGTGGAGTC[A/G]GTGGGGTGTAAAGTGTCTGAACTGAAGTAG
stSG3245	160	G C	---			ACATCTCATACCCAGTAAGATGCAAGAAAGGAATATCTGAGAGCAAGCAGCCCTGCTCCAGGGGCCC CAGGTATGTAGAGGCCAGTGGGGGTGGCCACTTGGTGTCTTACCACCCCTGCCATCCAGTCTG GCCCAAGTACCTACCTGGGAGGT[G/C]GTACTTGGCTTAAGTACTTCATGCTTTAT

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stSG3265	42 T C ---			AGGTGAAATGAGTTACTAAATGTAGCATTTATTTATAAGGAA[TC]GCATTGTGTAATAGTTTCTCAG TTTTCAATTATGGAAGATGATGATTTTCAGCCACATTCAGTGTATGTTTCTAAATAACACAATCGAC AGGACTGTCTGTTTCAGTACAATGGAGGACAGCTTTTCAGGGCAATGGGATTTCTTGATAATGCTAA ATCTGCTTGTGAGCTGAATTTCTGGGCTTTATGTGGCAGTGTGGTAAAAA
stSG3269 b	141 C T ---			TGTACTACTGTGTCATCCTATCCATTCCCTCCCTGAGCCTGGAGCTGCTTCCAAAGGGAGACTAGG AGTGAAGGGAGGAGTCCCTCCCAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCATGCTAAA GCATGA[CT]TGTAGATCCCAAGTCCCTGACACATTTTCTTCTAAGAAACT
stSG3269 a	24 A G ---			TGTACTACTGTGTCATCCTATCC[AG]TTCCCTTCCCTGAGCCTGGAGCTGCTTCCAAAGGGAGACT AGGAGTGAAGGGAGGAGTCCCTCCCAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCATGCT AAAGCATGACTGTAGATCCCAAGTCCCTGACACATTTTCTTCTAAGAAACT
stSG3284	130 C T ---			TTAACTCAAGAACTTTCAGTTACAGGAAGATTATCTAATATTAAATGACTAAATTACAAAAAGC ATAAAATGTTTGAAGCCATTTTAAAGTTGTTTGAATCCATATTAGCAGCTCAGACTTCCCCA[CT] TCCCTAACTTTTGTTAATTGCTGTAATGGGACATTTGTTGTTTGATCTACCC
stSG3292	99 A T ---			GTCTCAAGTGAATCTGTAATACATTTTAAAGTCTGACTTCAATCGGTACATGAGGCTTAGACATA CACATCATTTGGACAAGTGACTTAAATATCTAA[AT]TACAAATCAATAGCATTTTCTTAACCTTCAA TAAATGTCATATCTTTAGCTCTCACT[CA]CCAGTGTATCCATTTTCCCGAGCCGTAGAGCTTTTCTG TTTCTGTAGATTTGCCCTGCTCGGACATTTGATAATAATGGAGTTGCTGTATCATGTTGAGCTTCTCTC ACCTAGCATGATGTTTCAAGACACATCCATGCTGTAGCATGCGTCAGTCTTCATTTCTTTAA
stSG3323	26 C A ---			GATCCCCAGTATTATTTCTAATTTGAACCTGTTTGTGGAAATAAAAAATCTGAGGACCCTCAGAG GG[CT]ATAAGGGAACCCCTTTTGTCTTAGTTCATAAGGACTTTCT
stSG3369	69 C T ---			CAAGACTGTAAGAACGTAGGCCCTTGTGAGAGTGAAGGAAGGATGCTCGAATTTGCCAGGACTCAGG CTTCAGCTTCACAATCCCGAGGAAAGGAATGACATTTCCAACTGTCACCTTTGTAGC[GT]CTGGGT CAAAGTCTAAAGAGGACAAATAAATAGAGACT
stSG3398	125 G T ---			TCCTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCACG[AG]CTCACTGTAGCCTGGACCTCC TGGGTTCAAGTGATCCTTCCACCTCAGCCAACTGAGTAGCTGGCCTGCGAGGACAAGTCACCATGCCTA CCTAAGTTTTGTAGAGACAG
stSG3416 a	43 A G ---			GTAAGACAAAGGTTTGCATGTTGACCAGGCTGGTCTTGAATCCTTGGCTTCAAGCGACCGTACCA CCTTGGCCTCCCAAGTTGCTGATATTACAGGTGTAGCCACTGCCCCCGCGACTTTTAAACTGAAT GTTGAAAATCATCTGCTCTTTGCTGGTAAACACTGA[TA]CAAGTTGCTTAACCTTTGTGAAACCCAC TTTCTTATCTGTAACAAAATGGACAAACAGAACTTTTCTCTTCTCTCTC
stSG3424	173 T A ---			GTTCATGTTAAAGATTAGAAAGCTGTGGATGTGAGGGGTCAGGTGATGGAGGCGCTCACAGA ATGAGTGGCAGAGAGGGCCCTT[AGAAATAGCTTACTCTGTTTCTCTATC
stSG3436	88 T A ---			

stSG3463	103 C T	---	---	GATACAGAAGATAGTGGTATGGATGGATAGTATGAAGGACAAAATAATACAAATATATTTATTG AAATAACAAAAATGCATACACAGCTCAATGGGTAC[C]/TJGGAAACAACTTGCTTGACTATATTA CTGA
stSG3491	71 G A	---	---	CAAGATACCTCATTGTCTAAGTAGTGCAGTGTGGCAAAATATTTCTACGAACAAGGACGATTTG AAGA[G/A]GTGGAATTACTGTGCAAGGAGTACTTTACCTCCAAATAGCCTGCAATTTAGCAGTCTGA ACAACTCTCTAATCTTTACTGGCACCTGTGGATTTCTATTAAACCTCAATTTATCTATCTTTCTGTGATG ACAGAAAAATAAGTTAAC
stSG3523	33 C T	---	---	TAGCCATCTTACTCTAGTCTTTTGGGTTT[C]/TGCCATATATGTGTACAAAACACACACACACC CCTAATCTCTCAATGCTCTTGGCATAAGTTTATCTCTTACTGGTCTC
stSG3536	213 A G	---	---	AGTACAAACACAGATTTAAAGAGCTCAGCAGTATTGACACGCTGGAAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCCTACCTACACAGCTGCTACAAAAACCAAAATACAGAATGGCTTC TGTGATCTGGCCTTGTGAAACGCATCTCACGTGCTATTCTATTGTTTATAATTGTTAAATGAGCTTG TGCACCATTAG[A/G]TCCTGCTGGGTGTTCTCAGTCCCTTGCCATGAAGTATG
stSG3583	112 G A	---	---	GAAAAGCTTAACATACGATCCATGTGCAACCCCAACAGGATCTACGAACCTCTGGCATGATCCA CATCGCTACACATACCATGCTGGAAGTGCACATCCACACAGGCAC[G/A]TAACATACACAGTACTGT CTAGTTATCAACACCTAC
stSG3586	60 G C	---	---	CCTAGTAACATAGTAGACCTCGTCTCTACTAAAAATTTAAAAATCAGGTGTGGTGT[G/C]ACG CCTGTAGTCCCTACTTGGAGGCTGAAGTAGGAGACTGCTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGCGCCATTGCACCTCCAGCTT[GAGACTGTTTCAAAA
stSG3589	101 T C	---	---	ATATAGTGTGGTAGCATTATAAACTCCTTTAAAAAGCAATCTGGCCATATCAAAAGGCAAAAAAGT GTATATACCCCTGGCACAAAAACCCCAATGA[T/C]CCTATTTCCAAAGATGTATCCAGATGAAA GTATCCAACAACAAAAAGCTATATACAC
stSG3590	70 A T	---	---	GAGAGATGAGCTATTATCTTTTACTTAAAGAAGTGAAGAAATGATCTTCTGTTCTAAAAAAA AA[A]/TTTCTCIGATGCTCTTGACCCGTGAGGAACACATTCAGTTTCTACACT
stSG3619	78 A C	---	---	CAGTGAGACTTCTCATTTTATAGCAAAATACATTTTTCAGCTTAAATTTCTTGAATTCATATACGCT TCTGTCAATTT[A/C]AACAACTTCCAGAGAAAACTGGGCTCTATATATTTAAG
stSG3644	40 T C	---	---	ACATATGTAAGTCCATTAGTAGCCATATTTAGGATGAGAT[C/G]GATTGAGAGGCATGAACCAAGG ATCGGTAATAATCATTATGAATAATAAGTTATCTGGGGAAACGGCCATTTGTCCCAACATTTACTAA GTGCCTACTA
stSG3646	70 G A	---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATAATATGTCTTACT GGT[G/A]ATATAACTTTGATACCTTGGTTAAGATGGTGTCTGCTAAATTTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA

stSG3646 b	55 A G ---			CTCATAATTAGATTGAGATTGTGCAATTTGGCAAGAATATATGATGATAACAATAA/GJATGTCCTT ACTGGTGATATTAACTTTGATACCTTGTTAAGATGGTGCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCCTTTTGTA
stSG3646 a	43 A T ---			CTCATAATTAGATTGAGATTGTGCAATTTGGCAAGAATATATG/A/TJTGATAACAATAATATGTCCTT ACTGGTGATATTAACTTTGATACCTTGTTAAGATGGTGCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCCTTTTGTA
stSG3693 b	85 A C ---			ATTGTTTCCTGAACATTCCTGGTGCTCCCTCTGAAAGCCGATGACCATCCAAACCCTGGACTCACCT GAAATATCCTACGAGGC/A/CJTCGCCCTCCGAGACTGACGATTATTAAACCACCCACACGGAAAAAGG
stSG3693 a	30 C T ---			ATTGTTTCCTGAACATTCCTGGTGCTCC/C/JTCTGAAAGCCGATGACCATCCAAACCCTGGACTCA CCTGAAATATCCTACGAGGCATCGCCCTCCGAGACTGACGATTATTAAACCACCCACACGGAAAAAGG
stSG3698 b	145 G A --			TCCTGCCCTTTGTGTACCCCTAGAGAGATGGCACCCAAATCCCCAGGGTTGCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGGAGCTCCCAAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAGTCT TTATTGGG/G/AJAGAAATACCCACCCACTTCCCTCACTGCAGA
stSG3698 a	51 C G ---			TCCTGCCCTTTGTGTACCCCTAGAGAGATGGCACCCAAATCCCCAGGGTTG/C/GJTCTGACTTCCA CCATTCACTGACTTTTATTGCCAGAGGAGCTCCCAAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTA AGTCTTTATTGGGAGAAATACCCACCCACTTCCCTCACTGCAGA
stSG3724	107 C T ---			ACCAGCCTCATGTGCAGAGGGTGCTCCTGCTGGATCCCAACTGGAGCCATCCCTGGGCCCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGTCTCAGTGATGTGAAG/C/TAACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTGCT
stSG3725	104 G A ---			GCCAAACAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTAA ATCAATATATATTACCAGCCAAACAGCAACACAGCCC/G/AJAGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAATAACGGCACATTTA
stSG3751	128 G A ---			CGGAAGAAAGAAACACAAAATCCACAGGAACAATCTATGGTTCACTACCTTTTAGAAAAGATGATTTTG AGGGCTTCAGTATTTAAAGGGGAAAGCAGGCTGGAGGGGAAAGAGAGAGGATATGGTCCC/G/AJTT GCTGACTCCATGTGTTGCAAGAG
stSG3787	49 T A ---			TTCTGTGCAAAAGAAATCCACATCATTTGTTGGTAGCAGAGGATCTCTTATTA/JAAAGTTCCCTAAGA CACTGAGGGCATAAAACCAACAAAATAAAATAAGGAGTGATAGGCTAAAGCAGTATCTTCCCCT
stSG3880 b	115 G C ---			GACAAGAGGGGAAGAGATGCGCCAGAGACAGGGCTGGGGCAGCTGGGGTCCCTGAGTGCAGGGCGC CACCACACGTCTGTGGTGCAAGGCCCTCTCTGGGGAGCAGGTCTA/G/CJGGCACGGAGGATGCAG GGCTGGGAGGGGACCCACCTCGGGGACCCAAAAGAGTCCATTCTGCCCC

stSG3880 a	36 G C ---	---	GAC AAGAGGGAAGAGATGCGCCAGAGACCAGGGCTG/CJGGCAGCTGGGGTCCCTGAGTGCACGG CGCCACACACAGTCTGTGGGTCAAGGCCCTCTCTGGGGAGCAGGCTAGGGCAGGAGGATGCAG GGCTGGAGGGGACCCACCTCGGGGACCCAAAGGAGTCCATTTCTGCCCT
stSG3895	44 A G ---	---	AATCAGCCATTGTACACATTGCAGCTATGTATTGTTAGTGTG/A/GJTTTTTTTCCATTAACTAA TACATGCCCTCATAGATATATTCAATTAGTGTATCACCATGGGAACAAGATGCTGATTCGTCAACTG AAAAT
stSG3902	104 T C ---	---	TCTGTTGAGACTGGAGAGACCAGGTACCAAGCACCGACTCTGGTGGGAACCTGGCTTCCTGATAACA TCATCTATTTACCTAAATGTGAACCTGCTTTCTTTTC/JCJACGCTCAATAGCTTAACATCTAATTC ATGTTGCTCCCTTTGCTGGACAAT
stSG3935	50 G A ---	---	GGGTGCTGACGGACAGGCACACCCAGCAGTTTCAACAAGCAATTTGTCC/G/AJTAGTGTGCAGGC TCCTCCCCAGTTTCCACAGGCTGAGTACATATGGGGTCACAACTTCCTGGACGT
stSG40	25 A G ---	---	GAGGAAGAGGTTGAAGAAGTGTGA/JGJAAATATATTTAAGATTTCTTTGGGGAGAAATCTCGTGC CCAAACCTGGTGATGGATCCCTTACTATTTAGATAAGGAACAAAATAAACCCCTTGTGTATGTATCA CCCAA
stSG4009	32 A G ---	---	GTGTGGGCTGTCTGATGATGAATGGCGCGCTC/A/GJACTCTTTACGGTCTTACACTTTTATGCTCCT ATGAATCTCTGATGGCTTTAAGGGCTGAACCATATCTGAAGGTTTCCACACTGCTTACA
stSG4033	123 T C ---	---	AGAAAGCTTTGGGACAATGGCAGTGCCTTTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT TGAACCTACAGTGCAGTAACCAAAAGAACCTAATGTTTCAAGCATAAAGGTACTTTT/CJGTGAAC AGGTGGGCAACAC
stSG4038 a	29 G A ---	---	GCTGAGAGCACGTGTACAGCCACGCTGTG/AJCGCAGGCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCTCAGTCAGGAGGTTTCAGGCTCCCGGAGAGCACCTGAGGGTTCCATCACT
stSG406	53 T C ---	---	ACTGTGGTTCAACAGTATTGCGTTGTCAGACTAGGAAGCTAAACGAACAAAAT/CJGGTTTTAGTT TTGCTGAAGACTGGCCCTTATTAATGGACAGCTTTCCCTAACAGAGATTATTAACCTTTATCAGGTGTT AACATCTGTTTCAGGAACAIGGCA
stSG4095 b	55 G T ---	---	ATCTGGGCTGAATTAGTCAAGCAGGTCAAGTACTATTGCTGCTAGATGTATTAG/GTJATAAAAAA GTTTGTCTGTGTAATACITTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAAATCAAG CCITTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
stSG4095 a	27 A C ---	---	ATCTGGGCTGAATTAGTCAAGCAGGTG/CJGATACTATTGCTGCTAGATGTATTAGGATAAAAAA GTTTGTCTGTGTAATACITTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAAATCAAG CCITTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
stSG4120	65 G A ---	---	TGCATGTTCCACATCTTTTCATAACAGCAAAATGTATAATAAAGCTTACGTACTTATGGATAATCAC/G/ AJCTTTTCCCTCAGAGAGCCCCACAGTTAAACACGTTCCAGCACACCATTAATCCACCGAGCT

stSG4128	54 A G ---	---	CTTGGCAGATAAGGGACTCGTTTGCAGATATGACTTTCCTTTGTGTACATTTCT[AG]TATATTATTT TACTTCTCTGAAATGCCACATAATTTGCAATAAATGATTCACTCCTTAGCTCCAAAAGCAAGTCC TTTATCAAAATGCAAAATGTTCCAGAGGG
stSG4209 b	128 G A ---	---	CACGAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAAACATCCACATGGCACAAAGC AGGCCGGCCACTCCAGGCAACGAAGCCACCCCGAACCTTGCAGAGGCGCGACTCCCTC[G/A]GC AGGGGACCAACGGAGCGACAGGTGCTTTGATGCTCCGAAGAGCTGAGCTCCATTCCA
stSG4209 a	65 G A ---	---	CACGAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAAACATCCACATGGCACAA[G /A]CAGGGCCGGCCACTCCAGGCAACGAAGCCACCCCGAACCTTGCAGAGGCGCGACTCCCTCGGC AGGGGACCAACGGAGCGACAGGTGCTTTGATGCTCCGAAGAGCTGAGCTCCATTCCA
stSG4254 b	31 G A ---	---	CATTACCCAGAACGCCATGGAGGACCAAGAGC[G/A]CCACGGCCGGGACTCCCGGATGGCTGGGGGG GCTATGGCTCTGACAAGAGGATGAGCGAGGGCGGGGCTGCCTCTCCCCCAGGGGCAGACGTGAC TGGGGGACCATGGCCGAAGAGAGGATGACCGGTCAATG
stSG4301	81 T G ---	---	TGCAACAGCTCTGAGAGGAAATCCTTTGGCAGATCAAAAGAGAGGGTAGTGGTCCACACATTTCCAT TTAAGCAATAAATTT[G]AGCTTCTGAGTAGTGTTCCTCCAGTTTACCCCAACATTTTG
stSG4331 b	71 T G ---	---	CTCACAAAGGCCAACACAGAAAAAGATACAAATACATTCACAGCTAATATTAGTTTTATGACAC AGAGT[G/TTT]TCAACAAGTTTAAAGTGCACCTGAAGAGCATGTAAAAAGTTTAAAGTTATCACTT GGAGAGCAGATTCTTGGCCTCGCCCTTGATTTCTGTTTGGGGGTGTC
stSG4340	76 G A ---	---	TTTTGCAACAACATGGATGGACCTGGAGGCCATTAAGTGAAGTAATGATACAGAAAGTCAAAAACC ACATGTTCTC[G/A]TAAGTGGAGATAACAATGTGTACACCTGGACGTGGAGAGCAGAA
stSG4361 b	109 A C ---	---	TTCCCAACCATTTGAGTGACAGAGC[T/C]CAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATTAGG AAGTTCTTGGAAATTTCCATAAGGGATAACTGCATCTTTTGACCTTCACAACCTAGAAACGACTC AGCGACTTTTCTGTGAGCAAAATGTCGAGG
stSG4361 a	24 T C ---	---	TTCCCAACCATTTGAGTGACAGAGC[T/C]CAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATTAGG CACAAGTTCTTGGAAATTTCCATAAGGGATAACTGCATCTTTTGACCTTCACAACCTAGAAACGACTC AGCGACTTTTCTGTGAGCAAAATGTCGAGG
stSG4376	73 A G ---	---	TTTCACTGCTACTGGTTTCGGTGTCTGAGTCTCAAACTCTGCTTTGCAAGTGTCTCTCCAAGGGGAG AACAGT[G/CT]GGAACCTGGGCTCTGCAAGAGGCCATCTTTCCAAAGCCATTTCTTCAGCTGC
stSG4381	50 T C ---	---	GAAGGCCACAACACTCCATAGCCAGAGAATGACAACATACGATTTCTTTT[C/TT]CAGTCTTTGATG ATCCACAGTAGTGTCTGTCCATGTACAAGTGTCTGTCCAGAACCCCATTAATTCATGCC
stSG4410	79 A G ---	---	ACCAATGGTTCTGCTATGTGCATCCGATATTTTGGCCGATCTGAAATACTGCAAGGGCTTAACCAT TCAAAACACCGC[G/TT]GACAACGAACCCAGTGGACTGTGAAACTCAGGCTGCAGGGGGTGGCTTGT CAGCTGGGT

stSG443	65	C T	---	AGCAGATCAGTCAGCCACCTTGCTCTCTCTTTAGGGAGAGGCTAGGCAGTGAACACATCA/C/
stSG4430				TJGTATGCAATGAGAAATAACCAACTGGTAGGATGGGGAGGGAGGCGAGGGAATAGGCAC
a	54	A G	---	AAATGGAATTCATCTCTGGCTGCTCTCAGGTC
stSG4448	99	G A	---	ATGCACATTAAATGAATGGCCTAACTACTGGGAACCTTAGTAGTTCCTATAAGGTJ/A/JATTAACATA
				GGTAGGATCCAGTTCCTATGACAGGCTGCTGAAGGAACAGATATAGGCATCAAGAGGGCCATTTT
				CCTCCCTCCCTTCCCTTCCCTTCCAGTCTTTCCATACTGTTCCCTCCCGCCCCACCCAGGCTCT
				CGCCTAGCCCTGCCCTCTGGGTCACCTGC/G/JTGGGTTAGGCCCCCCAAAAA
stSG4449	92	T C	---	ATTAGCCATTCACTTGCACAATTCGCTTTACTGTAACAGAGTACTGTACTGATGATGTTTACAAT
				TAACTTTGGACAACCTTAAAACCTTA/J/CJTAGTGACATTGCTGTCTAATAATCAAATACTTCATCATA
				GGCTGAACATAATTATTAAGAGCAAAAGTTACCCCTCCC
stSG4467	42	C A	---	CAGACATGAGGGATGGCCCTGTCTCTCTGGGACAGAGCCCTCA/JAGATGATGTCCATGTTTTGTGT
				GAATGAAACTCAAACACTCTTCAGTTTTTAGAGTCATTTTCTGGTATCGAGCGACACACCGGAG
				CACACCTGCTTCCAAGGCTGCTGCCCTCTCGCACACAGT
stSG4475	21	A C	---	ACATGTCACTTCTGACCAGGJ/A/JATTAATAATGTTTATTTAGAAGAAATGAGTTGAAGTGAGCGGA
				TTAAGAGACACAACTGGACTTTTGTTTCTTTACTGTAGCACCCAGGTTTCATG
stSG4477	32	A G	---	GTAACATTCCTGGGGTGGGGTGAGACAACA/JA/JATGAACCAATAATTAATTACAATTATACATT
				TCAAGGAGACTTTTAATCTAGGTTAATGTGAACCGCAGCCATCAATGGTTGTGAGGAAAAGGGAGA
				TGAAGTCTGCTCTGGGCAACGTTTGGCCTCATTGCAGTCAGACTTGGC
stSG4531	79	C T	---	TGAATCAGAGCTGGGTGGGAGCTCAGCGAGGGAGGCTGGGGGCGCAGATGAGCCGCCGGGA
stSG4550	86	G A	---	CAGCAGGCTCG/C/JGCCACGCTCTGGCGTTGGTAGAAGAGGACATAGGCTGCCCTGGACTCGATCT
				GATTCCTATTGACAGGGGAGACGCTGTTGTCAATCA
stSG4550	85	C G	---	TGCATTAAGGAATGATACGGCATATTTGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT
a				AAAAGAGACAGTGGGCACC/G/AJCAATTTGGAGGGGAAGCGGGGAGGTTTAGAGAAC
stSG4590	47	A G	---	TGCATTAAAGGAATGATACGGCATATTTGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT
				AAAAGAGACAGTGGGCAC/C/GJGCAATTTGGAGGGGAAGCGGGGAGGTTTAGAGAAC
				AATCAGGCACAAGCTCGGGAGAGAAGCCAACAAAGCTCTTCTGCACJ/A/JATGGGAGGGAGACAC
				CATTGAAAAAGGCATCGTTCCTCTTCATGCAAGCGAGGCTGGCTCCACAGGCATGGTCTCCTTG
stSG4623	22	T C	---	AATCTGTATCACCCAGCGCTGGT/CJCAATGTACTAGTAGCTTCCACAGGGATTTTTTATACTATTC
				CTATAAGGTTTTATCATGAATAAAAAGCTCACAACCTCTTTTCAGGCCATTGCAGATTCACATTTATCT
				TAATATTCCTGTTCAAGATGCTCTGGAG
stSG4843	102	A C	---	TAAAAAAAACAACCCCCCAAAAAAACACCCAGAAGTTTTTGTAGTTTTATGTTTTTCAGATTTAAAG
				GTATTTCTTTCTTAGCTTCTAAATTTTGTAGTCA/JATCAGAAAAGTCTTCCCTACTCTCAAGGTGA
				GAAGAAGGA

stSG4850	38 C T	---	GGAACTAAACTGGGAATGCCGAGGAGGAAAGGGGCTC[CTGTGCACTTGCAGGCCACGTCAGGAG AGCCAGCGTGCTGTCCGGGAGGTTTCCAAGGTGCTCCGTGAAGAGCATGGGCAAGTTGTCTGACAC TTGGTGGATTCTTGGGTOCC
stSG4879	86 A G	---	AACTCTGAAGGGGGTGACCTCAACCCAGCCCTTGTTTCTGTGAGGTCTGCTTTTGCAGAATGGCCTG CCCTGGGACTGGAGCAG[AG]CTTGGGTGAGCTCTAGGTGGAGGGTGGTGGAGGGGCATAGAAAT AAACCTTCC
stSG4885	104 G A	---	ACTGGACTGGCTCGCTTGTGAGCCGGCTGAGCGGCTGGGACTCGGGTGAACACCTCGCTCTTCAG AGACTGCCCGCCGGTGACCCAGCACTACGCTCTGCC[GA]GTGGGAAGCAGAAGCAGGACC
stSG4896	112 C T	---	AAACAAATCAACCCAAATCCCAGCAGTCTATGTACAGGGCCACTCCCTGCTCTCTGCCATAGAGA GGTTGGGGGACGCTGAGGAGTGGTGGGGCTGGGCAACCTTTCT[CT]ACGCCACAGGCCCTTGAGG AATTAATTGACTG
stSG4932	22 G A	---	ACAGTGCCGATGGTTACACAAAT[GA]TTGTAATGTATTTAATCCACTTACGAATGATTAATAATGA TAAATCTTATGTTTATTTTCATCACTACCAAAAGGCTGTGGGTGCAGGGGTGCTGGTTCTGTGTCCT
stSG4950	24 A G	---	TCATGACTCCCAGGAAAAGGTC[TA]GTTAGCTTCCCTCCCTACTTTCTCTACATGGTCAAGC ACTGTAATGTAGCTAAGATATAGTAAGGCAATTGCTCCCTACCCCTACACTTCAAGG
stSG4957	136 G A	---	AGATACGGGCAAAACACTGGGATGGCTTCCCTGACAACTTAAGAGGCTCCGAGTTATATCTGGGT GGGAAACACTGACCCAGCCCTTATTCCTCAAGGACTTAGTCATTGGCAAGGAGGATTCATGAGCC CC[GA]GTGACACAGATGGGGCCCTGCTCTATATCAAC
stSG4961	91 C T	---	GAAGTGCTCTGAGGAGGTGTGACTCTCCCTGGCTGACAGGGGAAGGCTTAGCAGAGCTTTGTCTTAG AGGAGTAGATGAAAAGGAAAGTA[CT]AGAGAGGGCATTCAGGCCAAGTCAGCAACACAGACAA
stSG4967	72 A G	---	ACTGGTGCTCTCAGCAGATTCAGGGGTGCTGCAGGGCTGGTTACCAAACTCAGTAGGAGTGCAA GGGT[GA]TACCCCGGAGCTAGACAGCCTGGGTTTGAATCTCAACTTCTCCCTTTCTTGCTGTGC AACCTTG
stSG4997	22 T C	---	CAAAGGAGAGTAGGAGCCCCAA[CT]TTTAAATGGTTTCTCTCCCTCATGCTATTGTATCCAAAA CTATATACAAATTTGTAGCAGTCTCTGTATAGTTATACACATGTTTAGAAGGGAGGGGCAAGAA GGGATAGGGAGAATGGTGATCCAAAAT
stSG6312	37 C T	---	ACAGGTTCTCACACTTTGAGCCCTTAGTGCAAAAACA[CT]TATGCCATGCGGGAATAAAATGCTT ATCCAGTGGAGCGCTCCCTGATGCAATTGAATATTAGGATACTCAAGCAGAAGAC
stSG6345	107 G A	---	GCCTGTGTCGAAGCAAAATCTCCAGGACAGAAAGCAACAGGACAGTAACACACATGTATGACCCCTTA CAAGTGCTTTAAGATTTTAAAAATGTGATGTTTTGTCCAC[GA]ATAGTTCAAGGCAATTAAGAATAT GCAACCCAGAGAAATTTCTGTGAAAACATTTTGCTCTTTGGCCTGGTGTGGACAGAAAGGGTGGCCAA ATGGATTGAGTATGAGCAGACATG

stSG6362	88 G C ---			---	TGTGAAATGTACACTCAGGCTAACAAATACCTATTATTCTCTGGTTAAGAAAGGTTTAGCAGGAGC CTCCAATGAGCACTGTATGTAG/CJAGAAAAAGGAAAGGAGCAGGAGGAGAAACAGATCTGCACAGA AT
stSG8010	62 G T ---			---	CACATCTGTGTTTCTGGAGCAAAAGGGAAACCCACAGAAAGGCCAGGAGTTTGGGTGTGCACCTGG[G/J] GTCCTTCAACTGGGTGGAACCAAACTGAGTCTTGAAGTCTCGCTCCCTGAGGCTGCAGAAGAATAGA TGGCTT
stSG8022	53 G A ---			---	AGCTCTGACTCCCTGTTACGTGACGTGATGTTGGTAGCCTGAAATGGACCAC[G/A]GTGGGAGTTAT TTACACCATGGAACTGGAAACTCTACAAATCAATGCGTTTATTCTTTATTTTTCAGAGGGCAGGTT TATCAGCACACGCTGTATCTCC
stSG8032	67 G C ---			---	TGATTGTTAGGGATAAGTGGGCATTGTGTTTACAAATTAACCTCCAAAGAAATTCAGAAAAATTTGTGTGTT G/CJTGGGAGGCAGGGTAGCAAGATAAAAAAGAGGGAGGACAGCTGGGGTTGGTAAAA
stSG8064 b	46 C A ---			---	AGCTGGCTCTTCCTCTGTCGGTTCGGGAGGCTTCACGTCTCG[C/A]CCGTGGTCCCTGGGTGGCC TGCAGGACCAGGGGTGGGAAACAATGCCAGGGAGAAATTCCTGTACATCAAAACAGGGAACA
stSG8064 a	23 G C ---			---	AGCTGGCTCTTCCTCTGTCGGTTCGGGAGGCTTCACGTCTCGCCGTGGTCCCTGGGTGGCC TGCAGGACCAGGGGTGGGAAACAATGCCAGGGAGAAATTCCTGTACATCAAAACAGGGAACA
stSG8072	59 A G ---			---	CACCATCATCATCGAGTAGGCTGAGGAGCAGGAGGGGTGGGTCTTGCTGTCTTAGGG[G/A]TGGC AGAGGCAGAAGGAAGTCCGAGTATTAGTGGCCGCAATGCAGTTCAAGCCTGTGCTGTTCAAAA
stSG8100	40 A G ---			---	ATACACCCACACACCCCACTCAACCTTGATCAAAATCCCA[G/A]GAGTGTAACATAAGTATAAGAAT ATCATGACTAGTTAAAAGATAGCAAAATACCAATAAGGTACAAGTTCAAGTATTAGTATAACCAAGTAT CTGAGTAACAAATGTCTTGGAAATGGG
stSG8102	138 T C ---			---	AAGGCTCCTTTGAAAGCATGGTTATTGTTCCATTTAACTGTTCTCAGCTATACTGAAGTATGATT GACAAATAAACTTGCATATATTTGAGATGTACAGTGTGATGATACATATGTATACAAATGTGAAA TGA[T/C]TGTCAATAATCAATAATCAATAATTTGGTATATGGTTAGGAATGTGATGGT
stSG8105	110 A G ---			---	CAGTGGTCTCAAACTCCAGCTACACGAGGATGGTCTTGCTTGTTAATACACAGATGACTAGGCC CACCTGCGGAGTTCCCTGTTGGAGTCTAGGCCCTGAGAATATTC[G/J]TTCTAACAAGTTCCCAGGTGA CCCTGAGGCTCTGGACTGGGGAACATGCTTTGAG
stSG8130 b	96 T C ---			---	GTGTGTACATCATTTGGGAATGGAGGGAATAAATGACTGGATGGTCTGCTTTTAAAGTTTCAAATT GACATTCAGACAAGCGGTGCCTGAGCC[T/C]GTGCTGTCTCAGATCTTCACAGCACAGTCC
stSG8130 a	36 C G ---			---	GTGTGTACATCATTTGGGAATGGAGGGAATAAATG[A/C]GTGGATGGTCGCTCTTTTAAAGTTTCA AATTGACATTTCCAGACAAGCGGTGCCTGAGCCCTGTGCTGTCTTCAGATCTTCACAGCACAGTTC
stSG8145	124 T A ---			---	TTGTGGACTTCAAATCTTTCCCTTCAGATTTTAAATGACATTTATGCATGTACATATTTTAAAAATT AGACACATTTTAGAGAACACAATTTGTGAACACAAATCTAAGAAATGAATGAGATGT[T/A]CTGAAA TCTGATTCAAACACTTATCTTAACTGACTCTGTCAATCCCTCTGCTCTGTAAGG

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stSG8145 a	97	C T	---			TTGTGGACTTCAAATCTTTCTCAGATTTTAAATGACATTATGCATGTACATATTTTAAATTT AGACACATTTTAGAGAACACAAATGTGAAC/C/JACAAATCTAAGAAATGAATGAGATGTTCTGA TCTGATTCAAACACTTATCTTAAACTGACTTCTGTCAATCCTCTGCTCTGTGAAGG
stSG8150	36	A G	---			ATTGTTCTTGCAATTTGCTTGGATTTTTCAGAATAGTJA/GJATAAATAAAGCGGAATCCTTAGGCAT TCGTGTTTCTATGTTTTAACAGGATTTTCTCTAATGTTTCGCTATTAAATACCATGCAGGAAAT GGGAAAT
stSG8340	30	C T	---			AGAGGATTATGGAGAGAGCTGGCAGGATC/C/JCAACATTATGACCCCTGAACCTCCAGAACTGGAT TCACTAGAAGGAGAGAGAGAAAACGCTCATCAAAA
stSG8466	111	G A	---			TGTGATTGGGTGACTGTAGCCTAAGGATAAATAAATGACAGCAATGTTATAAGCAGTGGGA GGAGTGAACCTGGGAATACCTGGTTACAAGGTAATTTGCACACTACCTJG/AJGGAAGCAGCACAGCATTAT TTGAAAG
ESTD-ACE	--	--	---			GATCAAGCAGTGCACACGGGTACGATGGACCAAGCTCTCCACAGTGCACCATGAGATGGCCATATA CAGTACTACTGCAGTACAAGGATCTGCCCGTCTCCCTGGTGGGGGGCCAAAGCCCGGCTCCATGA GGCCATTGGGGACGTGCTGGCGCTCTGGTCTCCACTCCTGAACATCTGCACAAAATCGGCGTGC
ESTD-ADA	--	--	---			ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAAGAGCCCTCTCCCTGGGATTTGAGTGGGTC CCCAGTCCACCCAGAGCCCTGGGGAATCCAGGGTCACTGTTCTCTCTCTCCCTGTGGGAAAT CAAGCCAGTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGGCCCTCGGCACTGAGCTGCAGACCC GCAGACCAACTCCTGAGCTTCTGGGCCCTGAGTCTTGCTC
ESTD-AK- 168	--	--	---			GGGAGTGACAGCTAGAGCACCAAGGGGGCTCTACAGCTGTGTCTCATGGAGGACAGGCTTCTGCTC ATTCTGG
ESTD-ALB	--	--	---			AATCCAGCACTTTAGGAGGCTGAGGCAGGCATATCACCAGAGTCAAGGATTTGAGACCAGTCTGA CCAACATGGTGAACCCCATCTCTACTATAAAATACAAAATAGCCAGGCATGGTGGTGCATGCCGTG AATCCAGGAGGCTGAGGCAGGAGAAATCGCTTGAACCTGGAGGCGAAGGTTGTGGTGAGCCGAGAT GGCAACATTGCACCTCCAGCCTGGGCAACAAAGAGTAAACTCTGTCTTC
ESTD- ANT1	--	--	---			TCTCTGTCTACTCTACTCCATTAGTTCAAGGTCAAGTGAAGAACTGGGGCAATTAACCAAGTAATCA TGGACTGCCCAACTGCCAAACAAGAGGGCGCAGTGGAGCAGGAGTATTATGCTACGCGGTACCTT TTTTATGGAGGACCGAACTGAGGCTGAGCTCAGATGATCCTGT
ESTD- APOA2	--	--	---			CCAGGTGTTGTGGCACGTGCTGTATCCAGTACTCGGGAGACTGAGGCATGAGAATCTTTTGAAC CGGGAGGCGGAGGTTGCAGTGAGCTGACATCGCCCACTGCACCTCCAGCCTAGGTGACAGAGCAAG ACTCC
ESTD- APB8	--	--	---			GGAAAGAAATGGAGCCTGTGGGAAGGAGCGCTCCGAGGGGTGGGCTTTGTGGCAAGCCCCCTTGCCTGA AGCAGAAGGGCGTGAAGAACCGGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGGGAAACCATCAGTGAA GGAAGCCCATCCCCCAGAAATGAGCTGCTGCATAATAATTGACCCCAAC

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ESTD-C7	--	--	--	--	---	---	---	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-CB22	--	--	--	--	---	---	---	GGCAAGTTTTTATTGATAGAGAGGAATCAAATATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGCAGTGCCAACCCATAGGGCGGATACAAAAGAC AGGCAAGGAAGGGGTGAACCATCAAGAGGAATAGGCTGGTACCCCAAGCAAGGAGGACCTAG TAACATAATTGTCTTCATTATGGTCTTTCCCGGCCTTCTCTCACACAC
ESTD-CB23	--	--	--	--	---	---	---	TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCAATTATGGTCTTTCCCGGCCTTCTCTCACACATACAGAGCCCTACCAGGACCAGACAGCT CTCAGAGCAACCCTAGCCCATACCTCTTCCCTTCCAGAGGACCTGAAAAACGTGTTCCCAACCCGA GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAA
ESTD-CB24	--	--	--	--	---	---	---	ACCAGGACCAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAA AAACGTGTTCCACCCGAGGTGCTGTGTTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAAAG GCCACACTGGTATGCTGGCCACAGGCTTCTACCCCGACACCGTGAGCTGGTGGTGGTGAATGG GAAGGAGGTGCACAGTGGGTGACACAGACCCCGAGCCCTCAAGGAG
ESTD-CB25	--	--	--	--	---	---	---	GTTTTCTTCAGACTGTGGCTTCACTCCGCTAGTGAGTCTCTCTTTCTCTCTATCTTCGCCGTG TCTGCTCTGAAACAGGCGATGGAGATCCACGGACACAGGGCGTGAGGGAGCCAGAGCCACCTG TGCACAGGTACCTACATGCTCTGTTCTTGTCACAGAGCTTACCAGCAAGGGGTCTGCTGCCACC ATCCTCTATGAGATCTGTAGGGAAGGCCACCTTGATGCCGTG
ESTD-CB27	--	--	--	--	---	---	---	TTTTCTGTTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTGTTGGGCTGGTTGCATTTCAAGAGTGTCTGTGGAGTCTGCTCATCACTGACCTATCTCTGA TTAGGGAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTTCTCTCCACCCCAATGCTGCT TTCTCCTGTTTCATCCTGATGGAAGTCTCTCAACACCATTTCCATACC
ESTD-COL2A1c	--	--	--	--	---	---	---	AGAAATGATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTTCCGTGACATTTCAAGGTGGAAAAAGGT GAACAGGTCCTGCTGGTCTCCAGGCTCCAGGTAAGTCAACTCAAGCATATACAATACTGSCCTTG GTCAGCCTATTGAGCTGTAATCACCATAACCGTACCT
ESTD-COL2A1d	--	--	--	--	---	---	---	TGAGAGAACACACCTAGTCTCCATCCTCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGTGGACCTGGAACACTGGACTTCTTCTACTGCAGCAGACAAGACTTACCC AAGAGAGATTAAATGGCAAGATATACAATAACAATTTTATTGACCAAAACACTATCATGGAACAGC ATT
ESTD-CPT2	--	--	--	--	---	---	---	GCCGCAATGCCCGGAGTTTCTCCAATGTGTGGAGAGGCCCTTAGAAGACATGTTTGTATGCTTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGAGATGAAAAGCTACCATCACTCTCTCATCATGAAAAC TGGGAGGCCGGCATAGTGTCTATGCTGTATGCCAGCATTTTGAGAGGCTGAGCGGGTGGATCAC TTGAGGTCAGGAGTTTGAGACCAACCTTGGCCAAACAT

ESTD-CTLA-4	--	--	---	---	---	ATGGCTTGCCTTGGATTTCAGGGGCACAAGGCTCAGCTGAACCTGGCTACCAAGGACCTGGCCCTGCAC TCTCCTGTTTTTCTTCTTCATCCCTGTCTCTGCAAAAGCAATGCAGTGGCCAGCCTGCTGTGGT ACTGGCCAGCAGCCGAGGCATGCCAGCTTGTGTGAGTATGCATCTCCAGGCAAAGCCAC
ESTD-CYP2D6	--	--	---	---	---	CAGGCCAGCGTGGTGAGGTGGTCAACCATCCCGGACAGAACAGGTCAGCCACCCTATGCACAGGT TCTCATCTTGAAGCTGCTCTCAGGGTTCCTTGGCCTGAGCAGGGCCGAGAGCATACTCGG
ESTD-D11S1873	--	--	---	---	---	AAAAAACATTTTAACACCTTTTCAATCATATACACCATAAAATTTCCATTTTTCACATAAGTCAGTT TGAGCTGAGTTTTCCAAATTACTTGCAATCTAAATGTCAATACTGATTAATGCAAGTTCAACAGACA ACTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATATGCCCATAT CTGCATGTC
ESTD-D17S33	--	--	---	---	---	CATCCCCAAGCCCATCCTTAGCCACTGGCATTTTTTGCCGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCCTTACCCCTTTGTAGTCCATGGGAAAGGCTCCTCTGGGGCGGTG GGGTGTGTGGCTATGTGGTGGTCTGTGTAGACGGGGCTTTGGTTTCAGTTGCATTAATGCGTTATT GCAGATTGCTTTGTCTTTCCACCTGAGCGAGCCCTC
ESTD-D18S8	--	--	---	---	---	TTTGAGACCACCTGGCCAACATGGCGAAATCACATCTCTACCCAAAATTACAAAATTAGCTGGGTGT GGTGGTACATGCCTATCGTAATCCAGCTACATCGGGAGGCTGAGCGAGGAATGCTTGAACCCA GGAGGCAGAGCTTGCAGTGAGCCCAAGATCACACCCTGCACCTTACAGCCTGGGTGACACAGTGGAGA CTCTGCTCAA
ESTD-D3S11	--	--	---	---	---	AACTGATTAGAACCCTGAAAAATACATATTTTATCTGAAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAAAATCCAAATAAGTACACTGTAATAAAGAAATTTAACAGAAATATCATTTGT TTATCAAACCTATTATCACCTATTATTTTATGGTAAGCCATACTAAATTTCTAAAGCATGTTTCTGAAAG TTTA
ESTD-D3S12	--	--	---	---	---	AGGTTCCACATTATTGCTGATGTTGCTGATGTTTCCAGGAGCCTTGATGTCATCTGTATCTCCTCAG GTATCCACCTTGAGACGTACTTTTCAAAAACCTCTCTACAGCCGTTGTGTTATTAAATCAAGGTTGA ACATAAAGTA
ESTD-D3S2	--	--	---	---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGTAGCAGAACATTTCTCTGC TGAGCTTATTCAAAACTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGATTCCTCC AGAAGTGAACATACTGCTCCTAGAGCCAGAGTCATACTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGTCTTTATTTGGAAGGATGCCGGTATGT
ESTD-D4S338	--	--	---	---	---	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGGAATCCCTATATATGGCAGGTATATGAAATGTATTT CTTAACAATAAACTTGAAAGTCCAAAATTTACTCCTTGATCCATGGACTGCAGAAATAAATGTTATTT TAGCTGTCAGAAAAACAATACTAACTTTCGCATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGATT GCCAATAAGCAGTAATATTTGAGAGGAATCTTGTTTTCATGCAAGTAG
ESTD-D4S95	--	--	---	---	---	CTTTCATGCACGATAGGCTTTCCTACTAATCACAGAAATTTTGAGAGAGCAAAACAACCTTCAAGG ATAATGGGCAATCACTTCTTTCTCTTTTAGAGTCTACCGG

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ESTD- D7S399	--	--	---	---	---	TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCCTACATCATCTCTTTACAAACATTTTCATCCATGGACTCCATACCTAG AATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DM	--	--	---	---	---	GTGGGACACCGAGGGCTCCAGGCTGGGCGCTTGACGCTGGCTCAAGCAGCTGCTCGGCCTCCACT TCCATGGGTGGGCGCTGGACCTCACTGTCCTGGGAGAGGAGGAGGGAGTGGGAGGGAGACA GAATGCTGATTATCTGGTGGAGAACAGAACTTCTGGCCTGTGGTAGGGGAGCTGCTTCCAAGACC TCCTGATTGAGGAAGGGAGCAGCAGAGCGAAGAGAAGAGT
ESTD- DRD1	--	--	---	---	---	TCCCCAGCCTATCGGTCTATTTGGACTATGACACTGACGCTCTCTCTGGAGAAAGATCCAAACCCATCAC ACAAAACGGTCAGACACCAACCTGAACCTGCAGATGAATCTGTCCACACATGCTCATCCCCAAAAGCT AGAGGAGATTGCTCTGGGGCTCGCTATTAAAGAACTAAGGTAC
ESTD- DRD2	--	--	---	---	---	TCTGCTTTGGTGCAGGAGGCTGCCGGGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGACCGGTACAGCCCCATCCACCCAGCCACCCAGCTGACTCTCCCCGACCCG TCCCACACGGTCTCCACAGCACTCCGACAGCCCCGCCAACCCAGAGAAGATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	--	--	---	---	---	AAGACGATGGCCAGGATGAGCGCGCAGTAGGAGAGGGCATAGTAGGCATGTGGGGGGCGCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTCAAGTGCCACTCAGCTGGCTCAGAGATGCCATA GCCAGAGGGAGGTGCGTGATGCCAAGGGCTTCTCTGTGAGGAGA
ESTD- ERB82	--	--	---	---	---	TCTTCAGGATCCGCATCTGCGCTGTTGGGCATCGCTCCGCTAGGTGTAGCGGCTCCACCAGCTGG GGTAGGGGGTGGTGGTCACTGCGGGGGCGGTGCAGACCCACCGGGCTGGGAGACTTCACCC CGCCTCACCTCCGTTTCTGCAGCAGTCTCCGCATCGTACT
ESTD- ETS2	--	--	---	---	---	ACTCAGAGTGTCTTTAAGTGAAATGGTCGAGAAAGAGCAGCAGAGCCGCTGCTGGCGCTGGCA GTCCGTGGACGGGATGTTCTGGCTGTTTGAGATTTCAAGGAGCGAGCATGTCTGGACACACAC AGACTATTTTAGATTTCTTTTGCCTTTTGCACCCAGGAACAGCAATGCAAAAACCTCTTTGAGAGG GTAGGAGGGTGGGAAGGAACAACCATGTCTATTTTCAAGAGTTAGTTG
ESTD-F2	--	--	---	---	---	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCCCAACTGTGCATGCACGCTTAACCTCT GCACCAATGGCTCCAGGCCCGTAGGGGAACTGGGGGATCTAGGGGATGGGTAGGAATGGCCC AGCCCAGTCCCGGGCGGTGCTGGTCCCAACAGAGGAGGCGCTGGAGGAGACAGGAGATGGGC TGGATGAG
ESTD-F9	--	--	---	---	---	AGATCCTGATGATTTTTCCTATTTTTCCTAAATGTTTACAGTTTGAAGTTTAGATTTATGCCCA TGCTCCATTTGAGTTAATTTGTGTAAGATGATGTTTAAAGTCAAACTTCATTTTTTTTCCATA GGTATGTCCAATTTATCCAGCACAAATTTGTTAAACAAAAAAC

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ESTD- G0DH	--	--	---	---	---	CGCAGACCGGTGCTAGTGGGGTGGGAGTGTGGAGGAAGGAGGAGGAACTGGGGGTTTAGGGACT TTCCGGGGTGACTTTCCCGTTCTGTCTTGCAAGAGAAAGCGGGAGAACACAGAGCCAACTGGCTAA GTGTAAGGGACCTCTGGTGGCACCCTGTCTGCTGCCCTGTTGAGCTGTCTGTCTGCGCAGTGA CTCTGTCCCGAAATCCGAGAGCT
ESTD-GCK	--	--	---	---	---	GTTTTATGCATGGCAGCTCTAATGACAGGATGGTACGCCCTGCTGAGGCCACTCCTGGTCAACATGAC AACACAGGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGATCCCCACCCACACCTGGCTGG AGCAGGAAATGCCGAGCGGCCCTGAGCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTCACC TGCAGCCTAAITTACTCAAAGCTGTCCCCAGGTACAG
ESTD- GNAT2	--	--	---	---	---	GACCCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACCCACAGGCATATTG AAACCAAGTTTCCGTCAAAGACTTGAATTCAGGTAAGTGCATGGTCCCTAGG
ESTD- GPPK2L	--	--	---	---	---	AGTCTCATCTGCGGTGTCAGGTAGATCCCTTTCACCGCCGAGAACTGCTCGATATC
ESTD- HRAS	--	--	---	---	---	CTGGGCTCGCCGACAGCTGTGCACTGTGAGCGGGCGGCGCAGGCTCACTCTATAGTGGGTGG TATTCGTCCACAAAATGCATCTGGATCAGCT
ESTD- HSD3B1	--	--	---	---	---	TTGGAAGTTCTCCACTGTTAACCAGTCTATGTTGGCAATGTGGCTGGCCCCACATCTGGCCCTTG AGGCCCTGCAGGACCCCAAGAGGCCCAAGCATCCGAGGACAGTCTACTATATCTCAGATGACA CGCTCACCAAGCTATGATAACCTTAATTACACCTTGAGCAAGAGTTCGGCCCTCCGGCTTGATTCC AGATGGAGCTTTCCTTATCCCTGATGTATGGATTGGCTTCCTGCTG
ESTD-HT2	--	--	---	---	---	GGGCTAAAATTTCCGAGCACTTTGCATAGACTGTTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGGAGAGGAAGATGTGTACAGTTTGTACAGAGATAAAAGGATAAOCCTGGGGTTTTCTGTGC TTTGCTTCTTCACTCCCTGGGAGTTAATAGCTGCAATTTTCAAGAAGCGTATACAGGGACAGCA AAGCGCAGTCTGTGAAGTTTTCAAAACACACACACCTT
ESTD-HT4	--	--	---	---	---	ACCAACGAGCCGGATACAGACACTCTTAAGTTTGGCCCTAAGGCTCATTCAAATCATTAGGCATTTT CTGATAAACTAGGTCTTGGTGCTTCTATCGGCAAGAATGCGTACTTATTTGAATAGTAGAGGTAA ACCACACGCCCAAGAGTCACTGAGACTGGCAGCTTCTGCAGCAGGCGTGAACCCCCGTAGCCTAAA TGACAGCCGAAGAGGCGCCGAAGACATGCAGATGTGC
ESTD-HT5	--	--	---	---	---	AACACACAAGCCCCAGCGAGAATTGAACCTGCGACCCCTGGTTTACAAAGACCAGTGTCTAACCCCT GAGCTATGGAGCCCTCGTCTGCTGTGGTTTTCTTCTCTTCACTTATAGATTGATGTTATGCTCCTA GCATTCCGGCTACCGAATAGGATGTAGCTTGAGTAAATTCAGGATATTCCTCTACAAAATGAAA ACATTTTCGTGCTGTAAATCCCTCGAAAAGGTTCT
ESTD- IGFBP1	--	--	---	---	---	ACCCAGTGGAGCCCGCTCATTGCACGGTCTTGGCAGGAGGTGCCCTGGGAGAAGAAGAGATGTTTC CAGGGCACACATAGCTTAGTGGAGACTC

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ESTD- IGHV4-6	--	--	--	---	---	TTTACTATTCAATGGATACAGAATTGTGGGAGTCACTATATCCTATGAACAAAAATTCAGATTT CAGTGTTAAGTAATGTTGCTACATTTGTGTGAGTGACGGGAGTGGTGAGTCGAGAGTGGTGGG TGACGGACATAATGATTCAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAATACCTTCACAAAATACTAATAAACGGAGTTGAATATAAACCCCA
ESTD-IL1A	--	--	--	---	---	CAAGTAAGCACCCCAATAATGTTAGCTATTACTATCAATATTATTATTATTATTATTATTG AGATGGAGTCTGGCTCTGTCAACCCAGGCTGGAGTGCAGTGGCACAATCTCGGCTCACTGCAAGCTCTG CCTCCTGGGTTCAATGCCATCTCCTGCCCTCAGCTCCGAGTCCGAGTGGGAATACAGGCCGCCCACT GTTCCCGGCTAATTTTGTATTTTGTAGTAGACGGAGTTCACCGT
ESTD-IL1B	--	--	--	---	---	CCACTACAGATGGATAAATGGGTACAAATGAAGGCCAATAGCCCTCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTGTCTCTGCCCTCAGGAGCTCTCTGTCAATTGCAGG
ESTD- KRT10	--	--	--	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTGAGTGTACCTTTTGGCAATATT AAAGGAAGAAAATGCATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTAIGTAGCTCTTTTAAATAGTCTC TGCCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA
ESTD- KRT8	--	--	--	---	---	ACCTCACCCCTCCCTTAGCCCGTGGGAGCAGGAATCTCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCCCTGACATGAGACCTCAGACAGAATCTTCTAGAGTT TGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCATCTCTCCCGTCTCAGGTTTACCACGTCAACATTTGACACA
ESTD- LF79	--	--	--	---	---	GGGTGATTTGAGGCTCAGTTAATATTTCAAAATTTGAACCGTAGCAAACTGCATTGGTATTAGA AAAAATAAAATTTCCAATATGATGTGCTGTGTATACCTGCTCTGCCATGCAGCATCATAGCCTGT GGGAACACAGGAGGGCTCCCTTACCACCCAGA
ESTD- LMP2	--	--	--	---	---	TACACACTTTCCTTAGCCATTCACTGAAACGCACTCGGAACTGGAGCCTTGTAGGAATGGAGTTGA CCTTCCCCAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	--	--	--	---	---	TGTCAGTGTCCCCTAGGGGCACTCACCACCTCCAGCTTCTCAGCTCTGCGCTGCTGCTGCGCA AGGGTTTGTCTAATTCATCAATTCATCTCTCTCATCTTTAGCAGCTGTGGGTTTTGTGTTGTTTC TTCTGTTTTGCTTAGTATCTGACTACTTTTAAATTATAAAAGAGATGTATCTAAACAAAAATAGAG ATTGTTATCAGAAGTTCACAACATTTTATAAAATTTTTCACCTG
ESTD-MCC	--	--	--	---	---	TTGTCAGGAGTGTGCTGATGCTGCTGCCCTCCAGCTCTGTCCCTAGCCGAATTCAGGACAACGTGCAG CATCCATGTAGGAGAGCCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACACAGCATGCATCCCGGAA TCTCAGGAAGTCTCTGTCTTCCAAGGGTTTGGTCAAGTTGCTGATTACCCGGATTTTCTGACGATC TTTCAACTGCTAGAGCATCTGGTCTCTGTTTTCATG
ESTD-NF1	--	--	--	---	---	ATTATCCAGATGAATTTACAAAACATAACCAGATCCACAGACTGATATGGCTGGT

ESTD- NFB1	--	--	---	---	AAATGGACTTGATATTTGTACAAAAAAGTTTTATTTCTAAAAAAGAAAAAAGAGAAA AAATTTAAGGGTGTACTTATATCCACACTGCACACTGCCTAGCCCAAAACGCTTATTGGTAGG ATCAGCCCTCATTTTGTGCTTTTGTGAACCTTTGTAGGGACGAGAAAGATCATTTGAAATCTGAG AAACTCTTTTAAACCTCACCTTTGTGGGTTTTTGGAGAAGGTTATCA
ESTD- NPPA	--	--	---	---	TGTCCCTAGGCCCCAGCCCTGCTTGTCTCCCTGGCTGTTATCTTCAGTACTGCAAGAGAACACAGAC AT
ESTD- NPAMP	--	--	---	---	GGAGGAGGAGGGGGGGTCTGTCTGCTCCAGGTCACAGACAGAGAGAGGGCCTCAGTG TATCCCCACCCCCAATGTGGGCGCTGGGAGATGAAGAGGAGTTGATGCAGGT
ESTD- NRAS	--	--	---	---	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATATTTCTTTCTGCAGGCATATAGAAATTTGGT GGTTTTCTTTATGTAGGGTGATATGGATACCTTTTGTGTGATTATATATAGCAATTTGAGGG ACAAACAGATAGGCAGAAATGGCTTGAATAGTTAGATGCTTATTTAACCTTGGCAATAGCATTCG ATTCCCTGTGGTTTTTAATAAAAT
ESTD-OTC	--	--	---	---	GTGACCTTCTCACCTTTAAAAAATTTACCGGAGAGAAATTAATATATATGCTATGGCTATCAGCAGA TCTGAAATTTAGGATAAAACAGAAAGGAGGATGTATAACA
ESTD-PAH1	--	--	---	---	GCCACACACCCACCCAGCACACCTCCAACTCAGCCAGCAAGTTGTGACACAAGAGAGGCC TCAGGGGACAGAGAGAGCTGTGACACGTGGGAGTCAAGCTGTATCATCGGAGGGCGCGGCAC ATGGAGGATGAGGGAAGACCAAGAGTCTCTGTTGGGCCAAGTCTTAGACAGACAAAAACCTAG ACAATCACGTGGCTGGCT
ESTD-PAR	--	--	---	---	CTCTTCAGGAACCAACAGCTCTTACCAACACAGACTTATGCTGTCGAGAGGTACAACCCGTAGA ACTTCTCCTAACTGTAATTTAGTTAAAGGAATCGAAACTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTTCATTAGCTCTGTGAGTGTCTTCTTCACITTTCTGTGTTCTAGAACGTTTTCTAG GACTGGCAGTTTAAGCTTTCACCTTAGGCTTTCTGTATACCCCATGCC
ESTD- PBDA	--	--	---	---	CCTTCTCATGCCAGATGGAAATTCAGTCCCTTCAGGATCGCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAAGGGAGGACTAATCCAAATCTCTACCCGAGCTTGTCTGCATACAGACG GACAGTGTGGTGGCAACATTGAAGCCCTCGTACC
ESTD-PS-1	--	--	---	---	GGGGAGTAAACTTGGATTGGGAGATTTCATTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAACACACCATAGCCTATTTCTGAGCCATATTAATTTGGTTGTGCCCTTACATT ATTACTCTTGCCATTTTCAAGAAAGCATTGCCAGCTCTCCAATCTCCATCACCTTTGGGCTTGT CTACTTTGCCACAGATTATCTGTA
ESTD- PXMP1	--	--	---	---	ATGAACATGGTCTTTAATTTATGATATGTTTGTATAGCTATCTTAAAGGGCTCTCTTTTTTTA ATGCAGAAAGAGGGGAAAGAGCGAGCTGTGGTGACAAGGTGTTTTCTCAAGGCTCATACAGA TTCTGAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAAGTCTTATGAAATTAATCTT
ESTD- Per/RDS	--	--	---	---	ACCTACAGACGCTGCTGGATGGTGTGTCACCCAGGAAATCTGAGAGCGAGAGCAGGGCTGGCTG CTGGAGAGAGCGTCCGGAGACCTGGAAGGCT

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ESTD-RDS	--	--	--	---	---	CCCGAGGAATCTGAGAGCGAGAGCGGGCTGGCTGCTGGAGAAAGAGCGTGCCGGAGACCTGGAAGG CCTTTCTGGAGAGTGTGAAGAGCTGGGCAAGGCAACAGGTGAAGCCGAGGGCGCAGACGCGCAGG CCAGGCCCCAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCACCT CCAAGAAACGTGGATCTCCCTCATCCAACTCCGAAAGTCTGAA
ESTD- PVR1	--	--	--	---	---	CTTCGTACGGGAGGTCACGTCTCCGCTCTTTCATGGACATATGGATGAGTGTGACCAATTCC CTGCTGACAGTATGACCGCAGACTTGTCTACTATGAGAGGGAGCTGTGTCACCTCATGCCCGC TCCCTCTGGAGGCTGGAGCCACTGAGAAATCAGCTGGAGTGGAGCCACCTGCGCTGGGGCCAGCCACT CCGAGTCGGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD- SPTB	--	--	--	---	---	TGAACACCTGTGGTCCGGAGCCAGGTTGTCTCTCTGGAGCCTGAGGAGTTGTGTCTGTGTG CAGTCCCGGCGCACCTGTCTGGTTGAGCCTGGACATACACCTTCACTCTTTGGCCGGAGAGAC ATTTACCCACCTGGCCATGTCCCTGGCTGTGTGACACACCTCTGTGAAGACCCCAACCCCTGCCTCC CCCACCAAGCCAGTTTCTAGCAAGGGCAGGAC
ESTD- SSA1	--	--	--	---	---	TTACATTTGTGGATTGTTCTTTTGTGTGTCAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAG TTTGTCTTGGCTGCTGTGTGGGATATTTGAAGAGATCTTTGCCAGTCCATGTCTCTAGAGAG TTTTCCCAATGTTTCTTGAATAGTTTCATAGTTTGAGGCCCTAGATTTAAGTCTTTAATCCATTTTG ATTTGATTTCTGTA
ESTD-TAT	--	--	--	---	---	AAATGGTCAGGACCCCTGATCCACAAGAAGTGGTACCATTTTCATCAGGGCCATCAGTTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTTCATTCATCTTAAATGACTTGTGGACAGGATCA ATTTCTCTCACCTAGAACGTTTGTTTACAACCTTTCTTCCAGTATGGATGGGATATGATGGGGGG GAGAAGCAAAATTTTAAATAGGACCCCATGAGACACATCA
ESTD- THR8	--	--	--	---	---	TGCGGCTTTCTCTCGGCGAGGTAGACTTCTTACTGGCTGTTGATTTCCAAGAGAAAGAGTCCCAAG CACACGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAAATCACAGGATCAGTTTCATCCA CACTGGATTGGCCCAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG
ESTD- TNFA	--	--	--	---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACCTGGTCCCCAAAGAAATGGAGG CAATAGGTTTGGGGGCATGAGGACGGGTTTCAAGCTCCAGGGTCTACACACAAATCAGTCAGTG GCCAGAAAGACCCCTCAGAAATCGGAGCAGGGAGGATGGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGCCCAACTTTCCAAATCCCGCCCGCGGATGG
ESTD-TYR	--	--	--	---	---	TAGTGAAGTTTTCATCTCTGTCAGCTTCTGGAATTTCTTGTCCACCGCAACAAGAGAGTCTATGC CAAGGCAGAAAGCTGTGCTTTCATGGCAAAATCAATGTCTCCAGATTTCCAGATCCCAAGCA GTGCATCCATTGACACATAATAATGTCATCCAGACAAAGAGGTCAATAATATTGATGTCTGTTAAACAT GGGTGTTGATCCATTTTTCATTTGGCCATAGGTCCCTATGGGGATGACA

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ESTD- TYRP1	--	--	---	---	---	AGTAGTGATGAAGCTAACCCAGCCTCTCCTACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACAA AACCCACTGGTTGAATATAATAGATTGAGTTAATCTGATTTCTTTCACTTTATTACCTTCTTTCT AATACAAGCATATGTTAGAATTAAGTTCTAGGCATACCT
ESTD- VB12	--	--	---	---	---	TTCCCAAGCCTCAATACAAGCTTTTTCTTGGGATTACAACATCAGGGTCTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACAAAGGTCACAGACAGGAACACCCAGTG ACTCTGAGATGTCACCCAGACTGAGAACCCACCGTTATATGTACTGGTATCGACAAGACCCGGGGCATG GGCTGAGGCTGATCCATTACTCATAT
ESTD-VWF	--	--	---	---	---	AGGTAGGAAAGCAAGAGTTGATTAGTGAAGGAGAGAAATGGACCTACCTTCCACACTGTCTTTGG TCCCCTAGAGTCTG
ESTD-WT1	--	--	---	---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTTACTCTCTGCCTGCAGGATGTG CGACGTGTGCTGGAGTAGCCCCGACTCTTGACGGTCGGCATCTGAGACCAGTGAGAAACGCCCTT CATGTGTGCTTACCAGGCTGCAA
ESTD- s14544	--	--	---	---	---	TTGGGAAGTTAGAGCCTATATTAAATTACGGAATTACTAAGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGTCCTAGTTCGCTGTGTGGGTTAGATGCAGGATTATATGATCOGTTAACC TCT
EST71770 6	--	--	---	---	---	AGCACCACTCTCACGTCAAGCCTCAGCACCATGCTGTTCTATAAGGATGACGTGCTTTTACAA CATCTCCTCCATGAAGAGCACAGAGATTATTTATCTGAACTCCGGATCTATGACTCAGGGACAT ATAAATGTAAGTGTGATTGTGAACAACAAGAGAAACCCACTGCAGAGTACCAGCTGTTGGTGAAGG AGTGCCCAAGTCCCAGGGTGACACTGGACACAGAAAGAGGCCATCCAAGG
EST32418 6	--	--	---	---	---	CAAAATTACAGGGTCAACTGCTATGATGTGTTTGGAGCCAGTACCCCTTTGGTGGCTACAAGATGTG GGGAGTGGCCGGGAGTTGGCGAGTACGGGCTGCAGGCATACACTAAMGTGAACACTGTGAGTGTGG
EST13586 3	--	--	---	---	---	CCCACCTATTTGCCAGCCCGAGGGACAGAGCTGATCCTTGAACCTTAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCCAGGGCTGGCTTATCAGCTCCAGCCCGACACCCCTGGCTGCAGACAT AAATAGGCOCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAAGGAGGTGCGTCTGCTGCCTGCCCGG GTCACTC
EST51976 7	--	--	---	---	---	AGGCAGAAACTGGGCCCCCATGCGGGGGGACGTGGAAGGCCACTTGAGCTTCTCGGAGAAGGACCTGA GGGACAAGGTCAACTCCTTCTTACAGCACTTCAAGGAGAAAGAGAGCCAGGACAAGACTCTCTCCCT CCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGCAGCAGCAGGAGGTCAGATGCTGGCC CCTTGGAGAGCTGAGCTGCCCCCTGGTGC

EST11458	6	--	--	---	---	CCACITTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCTCCAGTGCTCATCTTGTTCTCGAGTTTTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCCAGCATGATTTACCATTTTCCACAGTGGTCCCATTAAAACATTCTATGAGCCAGGAGAGAGATTACGTATTCCTGCAAGCCGGCTATGTGTCCCGAGGAGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC
EST39852	8	--	--	---	---	CGGTCTCTCCAGGATTGTTGCAGAAGGCCGAGATGACCTCTATGTCCTCAGATGCATTCCTCATAAGGCAITTTCTGAGGTAGTACACCTTCCCACCTCTCTTACGGTACAGAAAGGAGATGCATGAACAGCA
EST62448	0	--	--	---	---	GGAAACACGTGGAAAGGCCCTGTTTCCAGTGTTAAGGCATGCAAAAGGCCCTCCACAGGCTGCTATAATACAGCCCT
EST36027	2	--	--	---	---	ACCTGGTGTGCTGGTGTGCTGGGTGAACCTGGTCTCTTGGCAATGCGGGCCCTCTGGGGCCCGTGGTCTCTGGTGTGGTAGTCTGGAGTCAACGGTGTCTCTAGTGAAGCTGGTGTGATGGCAACCCTGGGAACGATGGTCCCCCAGGTGCGGATGGTCAACCCGGACACAAGGGAGAGCGGGTTACCCCTGGCAATAT
EST12274	0	--	--	---	---	AGTGACTTCCAAGGAAATGGCTACCCAACTTGCCCTTCATGCGCCTGCTGGCCAACTATGCTCTCTCAGACATCACCTTACCCTGCAAGAACAGCATTGCATACATGGATGAGGAGACTGGAACCTGAAAAAGGCTGTCTATTACAGGGCTCTAAATGATGTTGAACTTGTGCTGAGGGCAACAGCAGGTTCACTTACACTGTTCTGTAGATGGTGTCTCTAAAAAGACAAATGAATGGGGAAGACAA
EST76807	3	--	--	---	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTGCTTCCAATAGAGCCTTACCAAAGTGTATACATAAAGAAAGTCAAGTGGTTTACTCTCTCATGACCAATATTCTTCCCTCTTAGGATGAGGTGATAGTAAATGACCCGATGGGTGAGAACTGTCTCTGTCACCATGGAGGATACTATAACTGTGGAAGATAAATTCAAGCCACAGAGCTTGCCAGATC
EST44438	7	--	--	---	---	ATGCTAAGGGGATCGGACATGAAGGACCCTGTGAGCCGATTGTCTATCTCCAGCGGCCCTGTCTATCAGCTACTCATCAATGGGCCAGTCAAGCCAGGCACTGGGCTCCGGAGGACTCAACCCTGCCCCCTGCTGCCATGTGGACTGTGCAAGTTGAGGACTTCTTG
EST12839	3	--	--	---	---	GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGACGCTCTGCTCCGACCTAAGCGGAGCAGCCTCAAGAGCCGAGCGAGGTGG
EST54419	5	--	--	---	---	TGCAAAACACACAAAATCTTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTTGCTCTTAACATCTATGTACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAGATCAAGTCCAAAGGCCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGGAACCTTGAATGTTATTCAACTGGATTCCAGTAGGTTTCAGTTACTTATGAATATATGATACTTAGCTTAG
		--	--	---	---	CTTCTGCCTAAATTTGAATGATAATGTTGTGCTGTGGGACCTGAGCACTTTTATGGCACAAATGATCACTATTTCTTGACCCCTACTTACAATCCTGGGAGATGATTTTGGGTTTAGCGTGGCTATGTTGCTACTATAGTCCAAAGTGAA

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EST10398 2	--	--	--	---	---	TGCTGGGGTGGCAAGGCTGCAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGATGATGTTACATTTGGGGCTTGACTTTCCAAACACGGAGAAG CATTGTTTCTTCGGGCCAAGAGTATCTACCAATAGTGTCTATTAGGCATTG
EST36751 7	--	--	--	---	---	CCAAAGTGTTCAATTTTACGTTTGCAGGTTTAACTCGATTACTTTTCTATTCAATCTCTGTAAAA TTGAAATATGAACCTTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
EST4J562	--	--	--	---	---	CACGTGGAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAACTGTCCTCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAGTTTCACTGGATGCATTAAACAAATATTTTACCTTTTGAAAAATAAATG AAGGATTGACCTGCTTCGCTCGCTGGAAGAGTATCCGTACCGTCTGACGTTTGAACAATACAGAT GCCTTCCCTGTAGCAGTTTTCAGCTCCTCTACCTA
EST18288 3	--	--	--	---	---	GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGTGAGAA GATTGACAGGTTTCATGACGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGACGGGAGCCAGTGTGG ACAGCACCTTGGCTTTCAACACCTAGCTCCACTTCCAAGTAAGGCAACCTCTCTGCTGGCTCTGGC CCTAGGACTTAGTATCC
EST70523 3	--	--	--	---	---	TTCCGGCAGCCCCCATCTTGGACCTTGGTCCCTCAGGGGCCACCCGGGCACTCACCGCTCT CGCTCTGGTAACATCCGGGGGGCGCTCTTGAGCACATAGCTGGACCGTTTCCGTATAGGAGG ACCGTGTAGGCTTCTGTCGGGGCTTGGCAGGGGCGAGCTGCAGAGAGAGGGGTCCTGTGGT TGAGCTGAACACAGCTGTGGAGTGTCTCCACGTG
EST58707 7	--	--	--	---	---	CAGTGTATCTGGAAGCCTACAGGACACCAAAATAACCTTAAATCATCAATTGTTACAGGAGGCTTT AAGTTCAGCATCTTTGGCTCAGATGAAGGCCAAATCCGAGAGACCCCTAGAAGATACACGAGACCGA ATGTATCAATGGACATTCAGCAGGAACTTCAACGATACCTGTCTGTGAGGCCAGGTTTATAGCA CACTTGTACCTACATTTCTGATTGGTGGACTCTTGTGCTAAGAACCTT
EST74167 6	--	--	--	---	---	AGACCATGAAGGAGTTGAAGGCTACAAATCGAACTGGAGGAACAACCTGACCCCGTGGCGGAGG AGACGGGGACGGCTGTCCAAGGAGCTGCAGCGGCGCAGCCCGGCTGGGGCGGACATGGAGGA CGTGGCGGGCGCTGTGTCAGTACCGGGCGAGGTGACGGCCATGCTCGGCGAGAGCAACGAGGAGC TGCGGGTGGGCTCGCTCCACCTGCGCAAGCTGCGTAAGCGGCTCCTC
EST43211 8	--	--	--	---	---	CGCTGGTGCAGTACCGGGGAGGTGCAGGCCATGCTCGGCCAGACACCGAGGAGCTGCGGGTGGG CCTCGCTCCACCTCGGCAAGCTGCGTAAGCGGCTCTCCGGGATGCCGATGACCTGCAGAAAGGCGC TGGCAGTGTACAGGCGGGCGGAGGGCGGAGGCGGCTCAGGCGCATGCGGAGCGGCTG GGGCGCTGTGGAACAGGGCGGCTGGGGCGGCGGCTGTTGGGCTC
EST36770 4	--	--	--	---	---	TGTAGCCAAAGTCACCTGCATCATCTTTGGCTGCTGGCAGGCTTGGCCAGTTTGCAGCTATAATCC ATCGAAATGTATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTTCATTATGAGTCCCAAAAT TCAACCTCCCGATAGGCTGGGCTTGACCAAAATATAGTGGTTTCTGTTTCTTCTGATCAT TCTTACAAGTTATACTCTTATTGGAAGGCCCTAAAGAAGGCTTATG

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EST26021 1	--	--	---	---	---	TAATGTAAAGCTCATCCACCAAGAAGCCTGCACCATGTTTGAGGTGAGTGACATGTTGGAACCTGT CCATAAAGTAATTTGTGAAAGAGGAGCAAGAGAACATTCCTCTGCAGCACTTCACATACCAATGA GCATTAGCTACTTTTCAGAAATGAAGGAGAAATGCAATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTCTTCTTTTGAACAAGACAAAGCAAAGCC
EST51212 0	--	--	---	---	---	ATCCTGAGCTCGCCAATAAGCTTCTTGTTCTACTCTCTCTCCACAAGCCCCAAATTTCACTTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCTTTGTGCTCCCACTCAATACAAAAGGCCCTCTCT ACATCT
EST20118 2	--	--	---	---	---	GTTCGAATCTCTCTCTGAAAGTGCCGGGTTTAAATCTGCTCATGACGCTGCGGCTGTGGTCCAGCT GAGGTGAGGGCCCTTGAAGCTGGAGTGGGGTTTAGGGACCGGGTCTCTGCGTGCATCCTAAGCTCT GAGAGCAACCTCTCTTGAAGCTGGAGTGGGGTTTAGGGACCGGGTCTCTGCGTGCATCCTAAGCT CTGAGA
EST53018 6	--	--	---	---	---	ACAATCCAGGTCAACATTCAGAAAGAGGAGGGGTGGTGCAGTGAGCCTGGGTAGGTCCAGTAATCCA AGGATTCAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC
EST68787 5	--	--	---	---	---	CTTCTATGGGATTGACTTTATTTCTCCATTGTCTTACCCTTTACAGGTGTTAATATAGTGAAAAG GAAGCTTGAGCTCATGACAAATTTGAAGCTGACAAATACACAAGAAGGAAATAAATTCACAGTCAA AGAATCAAGCACTTTTCGAAACATTGAAGTTGTTTGAACCTGGTGTACACCTTTAATTACAACCTAG CAGACGGAACCTGAACCTCAGGGTAAGAAT
EST34088 2	--	--	---	---	---	GTGGGGCAACAGTGGGAGAGAGGGGCCAGGGTATAAAGGGGGCCACAAAGAGAACCGGCTCAAGG ATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCTCTGTGGACAGCTCACCTAGCTGCAATGGCTACA GGTAAG
EST37382 5	--	--	---	---	---	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCCACCCCTCTTCTCTCCCTTGGA CTTTGAGTCAAAATGGCCTGGACTTGAGTCCCTGAACCAAGCAAGAGAAAGAGGACCCAGAAAT CACAGGTGGGCACGTGCGTCTACCGCCATCTCCCTCTCACGGGAATTTTCAGGGTAAACT
EST74082 --	--	--	---	---	---	TCCAGGGTGGCTGGACCCAGGCCCAAGCTCTGCAGCAGGAGGACGCTGGCTGGCTCGTGAAGCATG TGGGGTGAGCCAGGGGGCCCAAGGCAGGGCACCTGGCTTCAGCCTGCCTCAGCCCTGCCTGTCAC CCAGATCACTGTCTTCTGCCATGGCCCTGTGGATGCGCCTCTGCCCCCTGCTGGCGCTGCTGGCCCTC TGGGACCTGACCCAGCCGAGCCCTTTGTGAACCAACACCTGTGGC
EST45311 0	--	--	---	---	---	GGCCTCCTCTCTCCAATTCGTCCCTATAGTTTCTCTATTAAAGTGAACATCATGCTCTTTTAGT GGATAGATGCACACAAACACAAAGCCATTATGGGAAGGATCCACGTGTGTGGCCATATTGTAACA CATTTTCTGCAAAATCACCTCTTTTCATTTAACAGCCCTATTCAATGGCCCTTTTCTTTTTCAGTAGTA CATACACATCTGTGTCAATTTGTTGAAT

EST65258 8	--	--	---	---		TGCCCCATCAGCGGCCGAGACATGGCTTGCCACAGCTCTTGAGGATGTACCAATTAAACCAGAAAT CCAGTTATTTCCACCCTCAAAATGACAGCCATGGCCGGCGGGTCTCTGGGGCTCGTCGGGGGG ACAGCTCCACTCTGACTGGCACAGCTTTGTCATGGAGACTTGAGGAGGGAGGCTTGAGGTTGGTGAG GTTAGGTGGTGTTTCTGTCGCAAGTCAGGACATCAGTCTGATTAAA
EST38216 3	--	--	---	---		ATGCAGGATGAAGGTGGACAGGGAGGAGAGGGCCAACTGTATCCAGGGCTGCAGATGTCGCTG GACTATGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782	--	--	---	---		ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATTATTAGCAATTTGTTTAGCATTACCTAA TTTTTTCTCTGCTCCATGCAGACTGTAGCTTTTACCTTAAATGCTTATTTTAAATGACAGTGGAAAG TTTTTTTTCTCGAAGTGCAGTATCCCAAGAGTTTTGGTTTTTGAAGTGAATGCCTGTGAAAAA GAACTGAATACCTAAGATTCTGCTTGGGGTTTTTGGTGCATGCA
EST35879 9	--	--	---	---		GAGATCGGTGTGTGAGTATTAGGCATGGTTACCTGTGATTCTCCCAATCTTGTGCGTTCACCGCATG GAACTGCCGGCAATCTGACACGTGTGCCACCGCTGTACCCAGGCTGTACCCAATTAGGTGAACATGGCTTCGAG AGAGTTGAACAGATTCTCTGGAAGACAGCAGCGGGATGGGGCAGGAGAGCTGCCTGGATGAA
EST68308 5	--	--	---	---		GGAAAGAGATTAAAGAGCTTGATTTGGACAATCTCGGTTCTTTGAGTGTGGAAGAGTTCATGCTCT GCCTGAGTTACACAGAACTCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAATGGA GAAGTAGACTTTAAAGGTAAAGAAAGTAGTATTTTTTA
EST54045 6	--	--	---	---		GGAATATTAAAAATATTTTAAAAATACCTCCATTTTGTCTATCTCTTTAGTGAAGATGATACCTGCAA AAGCATGGCTAAAGTTATGATTGTCATGTTGGCAATTTGTTTCTTACAAAATCGGATGGGAAATCT GTTAAGTAAGTACTGTTTGGCTTGAATGGATTTTAAATGTGACTTTATCAT
EST52908 0	--	--	---	---		ATCACAGGCTCTGGTCTCTGGCCATCATTTCTCTGGGAGAGATGGATGGTGTGCAAGCCCTTTGG CAATGTGAGATTTGATG
EST19590	--	--	---	---		AGGAGAAGCTGAGGAGGGGAAGAGAGACAAAGNATGACATTGATGAGTGAAGATGTCGGCTCAGGAT GCCGGAAATGAC
EST76136	--	--	---	---		TGAAGCTTCTGCCAGCTTGCAATGTTTCTAGGAGAACCCGCGTCATACCTTTATCTATAGCCTTCGCC TAGGTCCT
EST58607 0	--	--	---	---		CTCTGGATGGGTTACAGGTGGCAGGCACAAAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCCTCACTGGAGAACAAAGGACAGCCACATGGCGGGGATGGCCGGGGAGTCTGGT TGCGGCCACGGCTGTGGCTCTGTTGTGAACGGTAGCCTTTGCGGTTGCGATGCCTAAACCTTTGTTTCT TGCCCAAGGAGGGGGGTGCCATGCTGAGATGTAGATGCGGCC
Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer 6=SNP Reverse Primer 7=Sequence						

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EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that

5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the

10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,
or a portion thereof which includes a polymorphic site,
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is
biallelic.
8. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is the reference base
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is an alternative form
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a
20 segment of a fragment shown in the Table, column 7 or
its complement.
11. The allele-specific oligonucleotide of claim 10 that is
a probe.

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12. The allele-specific oligonucleotide of claim 10,
wherein a central position of the probe aligns with the
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is
5 a primer.
14. The allele-specific oligonucleotide of claim 13,
wherein the 3' end of the primer aligns with the
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which
10 is selected from the group consisting of the nucleotide
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which
is selected from the group consisting of the nucleotide
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the
Table, column 7 or the complement thereof, wherein the
polymorphic site within the sequence or complement is
occupied by a base other than the reference base shown
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising
obtaining the nucleic acid from an individual; and
determining a base occupying any one of the polymorphic
sites shown in the Table.
19. The method of claim 18, wherein the determining
25 comprises determining a set of bases occupying a set of
the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method
5 further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12Q 1/68, C12N 15/11	A3	(11) International Publication Number: WO 98/20165 (43) International Publication Date: 14 May 1998 (14.05.98)
(21) International Application Number: PCT/US97/20313 (22) International Filing Date: 5 November 1997 (05.11.97) (30) Priority Data: 60/030,455 6 November 1996 (06.11.96) US (71) Applicant (for all designated States except US): WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH [US/US]; Nine Cambridge Center, Cambridge, MA 02142 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): LANDER, Eric, S. [US/US]; 151 Bishop Allen Drive, Cambridge, MA 02138 (US). WANG, David [CN/US]; Apartment 314, 276 Mass- achusetts Avenue, Arlington, MA 02173 (US). HUDSON, Thomas [CA/US]; 361 Metcalfe Avenue, Westmount, Quebec H3Z 2J2 (CA). (74) Agents: GRANAHAN, Patricia et al.; Hamilton, Brook, Smith & Reynolds, Two Militia Drive, Lexington, MA 02173 (US).	(81) Designated States: JP, US, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims</i> <i>and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 12 November 1998 (12.11.98)	
(54) Title: BIALLELIC MARKERS (57) Abstract The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.		

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EE	Estonia						

INTERNATIONAL SEARCH REPORT

International Application No

P S 97/20313

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12Q1/68 C12N15/11

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12Q C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 95 12607 A (MOLECULAR TOOL INC) 11 May 1995 see the whole document ---	1-20
X	WANG D ET AL: "TOWARD A THIRD GENERATION GENETIC MAP OF THE HUMAN GENOME BASED ON BI-ALLELIC POLYMORPHISMS" AMERICAN JOURNAL OF HUMAN GENETICS, vol. 59, no. 4, October 1996, page A03 XP002050641 see abstract --- -/--	1-20

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents:

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- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *Z* document member of the same patent family

Date of the actual completion of the international search

17 June 1998

Date of mailing of the international search report

23. 09. 1998

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Authorized officer

Knehr, M

INTERNATIONAL SEARCH REPORT

International Application No

PC

97/20313

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMBL10 embl Accession number: hst27766, 12 January 1995 ADAMS M D ET AL.: "Initial assessment of human gene diversity and expression patterns based upon 52 million basepairs of cDNA sequence" XP002067789 * Sequence *</p>	1-3,10, 11
X	<p>SYVANEN A -CH ET AL: "IDENTIFICATION OF INDIVIDUALS BY ANALYSIS OF BIALLELIC DNA MARKERS, USING PCR AND SOLID-PHASE MINISEQUENCING" AMERICAN JOURNAL OF HUMAN GENETICS, vol. 52, no. 1, January 1993, pages 46-59, XP002050638 see abstract see page 47, column 1, paragraph 3 - page 50, column 1, paragraph 1 see page 51, column 1, paragraph 3; figure 1; table 1</p>	1-3, 7-10,13, 14,17-20
X	<p>FR 2 722 295 A (ROUSSY INST GUSTAVE) 12 January 1996 see abstract see page 1, line 5 - page 2, line 17 see page 9, line 9 - page 10, line 15; tables 2,3</p>	1-3,7-9, 17-20
X	<p>HRUBAN R H ET AL: "K-RAS ONCOGENE ACTIVATION IN ADENOCARCINOMA OF THE HUMAN PANCREAS A STUDY OF 82 CARCINOMAS USING A COMBINATION OF MUTANT-ENRICHED POLYMERASE CHAIN REACTION ANALYSIS AND ALLELE-SPECIFIC OLIGONUCLEOTIDE HYBRIDIZATION" AMERICAN JOURNAL OF PATHOLOGY, vol. 143, no. 2, 1 August 1993, pages 545-554, XP000572114 see the whole document</p>	10-16, 18-20
X	<p>GROMPE M: "THE RAPID DETECTION OF UNKNOWN MUTATIONS IN NUCLEIC ACIDS" NATURE GENETICS, vol. 5, no. 2, October 1993, pages 111-117, XP000615290 see the whole document</p>	18-20

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INTERNATIONAL SEARCH REPORT

International Application No
US 97/20313

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>NIKIFOROV T T ET AL: "GENETIC BIT ANALYSIS: A SOLID PHASE METHOD FOR TYPING SINGLE NUCLEOTIDE POLYMORPHISMS" NUCLEIC ACIDS RESEARCH, vol. 22, no. 20, October 1994, pages 4167-4175, XP002015765 see the whole document</p> <p>-----</p>	18-20

INTERNATIONAL SEARCH REPORT

I. International application No.
PCT/US 97/20313

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-20 (partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: 1-20 (partially)

INVENTION 1: An isolated nucleic acid segment including a polymorphic site having the nucleotide sequence of SEQ ID NO:1149, or the complement of that segment or portions thereof, an allele-specific oligonucleotide probe or primer hybridizing to such a segment or its complement, and a method of analyzing such a nucleic acid by determining the bases occupying the polymorphic site(s).

2. Claims: 1-20 (partially)

INVENTION 2 to INVENTION 2669:

-Idem as invention 1 but limited to the sequences having SEQ ID Nos. 1150 to 3817. (Invention 2 is limited to SEQ ID NO:1150, invention 3 is limited to SEQ ID NO:1151, ..., invention 2269 is limited to SEQ ID NO:3817).

For the sake of conciseness, the first group is explicitly defined, the other groups are defined by analogy hereto.

INTERNATIONAL SEARCH REPORT

..or.. in patent family members

International Application No

F S 97/20313

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9512607 A	11-05-95	AU 8132194 A	23-05-95
		CA 2175695 A	11-05-95
		EP 0726905 A	21-08-96
		US 5762876 A	09-06-98

FR 2722295 A	12-01-96	NONE	
